

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Anish Gupta

Art Unit: 1654

Location: REM/3C15/3C18 Serial Number: 10/083768

Friday, September 02, 2005

From: Beverly Shears

Location: Biotech-Chem Library

REM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

Searon Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.



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OSTO ACCESS DB # 144518
PLEASE PRINT CLEARLY

Scientific and Technical Information Center

SEARCH REQUEST FORM

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Requester's Full Name: Auch Course Examiner # : 13121 Date: 8/31/05 Art Unit: 1654 Phone Number: 2-0965 Serial Number: 10/093,718 Location (Bldg/Room#): Results Format Preferred (circle): QAPER) DISK	
To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:	
Title of Invention: Paphde & Compands that but to a Geespher	
Inventors (please provide full names): William Dower, Ronal Barrett, Stern Civilera,	
David Duffin, Christian Gates, Send Haselden, Lang Madealcis, Peter Schatz	
Earliest Priority Date: 6/7/96 Christopter hayshm, Nicholars Wri	فعنح
Search Topic: Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.	e
For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.	8
Ej Please Search Seay Id No. 6-13 7 / 19	
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an ICSO of no more than about 100 mum. compound (especially if modified, see features table) can be used for
                                                                                               Thrombopoietin receptor-binding/activating peptide(s) and pep mimetic(s) - useful in treatment of haematological disorders, thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                      Claim 18; Page 89; 106pp; English
                                                                                                                                                         WPI; 1997-051883/05.
                                                                                                                                                                                    Mattheakis LC,
                                                                                                                                                                                                    Dower WJ
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LC, Schatz PJ,
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51.4
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95US-00473604.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Preferably C-terminus is -C(0)R2 where R2 is selected from hydroxy, lower alkoxy, and -NR3R4, where R3 and R4 are independently selected from hydrogen and lower alkyl, and where the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide forming a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)]
; -NHC(O)NH; where R is hydrogen or lower alkyl and R6
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CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6
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                                                                                          The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a Ta binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia
                                                                                                                                                                                                          Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haematological disorder; thrombocytopaenia; radiation therapy; bone marrow transfusion; signal transduction; receptor activation; ce
                                        resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor; binding peptide; treatment; agonist;
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95US-00485301.
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                                                                                                                                                                                                                                                                                             Schatz
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Matches Query Match Best Local &

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                                                                                                                                                                                                                                                                                                                The present invention describes composition of matter (I) comprising an CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each (I) c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(I)c-P1-(
                                                                                                                                                             Query Match
Best Local (
                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter active peptides, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-350702/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; Page 220; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024782-A2
                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      μ
                                                                                                                                 18;
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                                                                                                                                                                 Similarity
                               GGCADGPTLREWISFCGG
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GGCADGPTLREWISFCGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical.
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                                                                                                                                 Conservative
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99US-00428082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US025044
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                                                                                                                                                                 Score 109; DB 3;
Pred. No. 4.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain and pharmacologically and autoimmune diseases.
                                                                                                                                     0,
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                                                                                                                                                                                                Length
                                                                                                                                     Indels
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                                                                                                                                     Gaps
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1 GGCADGPTLREWISFCGG

Best Loc Matches Query Match

Local

l Similarity

100.0%; larity 100.0%; Conservative 0

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Score 109; DB 4; Pred. No. 4.6e-09; Mismatches 0;

Length 18; Indels

0

Gaps

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RESULT 4
AAU25820
ID AAU2
  Sequences AAUZ5815-AAUZ6049 represent peptides and peptide mimetics that CC bind to and activate the human thrombopoietin receptors (TPO-R). Methods CC of activating thrombopoietin receptors in cells comprise contacting the CC ells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such CC as that due to chemotherapy, radiation, therapy or bone-marrow CC transplantation and to prevent thrombocytopenia in patients at risk. The CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC in purified or natural biological fluids, in tissue homogenates, and CC in purified or natural biological materials. They may also be used for in CC in staining, fluorescence-activated cell sorting, Western blotting and CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed CC progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELLSA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
15-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human thrombopoietin receptor (TPO-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-2001
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Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 65-66; 128pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting with peptides and peptide mimetics attached to hydrophilic polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-564142/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dower WJ, Barrett RW, Cwirla S
Balasubramanian P, Wagstrom CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROUP LID
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95US-00485301.
96WO-US009623.
96US-00699027.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schatz PJ;
Deprince R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymers.
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GGCADGPTLREWISFCGG

Gaps

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TPO mimetic peptide SEQ ID NO:76
                                                                                                           Claim 39; Page 44; 176pp; English.
                                                                                                                   diabetic
                                                                                                                                     WPI; 2002-130313/17.
                                                                                                                                                               03-MAY-2000; 2000US-00563286
                                                                                                                                                                       02-MAY-2001; 2001WO-US014310.
                                                                                                                                                                                                                                                                              05-APR-2002
                                                                                                                                                                                                                                                                                               ABB72906 standard; peptide; 18
        exemplification of the present invention
                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                08-NOV-2001
                                                                                                                                                                                         WO200183525-A2
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                             Fanconi's syndrome.
                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                              Cheetham JC,
                                                                                                                                              Boone TC,
                                                                                                                                             Gudas JM;
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The present invention describes a vehicle-peptide molecule (I) or its complitimers (I) can have antiinflammatory, antitumour, immunosuppressive, cc cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological, antianaemic, anorectic, antiinfertility, haemostatic, dermatological and consurprotective activities. (I) can be used as a therapeutic or cc prophylactic agent as well as for screening purposes. (I) is useful for cdiagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, crimentation arthritis, diabetic retinopathy, obesity, sleep disorders, cinfertility, and neurological degenerative diseases. (I), comprising EPO-cc mimetic compounds are useful for treating disorders characterised by low cred blood cell levels such as anaemia. The TPO-mimetic comprising EPO-cc megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet cc deficiency, such as thrombocytopaenia, spatemic lupus erythematosus, cand Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 cc exemptification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TMP; TNF-alpha inhibitor; interleukin 1 antagonist; II-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antitheumatic; antiarthritic; antidiabetic; ophthalmological; antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retinopathy, obesity, sleep disorders and infertility.
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                                                                                                                                            portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one ligand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is a TPO mimetic peptide sequence used to make a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches 18
                                 Matches
                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding regionseful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mimetic; CDR mimetibody; gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ73058 standard; peptide; 18
                                                                                                    Sequence 18
                                                                                                                                  peptide sequence is a mimetibody of the inve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2002; 2002US-0368791P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO mimetic peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to novel mammalian CDR mimetibodies, specific
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 512; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-804237/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heavner GA, Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-2003; 2003WO-US009139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                 18;
1 GGCADGPTLREWISFCGG 18
                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCADGPTLREWISFCGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCADGPTLREWISFCGG 18
                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                 100.0%; Score 109; DB 7; 100.0%; Pred. No. 4.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scallon BJ, Ghrayeb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SeqID 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 109; DB 5;
Pred. No. 4.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                    which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, noutropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases (for example multiple sclerosis, conditions, or infectious diseases (for example bacterial, viral or fungal infection. The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovasculor neurodegenerative disease or disorder, anemia, cancer, or infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-2003; 2003WO-US020347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis; dementia; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH1 deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-082870/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004002417-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral infection;
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 512; 129pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancerous condition; infectious disease; bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fungicide; gene therapy; immune disorder; cardiovascular di
arrhythmia; hypertension; heart failure; neurodegenerative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ypotensive; neuroprotective; nootropic; antibacterial; virucide
                                _
                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                    Similarity
                                                                                                                                      18
                                GGCADGETLREWISECGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mimetibody-related peptide SeqID512
                                                                  100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                      Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ghrayeb
 18
                                                                  0
                                                                                  Score 109; DB 8;
Pred. No. 4.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scallon BJ,
                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nesspor
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiovascular, or infectious
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                                                                    Gaps
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ADJ51654
ADJ XX
ADJ XXX
ADJ XXX
ADJ DT 06-1
ADJ DT XXX
CH1
XX
CH1
XXX

                                                                                                which encode them), compositions, methods and uses. The invention may be competed to the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, cen, composition, muscular-Gen, cytostatic, cardinal-Gen, gynaecological-Gen, hepatotropic, haemostatic, cardinal-Gen, auditory, endocrine-Gen, cytostatic, cardinal-Gen, cytostatic, gastrointer, file methods and compositions of the cytostatic particular, dental or conditions associated with aberrant expression cor activity of the CH1 deleted mimethody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, cardiovascular, dental or oral, dermatological, ear, nose or throat, conditions, musculoskeletal, oncological, musculosic, infectious, musculoskeletal, oncological, musculosic, infectious, musculoskeletal, oncological, neurological, nutritional, ophthalmologic, cediatric, psychiatric, renal or pulmonary disorders. The present correct sequence is that of a peptide which may be used during the creation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; troat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; musculosteletal disorder; oncological disorder; neurological disorder; nutritional disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavner GA, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUN-2002; 2002US-0392431P.
19-SEP-2002; 2002US-0412144P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2003; 2003WO-US020495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-082872/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to CH1 deleted mimetibodies (and the DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 512; 123pp; English.
                                                                          of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mimetibody-related peptide SeqID512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ghrayeb J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder.
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Sequence 18

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Length 18;

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AAW AAW09458

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haematology; thrombocytopenia; TPO; TR; proliferation; bone marrow transfusion; chemotherapy; radiation therapy.
                                                                                                                                            Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
07-JUN-1995;
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                                                                       Claim 18; Page 89; 106pp; English
                                                                                                                       thrombocytopenia resulting
                                                                                                                                                                                                                        WPI; 1997-051883/05
                                                                                                                                                                                                                                                                         Mattheakis
                                                                                                                                                                                                                                                                                                Dower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin receptor binding compound peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO
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                                                                                                                                                                                                                                                                    Barrett RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                GROUP LID.
                                                                                                                                                                                                                                                                                                                                                                                         95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US008998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Preferably C-terminus is -C(0)R2 where R2 is selected from hydroxy, lower alkoxy, and -NR3R4, when selected from hydroxy, lower alkoxy, and the selected from hydrogen and halkyl, and where the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide forming a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Preferably linkages are selected from: -
CH2OC(0)NR-; phosphonate; -CH2S(0)2NR-; -CH2NR-; -C(0)NR6
; -NHC(0)NH; where R is hydrogen or lower alkyl and R6 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Preferably N-terminus is selected from: -NRR1;
NRC(0)R; -NRC(0)OR; -NRS(0)2R; -NHC(0)NHR; succinimide;
benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alkyl"
                                                                                                                                                                                                                                                                         PJ,
                                                                                                                                                                                                                                                                                                  Cwirla SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0%;
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                                                                                                                                                                                                                                                                      Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 4.6e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
                                                                                                                       chemotherapy, etc.
                                                                                                                                                                                                                                                                    Duffin DJ, Gates CM, m CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrogen and lower
the -NR3R4 group
he N-terminus of
                                                                                                                                                                                                                                                                                                  Johnson
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                                                                                                                                                                                                                                                                                                  ss;
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The present receptor (TH

ent sequence is (TR). It has a

a compound which molecular weight

binds to thrombopoietin (TPO) of < 8000 Da, and a binding

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RESULT 10
AAW33025
ID AAW33
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Matches
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        affinity to TR as expressed by an IC50 of no more than about 100 mum. compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bor marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                     or to
                                                                                                                                                                                                                                                     Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW33025 standard;
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                                          Sequence
                                                                                                                                                                                                                            Claim
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Mattheakis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal transduction;
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                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCADGPTLREWISFCGG
                                                                                                                                                                                                                            Page 89; 106pp; English.
                                                                                                                                                                                                                                                                                                                                         Barret
LC, Sc
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95US-00485301.
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Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide; 19
 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
                                                                                                                                                                                                                                                                                                                                       Cwirla SE, Du
PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding peptide.
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 Score
Pred.
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 109; DB 2;
No. 4.8e-09;
                                                                                                                                                                                                                                                                                                                                            DJ, Gates
Wrighton N
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              Length
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Best Local Similarity

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AAU2258222
ID 26222
ID 26222
ID 26222
XX AAU22
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XX Pept:
KW haemw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                 transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological fluids, in tissue homogenates, and situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (BLISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; RIISA; bone marrow transplantation; heamotherapy and disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                       of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises con with peptides and peptide mimetics attached to hydrophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 67-68; 128pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Balasubramanian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU25815-AAU26049 represent peptides and peptide mimetics that nd activate the human thrombopoietin receptor (TPO-R). Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrett RW,
anian P, Wag
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96WO-US009623.
96US-00699027.
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Hendren
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Sequence

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RESULT 12
AAW09466
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Best Local (
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptimay also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting
                                                                                                                                                                                   Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-1997
                                                                                                                                                                 Claim 30; Page 91; 106pp; English.
                                                                                                                                                                                                                          WPI;
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                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone
                                                                                                                                                                                                                                                                        (GLAX ) GLAXO GROUP LTD
                                                                                          receptors on
                                                                                                                                                                                                                           1997-051883/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marrow
                                    14;
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                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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CADGPTLREWISFC
        CADGPTLREWISFC
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LC, Schatz
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                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transfusion;
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95US-00478128.
95US-00484090.
95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor binding
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                                                                                                                                                                                                                                                                                                                                                                                                              /note= "In amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                          living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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                                            78.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   penia; TPO; TR; proliferation; cyclic;
chemotherapy; radiation therapy.
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                                             Score Fred.
                                                                                                                                                                                                                                            Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compound
                                     Mismatches
                                             . 85;
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om CR, W
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                                              1.3e-05;
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                                                      Length 14;
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ton NC;
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RESULT 13
AAW09462
      07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mum. The compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                      Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
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07-JUN-1995;
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                                                                                                                                                                    Claim 18; Page 89; 106pp; English
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                                                                                                                                                                                                                                                                                                                                                          (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                         Barrett RW, Cwirla SE, I
LC, Schatz PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transfusion; chemotherapy; radiation therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombocytopenia; TPO; TR; proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Preferably N-terminus is selected from: -NRR1; NRC(O)R; -NRC(O)OR; -NRS(O)ZR; -NRC(O)NIR; succinimide; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl lower alkoxy, chloro, bromo; where R and R1 are alkyl lower alkoxy, chloro, bromo; where R and R1 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Preferably linkages are selected from: -
CH2OC(0)NR-; phosphonate; -CH2S(0)2NR-; -CH2NR-; -C(0)NR6
; -NHC(0)NH; where R is hydrogen or lower alkyl and R6 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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RESULT 14
AAW09465
ID AAW09
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Matches 14
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                        chemotherapy, radiation therapy or bone marrow transfusions. The peptimay also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
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bone marrow transfusion; chemotherapy; radiation therapy
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                                                                                                       Local
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                        CADGPTLREWISFC 16
CADGPTLREWISFC
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LC, Schatz
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                                                                                 Conservative
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95US-00476168.
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95US-00485301.
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100.0%;
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                                                                                 Score 85; DB; Pred. No. 1.3
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Pred. No.
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                                                                                                       DB 2; Lo
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Wrighton NC;
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-051883/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dower WJ, Barrett RW, Mattheakis LC, Schatz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haematology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombocytopenia resulting from chemotherapy,
Thrombopoietin receptor; binding peptide; treatment; agonist;
                                                    Thrombopoietin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                    11-MAR-1998
                                                                                                                                                                                                      AAW33031 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptors on living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                  μ.
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                                                                                                                                                                                                                                                                                                                                     CADGPTLREWISFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 26; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombocytopenia; TPO; TR; proliferation; transfusion; chemotherapy; radiation therapy.
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                                                                                                       (first entry)
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95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.0%;
100.0%;
                                                  binding peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85; Pred. No.
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n CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3e-05;
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RESULT 17
AAW36633
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                           Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                          Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 30; Page 91; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dower WJ, Barret RW, Cwirla SE, Du
Mattheakis LC, Schatz PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
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                        WO9640750-A1
                                               Synthetic
                                                                         signal transduction;
                                                                                                                                                                    11-MAR-1998
                                                                                                                                                                                              AAW36633;
                                                                                                                                                                                                                     AAW36633 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                           14;
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                                                                                                                                                                    (first entry)
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                                                                                                                                          receptor binding peptide.
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95US-00485301.
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1. .14
                                                                                                                                                                                                                                                                                                                                                       78.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                         Score 85;
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rom CR,
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                                                                                                                                                                                                                                                                                                                                                         1.3e-05;
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Wrighton
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19-DEC-1996

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RESULT 18
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
07-JUN-1995;
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Peptides
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1998
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                                                 WPI; 1997-052226/05
                                                                                                  Mattheakis
                                                                                                                            Dower WJ,
                                                                                                                                                                                                                                                                                                                                                       19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                        WO9640750-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dower WJ,
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                                                                                                                                                                              (GLAX ) GLAXO GROUP LTD
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14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transduction; receptor activation; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CADGPTLREWISFC 16
and peptide mimetics which bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CADGPTLREWISEC
                                                                                                Barret RW,
LC, Schatz
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LC, Schatz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00478128.
95US-00485301.
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95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which binds the thrombopoietin receptor (TR),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.0%;
                                                                                                Cwirla SE, Du
PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cwirla SE, Duffin DJ, Gates C
PJ, Wagstrom CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
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                                                                                                Duffin DJ, Gates CM, om CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; 1, 1, 1, 3e-05; 0;
     6
     and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemotherapy, etc.
     activate
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     the
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                                                                                                                            Johnson
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RESULT 19
AAW35401
ID AAW35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
The present peptide, which binds the thrombopoietin receptor (\mathtt{TR}), used to treat disorders which are susceptible to treatment with a
                                                                            Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                          07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW35401 standard;
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                                                               disorders,
                                                                                                                                             Mattheakis
                                                                                                                                                        Dower WJ,
                                                                                                                                                                                                                                                07-JUN-1996;
                                                                                                                                                                                                                                                                                                   WO9640750-A1
                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                    signal transduction; receptor activation; cell culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW35401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                  (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                         L9-DEC-1996.
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                                                                                                                    1997-052226/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 89;
                                    Page
                                                              евр.
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                                                                                                                                         Barret RW,
LC, Schatz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor binding peptide.
                                                                                                                                                                                                          95US-00478128
95US-00485301
                                                                                                                                                                                                                                                 96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombocytopenia resulting from chemotherapy, etc
                                       63;
                                                                thrombocytopenia resulting
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .14
                                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide;
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                                       106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.0%;
                                                                                                                                           Cwirla SE, Duffin DJ, Gate PJ, Wagstrom CR, Wrighton
                                                                                                                                                                                                                                                                                                                             "NH2-D-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
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1.3e-05;
                                                                   from
                                                                                                                                                         Gates CM,
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                                                               chemotherapy, etc
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                                                                                                                                             NC;
                                                                                                                                                           Johnson
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RESULT 20
AAW36647
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            Query Match
Best Local Similarity
  Matches
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                                                                      marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                     The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin aponist, preferably haematological disorders and thrombopotepian resulting from chemotherapy, radiation therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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                                                                                                                                                                                                                                   Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                        Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin receptor binding peptide.
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                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                    Dower WJ,
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                                                      Sequence
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14; Conser
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                                                                                                                                                                                                                                                                                                                    Barret RW,
                                                                                                                                                                                                         Page 26; 106pp; English.
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95US-00485301
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                                                                                                                                                                                                                                                                                                                        Schatz
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100.0%;
78.0%; Score 85;
100.0%; Pred. No.
Live 0; Mismatc
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Pred. No.
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  Mismatches
                                                                                                                                                                                                                                                                                                                     Duffin DJ, Gates CM, om CR, Wrighton NC;
            DB 2; Le
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CADGPTLREWISFC 16

AAW33032 ID AAW:

AAW33032 standard; peptide;

RESULT 22

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RESULT 21
AAW35400
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Best Local S
Matches 14
                                                                                                                            The present peptide, which binds the thrombopoietin receptor (TR), c used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor; binding peptide; treatment; agon; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                             Sequence 14
                                                                                                                                                                                                                                                       Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                              Dower WJ, Barret
Mattheakis LC, Sc
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                                                                                                                      thrombopoietin
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                                                           Similarity
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             CADGPTLREWISFC 16
 CADGPTLREWISFC 14
                                            78.0%; Score 85; DB ilarity 100.0%; Pred. No. 1.: Conservative 0; Mismatches
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                                                                                                                      dependent cell lines
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95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "NH2-D-Cys"
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PJ, Wagstrom CR,
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                                                                                                                                                                                                                                English.
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                                                          DB 2; Lo
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Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment; agonist;
                                                                                                                                                                                                                                                        from chemotherapy, etc
                                                                       Length 14;
                                                 Indels
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                                                                                                                                                                                                                                                                                                                                             Johnson
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                                                                                                                                                                                                                                                                                      The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an ICS0 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transflusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
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07-JUN-1995;
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              31-OCT-2000
                                                                 AAB17014 standard;
                                                                                                                                                                                                                                     Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 30; Page 91; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-052226/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                            to maintain the proliferation and growth
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                                                                                                                                                                                   14;
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LC, Schatz PJ, Wagstrom CR, Wrighton NC;
                                                                                                                                                                                   Conservative
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              (first entry)
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95US-00485301.
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                                                                 peptide; 14 AA
                                                                                                                                                                                                78.0%;
100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                            of thrombopoietin dependent
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                                                                                                                                                                                                                                                                                                                                                                                                                                     chemotherapy, etc.
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                                                                                                                                                                                                                                                                                                                 RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC domain, pharmacologically active peptides, and linkers. Where (I) is:

(XI)a-Fi-(X2)b, where: Fi = an Fc domain; XI and X2 = are each
independently selected from -(Li)c-Pi, -(Li)c-Pi-(Li)d-Pi, -(Li)c-Pi-

(CC (Li)d-P2-(L3)e-P^3, or -(Li)c-Pi-(L2)d-P2-(L3)e-P3-(L4)f-P4 where Pi, P2,

(CC P3, and P4 = are each independently sequences of pharmacologically active

(CC peptides; Li, Li, Li, A3, and Li = are each independently linkers; and a, b,

(CC c, d, e, and f = are each independently 0 or 1, provided that at least 1

(CC c, d, e, and bis 1. The composition can have cytostatic, antiasthmatic,

(CC cthrombolytic and immunosuppressive activities. DNAs, vectors and host

(CC compositions. The compositions are useful for treating cancer, asthma,

(CC cthrombosis, or autoimmune diseases. The use of an Fc domain (rather than

(CC compositions or provide a longer half-life or incorporate functions

(CC such as Fc receptor binding, protein A binding, complement fixation, and

(CC possibly placental transfer. AAA6943 to AAA6936 and AAB16955 to

CC AAB18003 represent nucleotide and amino acid sequences used in the

(CC exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; autoimmune disease; cytostatic; antiasthmatic; thrombol; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
22-OCT-1999;
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                                                             Human thrombopoietin receptor (TPO-R) activator peptide #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                           17-DEC-2001
                                                                                                                                                                                         AAU25826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:70
                                                                                                                                                                                                                                                AAU25826 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CADGPTLREWISFC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease; cytostatic; antiastnmatt, con-
disease; cytostatic; antiastnmatt, con-
ressive; EPO; TPO; CTLA4; mimetic; II-1; TNF; antagon
erythropoietin; thrombopoietin; interleukin 1;
erythropoietin; thrombopoietin; interleukin 1;
erythropoietin; thrombopoietin; interleukin 1;
erythropoietin; antigen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention describes composition of matter (I) comprising pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                           (first entry)
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99US-00428082.
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100.0%; Pr
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                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 85; DB; pred. No. 1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombolytic; VEGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antagonist; MMP;
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Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

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RESULT 25
AAU25852
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SEXEXEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC bind to and activate the human thrombopoletin receptor (TPO-R). Methods colls with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such cC as that due to chemotherapy, radiation therapy or bone-marrow cC transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders compounds that bind to and activate the TPO cas unique tools for understanding the biological role of thrombopoietin cC (TPO) and to develop other compounds that bind to and activate the TPO cells and fixed cells, in biological fluids, in tissue homogenates, and conjunctified or natural biological materials. They may also be used for in purified or natural biological materials. They may also be used for in bused for in vitro expansion of megakaryocytes and their committed cc progenitors alone or in conjunction with additional cytokines
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
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07-JUN-1995;
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                             Human
                                                                                    17-DEC-2001
                                                                                                                                                                                                 AAU25852 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO
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                             thrombopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                    (first entry)
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95US-00485301.
96WO-US009623.
96US-00699027.
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                                                                                                                                                                                           peptide; 14
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                                receptor (TPO-R) activator peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85; DB 4; I
; Pred. No. 1.3e-05;
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Deprince RB,
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RESULT 26
AAU25866
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AC AAU25
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DE Humar
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                                                                                                                                                                                                                                                                                                                                                      Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that CC bind to and activate the human thrombopoietin receptors (TPO-R). Methods CC of activating thrombopoietin receptors in cells comprise contacting the CC ells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such CC as that due to chemotherapy, radiation therapy or bone-marrow CC transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders CC including thrombocytopenia and platelet disorders. They are used in vitro CC as unique tools for understanding the biological role of thrombopoietin CC (TPO) and to develop other compounds that bind to and activate the TPO creceptor. The peptides can be used to detect TPO receptors on living CC ells and fixed cells, in biological fluids, in tissue homogenates, and CC in purified or natural biological materials. They may also be used for in Situ staining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed committed committed or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                          Matches
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07-JUN-1995;
07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting with peptides and peptide mimetics attached to hydrophilic polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                          Sequence 14
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Balasubramanian P, Wagstrom
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                                                                                                     AAU25866
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                                                                                                                                                                                                                        CADGPTLREWISFC
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95US-00485301.
96WO-US009623.
96US-00699027.
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                                                                                                   peptide;
                                                                                                                                                                                                                                                   78.0%; >---
100.0%; Pr
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strom CR, Hendren
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                                                                                                                                                                                                                                                                          Score 85;
Pred. No.
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                             NO.
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                                                                                                                                                                                                                                                                                          Length 14;
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Deprince RB,
                                                                                                                                                                                                                                                           Indels
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Human thrombopoietin receptor

(TPO-R)

activator peptide

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17-DEC-2001

(first entry)

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of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to cells with effective amounts of peptides and peptide mimetics attached to chaydrophilic polymers. The methods are used to treat thrombocytopenia such contacting the content of the content of
BXXXXX
                                                                                                                                                               RESULT 27
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Best Local
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises con with peptides and peptide mimetics attached to hydrophilic
                      05-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 20; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-564142/63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6251864-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                  ABB72900 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ences AAU25815-AAU26049 represent peptides and peptide mimetics that to and activate the human thrombopoietin receptor (TPO-R). Methods
                                                                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                    CADGPTLREWISEC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barrett RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                  A
A
                                                                                                                                                                                                                                                                                                                                     Conservative
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                      (first entry)
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95US-00485301.
96WO-US009623.
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                                                                                                               peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagstrom
                                                                                                                                                                                                                                                                                                                                                         78.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cwirla SE, Gates CM, strom CR, Hendren RW,
                                                                                                                                                                                                                                                                                                                                     <u>,</u>
                                                                                                                                                                                                                                                                                                                                                            Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                     . 1.3e-05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprises contacting cells o hydrophilic polymers.
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Deprince RB,
                                                                                                                                                                                                                                                                                                                                                                                  Length 14;
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                                                                                                                                                                                     neuroprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of compression of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, infertility, and neurological degenerative diseases. (I), comprising EPO-mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic compounds are useful for treating disorders characterised by low megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic tumour which result in thrombocytopaenia, systemic lupus erythematosus, and Fanconi's syndrome. AbB73403 to AbB73426 and AbJ35695 to AbJ35777 cerepresent amino acid and nucleic acid sequences used in the
                                                                           Matches
                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erythropoletin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EMP mimetic peptide; EMP WEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; antianaemic; antorectic; antiinfertility; haemostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-2000; 2000US-00563286
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                                                                                                                                                      Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 39; Page 44; 176pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-130313/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2001; 2001WO-US014310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPO mimetic peptide SEQ ID
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                                                                                             Similarity
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                              CADGPTLREWISFC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       retinopathy, obesity,
                                                                                                                                                      AA;
                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mimetic; Fc domain;
                                                                     78.0%; SUL
100.0%; PY
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                                                                           Score 85; DB; Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion; immunoglobulin G;
                                                                       DB 5,
1.3e-05;
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                                                                                                                 Length 14;
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th, cancer,
                                                                               Gaps
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RESULT

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ADJ73051
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ADJ73051
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RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to novel mammalian CDR mimetibodies, specific CC portions or variants thereof. Specifically, it refers to an antibody CC fragment where a protein has been inserted into, or replaces a portion of of, one or more CDR regions, such that each CDR mimetibody comprises at CC least one portion of a heavy chain or light chain variable region, which CC itself comprises at least one human framework region and at least one CC ligand binding region (LBR). The present invention describes human CC mimetibodies, including modified immunoglobulins and cleavage products CC that can be useful in gene therapy and the generation of transgenic CC plants and animals. Furthermore, the CDR mimetibody is useful for CC preparing compositions for modulating, treating or reducing the symptoms CC of immune, cardiovascular, infectious, malignant and/ or neurologic CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This CC peptide sequence is a TPO mimetic peptide sequence used to make a
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
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cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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                                  06-MAY-2004
                                                                                                                                                    ADJ52686 standard;
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                                                                                           ADJ52686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knight DM,
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                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO 505; 97pp; English.
                                                                                                                                                    peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,</u>
                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; L
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RESULT 30
ADJ51647
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                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to CHI deleted mimetibodies (and the DNA sequences cc which encode them), compositions, methods and uses. The invention may be cuseful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, compounds with an immunosuppressive, cc antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, ct issue, organ or animal, specifically for modulating, treating, calleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart cf failure), or neurodegenerative (for example multiple sclerosis, dementia cor Alzheimer's disease) diseases or discorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or cf fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                 CH1 deleted
                                                                                                                                                                                                                                                                                                                                                            Sequence 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancerous condition; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant; hypotensive; neuroprotective; nootropic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CH1 deleted mimetibody-related peptide SeqID505.
CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
                                                                   06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                    ADJ51647;
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                                                                                                                                       ADJ51647
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                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                      standard; peptide;
                                                                                                                                                                                                                          CADGPTLREWISFC
                                                                                                                                                                                                                                                          CADGPTLREWISFC
                                                                                                                                                                                                                                                                                          78.0%; Silarity 100.0%; Conservative 0;
                                 mimetibody-related peptide SeqID505
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                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                            Score 85;
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                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                         gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic, immunomodulator, antiallergic, muscular-Gen, cytostatic, antininflammatory, neuroleptic, ophthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-modulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant express or activity of the CH1 deleted mimetibody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, endocrine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, haematologic, immunological, allergic, infectious, besterric, haematologic, immunological, allergic, infectious.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis facto; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; mimunological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; oncological disorder; neurological disorder; psychiatric disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder;
                                                                                                                                                                                                               musculoskeletal, oncological, neurological, nutritional, ophthalmologic, pediatric, psychiatric, renal or pulmonary disorders. The present sequence is that of a peptide which may be used during the creation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to CH1 deleted mimetibodies (and the DNA which encode them), compositions, methods and uses. The inventio useful for the development of compounds with an osteopathic, cardiovascular Gen, dermatological Gen, auditory, endocrine Gen,
                                                                                                                                                        Sequence
                                                                                                                                                                                                  mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-082872/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kutoloski KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2002; 2002US-0392431P.
19-SEP-2002; 2002US-0412144P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     renal disorder; pulmonary disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CENZ ) CENTOCOR INC
                                                                           14;
                                                                                                Similarity
                                                                                                                                                          14
CADGPTLREWISFC
                             CADGPTLREWISFC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 505; 123pp; English.
                                                                                                                                                          A
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knight DM,
                                                                                              78.0%;
100.0%;
14
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                                                                           0;
                                                                                              Score 85;
Pred. No.
                                                                               Mismatches
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                                                                  DB 8; L.
J. 1.3e-05;
                                                                                                                Length 14;
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                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                               expression
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RESULT 31 AAW09467

RESULT 32
AAW35399
ID AAW35
XX
AC AAW35

AAW35399 standard; peptide; 13

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AAW35399;

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                                            Matches
                                                      Query Match
Best Local 9
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                   The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptimary also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting
                                                                                                                                                                                                                        Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
07-JUN-1995;
                                                                                      Sequence 13
                                                                                                                                                                                                    Claim 30; Page 91; 106pp; English.
                                                                                                                                                                                                                                                                       WPI; 1997-051883/05
                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haematology;
bone marrow t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW09467 standard; protein; 13 AA.
                                                                                                                                                                                                                                                                                             Mattheakis
                                                                                                                                                                                                                                                                                                         Dower WJ,
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                                                                                                                                                                                                                                                                                                                              (GLAX ) GLAXO
                                                                                                             receptors on
                                            13;
                     4 ADGPTLREWISEC
                                                        Similarity
                                                                                                                                                                                                                                                                                             Barrett RW,
LC, Schatz
                                                                                       AA;
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transtusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombocytopenia; TPO; TR; ransfusion; chemotherapy; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                            GROUP LID
                                                                                                                                                                                                                                                                                                                                                 95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US008998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "S-carboxymethyl-cysteine alpha-carboxamide;
forming a linkage onto the Ala at position one with
delta C of this residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                            living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "The Ala is linked with position 13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= OTHER
                                                      69.7%;
100.0%;
                                                                                                                                                                                                                                                                                            Cwirla SE,
PJ, Wagstro
                     16
                                            0
                                                                                                                                                                                                                                                                                            Wagstrom
                                                      Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     compound cyclic peptide
                                            Mismatches
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radiation theray
                                                      DB 2; L
                                                                                                                                                                                                                                                                                             n DJ, Gates
Wrighton NC;
                                                                  Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy
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                                            Gaps
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RESULT 33
AAW35417
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DT 11-W3
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DT 11-W3
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Thron
KW Thron
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Best Local
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                                                                                                                                                                                                                                                                         investigate the mechanism of thrombopoietin signal transduction a receptor activation, or to maintain the proliferation and growth thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                           The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dower WJ,
Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                     Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-1998
Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy;
                                                                                                    AAW35417 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 63; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     disorders, esp. thrombocytopenia resulting
                                                                                                                                                                                                                                                                                                                                                                                                                Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-052226/05.
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                                                                                                                                                                                 4
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                  ADGPTLREWISFC 16
                                                                                                                                                            ADGPTLREWISFC
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LC, Schatz
                                                                                                                                                                                                         Conservative
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                                                         (first entry)
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95US-00485301
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                                   receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ala1"
                                                                                                                                                                                                                    100.0%;
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PJ, Wagstrom CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "NH2-cytosine linked via sulphoxidised thiol group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "COCH2-alanine linked via CH2 group to Cys13"
                                 binding peptide.
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                                                                                                                                                                                                         0
                                                                                                                                                                                                                     Score 76;
Pred. No.
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                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                  DB 2; L
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                                                                                                                                                                                                                              Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                     chemotherapy, etc
                                                                                                                                                                                                                                                                                                              therapy or e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson SS;
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Query Match
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Matches 13
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Cross-links
Key
Modified-site
                                         Synthetic
                                                                Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                     Thrombopoietin
                                                                                                                                                                  11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dower WJ, Barret RW,
Mattheakis LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                      AAW33033 standard; peptide; 13 AA
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                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Page 73; 106pp; English.
                                                                                                                                                                                                                                                                                                                  CADGPTLREWISF 15
                                                                                                                                                                                                                                                                                          CADGPTLREWISF
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                                                                                                                                                                  (first entry)
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95US-00485301.
                                                                                                                                       receptor binding peptide.
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13
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           69.7%; 500
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cwirla SE, Duffin DJ, PJ, Wagstrom CR, Wri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "linked via disulfide bond to
                                                                                                                                                                                                                                                                                                                                              ; Score 76; DB
b; Pred. No. 0.0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                           Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                         Length
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia
                                                                                                                                                                                                                                                                                         Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
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07-JUN-1995;
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                           WO9640750-A1
                                                                                                        Modified-site
                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW35413 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 30; Page 91; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-052226/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dower WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9640750-A1
                                                                                                                                                       Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADGPTLREWISFC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADGPTLREWISFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barret RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GROUP LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-00478128
95US-00485301
                                                                                                                                                                                                                                                                                                                                                                                                                          receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               et RW, Cwirla SE, Duffin DJ,
Schatz PJ, Wagstrom CR, Wrig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "NH2-cytosine linked via thiol group to Ala1"
                                                                               note=
                                                                                                                              /note= "Br-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "COCH2-alanine linked via CH2 group to
                                                                               "NH2-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gates CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 36
AAW35406
ID AAW35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present peptide, which binds the thrombopoietin receptor (TR), can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders. esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                     AAW35406 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
07-JUN-1995;
                      07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                             Thrombopoietin
                                                                                                                                                                                                                                                                                                                     11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Page 73; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mattheakis LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1996;
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                                                         07-JUN-1996;
                                                                                                                                              Modified-site
                                                                                  19-DEC-1996
                                                                                                           WO9640750-A1
                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ADGPTLREWISFC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADGPTLREWISFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barret RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00478128
95US-00485301
                                                                                                                                                                                                                                                                                             receptor binding peptide.
                     95US-00478128.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US009623
                                                          96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schatz
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                   /note=
                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cwirla SE, Duffii
PJ, Wagstrom CR,
                                                                                                                                  "NH2-cytosine linked via thiol
                                                                                                                                                           "CO-CH(Ph)-alanine linked via CH group to Cys13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duffin DJ, Gates Com CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                  group to Ala1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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(GLAX) GLAXO

GROUP LTD

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ARBSULT 37
AAW35422
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XX Thron
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically a continuesticate the machine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dower WJ,
Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haematological radiation thera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombopoietin dependent cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction receptor activation, or to maintain the proliferation and growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 64; 106pp;
                                                                                                                                                                                                                                    07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                   19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-links
                                                   WPI; 1997-052226/05
                                                                                                      Dower WJ,
Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                      WO9640750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transduction; receptor activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADGPTLREWISFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADGPTLREWISFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ietin receptor; binding peptide; treatment; agon
gical disorder; thrombocytopaenia; chemotherapy;
therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barret RW,
LC, Schatz
                                                                                                   Barret RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
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                                                                                                                                                                                                                                    95US-00478128.
95US-00485301.
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13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "linked via disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cwirla SE, Duffin PJ, Wagstrom CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "optionally acylated
                                                                                                      Cwirla SE, Duffin DJ, Gate PJ, Wagstrom CR, Wrighton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
5. 0.00025;
0;
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Wrighton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gates CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                culture
                                                                                                                                 Gates CM,
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                                                                                                           NC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy or e.g. to
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The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and

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                                                                                                                                                                                                                                                                                                                                                                                                          'inrombopoletin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                             Example
                                                                    Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                     WPI;
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Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                                                                                                 of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow of the methods are used to the contact of the contact 
                                                                                                                                                                                                               Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barrett RW, Cwirl
anian P, Wagstrom
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95US-00485301.
96WO-US009623.
96US-00699027.
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Jstrom CR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SE, Gates
R, Hendren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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No.
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Deprince
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹ PJ;
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                                                                                                                                                                                                                                                                                                                                     polymers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokine;
by; ELISA;
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transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO

at risk.The

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RESULT 41
AAW35398
ID AAW35
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, a in purified or natural biological materials. They may also be used for situ staining, fluorescence-activated cell sorting, Western blotting enzyme-linked immunosorbent assay (ELLSA). In addition, the peptides be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
            The present peptide, which binds the thrombopoietin receptor (TR), cused to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and investigate the mechanism of thrombopoietin signal transduction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                             Example 6; Page 63; 106pp; English.
                                                                                                                                                                                                                           Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                         WPI; 1997-052226/05
                                                                                                                                                                                                                                                                                                                                Mattheakis
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13; Conser
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activation, or to maintain
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                                                                                                                                                                                                                                                                                                                              Barret
LC, Sc
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                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00478128.
95US-00485301.
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                                                                                                                                                                                                                                                                                                                              et RW,
Schatz
                                                                                                                                                                                                 thrombocytopenia resulting from chemotherapy, etc
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "NH2-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Homocysteine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76;
Pred. No.
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the proliferation
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0.00025;
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                                                                                                                                                                                                                                                                                                                              DJ, Gates CM, Wrighton NC;
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  and
growth
                                                                                                                                                                                                                                                                                                                                                        Johnson
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              Query Match
Best Local S
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                                                                   The present peptide, which binds the thrombopoietin receptor (TR), cused to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                          Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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                                                                                                                                                                     Example 6; Page 63; 106pp; English.
                                                                                                                                                                                                                                         WPI; 1997-052226/05
                                                                                                                                                                                                                                                              Dower WJ, Barret RW,
Mattheakis LC, Schatz
                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
07-JUN-1995;
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                                              AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor binding peptide.
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95US-00485301.
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69.7%; Pr
100.0%; Pr
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100.0%;
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PJ, Wagstrom CR,
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                                                                                                                                                                                                                                                                                                                                                                                                                        "NH2-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Penicillamine"
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               Score 76; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                          DB 2;
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Wrighton NC;
                         Length 14;
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                                                                                                                                                                                                                                                                            Johnson SS;
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RESULT 43
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                                                                                                                                                                                                                                    marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                   The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombopotetin agonist from chemotherapy, radiation therapy of
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                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 64; 106pp;
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07-JUN-1995;
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LC, Schatz
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95US-00485301.
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100.0%; Pred.
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PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
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anian P, Wagstrom CR, l
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96US-00699027.
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RESULT 44 AAU25987

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Balasubramanian P,
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C;Species: Ca
C;Date: 29-Oc
C;Accession:
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T33943
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A;Experimental source: cultivar Columbia; BAC clone C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Smith, A.; Wamsley, P.; Fronick, W. submitted to the EMBL Data Library, February 1999 A; Description: The sequence of C. elegans cosmid (A; Reference number: Z21443 A; Accession: T33943
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A; Note: F1I16.30
C; Superfamily: co
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandsubmitted to the Protein Sequence Database, A;Reference number: Z25022
                                              hypothetical protein B24B19.30 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change C;Accession: T49731
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A; Introns: 45/2;
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;Residues: 1-475 <SMI>
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Pred. No.
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                                  Brandt,
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C; Superfamily:
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A;Accession: T49731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <SCH>
A;Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.30
A;Experimental source: BAC clone B24B19; strain OR74A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Mattar, S.; Engelhard, M.
Eur. J. Biochem. 250, 332-341, 1997
Eur. J. Biochem. 250, 332-341, 1997
A;Title: Cytochrome ba3 from Natronobacterium pharaonis:
A;Reference number: Z22876; MUID:98088958; PMID:9428682
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A;Map position: 6
C;Superfamily: Neurospora crassa
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A;Cross-references: UNIPROT:Q9XUV7;
A;Experimental source: clone F59A1
                                                                                                                                                                                                                                                                                                                                               hypothetical protein F59A1.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 5 [imported] - Natronobacterium pharaonis
C;Species: Natronobacterium pharaonis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A;Reference number: Z19644
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A; Residues: 1-180 < MAT>
                                                                           A; Map position: 5
A; Introns: 27/1; 116/1;
                                                                                                                    A;Gene: CESP:F59A1.13
                                                                                                                                                                                                                A; Molecule type: DNA
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50.0%;
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Pred. No. 53;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S51089
A; Accession: S51089
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N;Alternate names: NH3 permease; protein JTA499; protein N1207; protein N1820;
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A;Residues: 1-499 <MAF>
A;Cross-references: EMBL:Z71418; NID:g1302090; PIDN:CAA96025.1; PID:g1302091; MIPS:YNL1
A:Experimental source: strain S288C
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Yeast 11, 1195-1209, 1995
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A; Residues: 1-499 < MAR>
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R;Mallet, L.; Bussereau, F.; Jacquet, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-499 <MAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Description: ammonium transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: SGD:S0005086; MIPS:YNL142w;Map position: 14L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reference number:
Accession: S63087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Saccharomyces cerevisiae; Date: 10-May-1995 #sequence_revisic; Date: 10-May-1995 #sequence_revisic; Accession: S51089; S55142; S59247;
                                                                                                                                                                                                                                                                                                                                                      ;35-51/Domain: transmembrane #status predicted <TM1>;62-78/Domain: transmembrane #status predicted <TM2>;123-139/Domain: transmembrane #status predicted <TM3>;124-170/Domain: transmembrane #status predicted <TM4>;228-244/Domain: transmembrane #status predicted <TM5>;288-304/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keywords: ammonium transport; transmembrane protein; 35-51/Domain: transmembrane #status predicted <TMl>
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Best Local
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                                                                                                    ĠĠSĀGNAŤIŘAŴYŚIMSTNLAAAĊĠĠ 272
                                                                                                                                                       GGCADGPTLREWISF-----CGG 18
                                                                                                                                                                                                                                                                                                                                transmembrane
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                                                                                                                                                                                                                            41.3%;
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359247; S63087
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Pred. No.
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                                                                                                                                                                                                                                                         <u>ب</u>
                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                      Length 499;
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                                                                                                                                                                                                         Gaps
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A;Title: Genome sequence of the radioresistant bacterium A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: D75266
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A;Introns: 109/1; 135/2; 160/2; 310/1
C;Superfamily: Caenorhabditis hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C06C6.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: iap38
F;148-167/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: spleen cell C;Comment: This protein is a plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: A58583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 25-Apr_1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chabaudi malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P70224; GB:Y08026; NID:g1550784; PIDN:CAA69283.1; PID:g1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
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A;Experimental source: clone C06C6
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Best Local
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                                                                                                                                                                                                                                                                                             3 CADGPTLREWISFCGG 18
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Similarity 43.88;
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                                                                                                                                                                                                                                                              CTONRALRDLVAECGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ys. Res. Commun. 230, 167-170, 1997
gene expressed in spleen cells mediating acquired testosterone-resistant
mbor: A58583; MUID:97148595; PMID:9020038
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Pred. No.
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                                                                                       J.D.; Dodson,
T.; Zalewski,
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C;Accession: A86440
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Recession: A86440
A;Accession: A86440
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A;Residues: 1-371 <WHI>
A;Cross-references: UNIPROT:Q9RRJ3; GB:AE002079; GB:AE000513; NID:g6460315; PIDN:AAF1203
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                      58.5K hypothetical protein - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) (;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: A86440
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A;Experimental source: strain cw-15
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C;Species: Chlamydomonas reinhardtii
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C; Superfamily: roo
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                                                                                                                                                             A; Status: preliminary
                                                                                                                         :Residues:
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Best Local (
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Best Local Similarity
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                                                                                                                                            Molecule type: DNA
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                                                                                                                         1-526 <STO>
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                                                                                                        UNIPROT: Q9C868;
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Pred. No.
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    Score 44;
Pred. No.
                                                                                                        GB:AE005172;
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Maiti, R.;
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C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 0 C;Accession: S53489; S34189 R;Sonnewald, U.; Basner, A.; Greve, B.; Steup, M. Plant Mol. Biol. 27, 567-576, 1995 A;Title: A second L-type isozyme of potato glucan phosphorylase: A;Reference number: S53489; MUID:95201249; PMID:7894019
                          F;291-313/Domain: transmembrane #status predicted <TM3>
F;320-348/Domain: transmembrane #status predicted <TM4>
F;320-348/Domain: transmembrane #status predicted <TM4>
F;349-785/Domain: intracellular #status predicted <TM7>
F;586-782/Domain: ATPase nucleotide-binding domain homology
F;786-809/Domain: transmembrane #status predicted <TM5>
F;848-873/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ohta, T.; Nagano, K.; Yoshida, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986
A;Title: The active site structure of Na(+)/K(+)-transporting ATPase: location of the A;Reference number: S29880; MUID:86177549; PMID:3008150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - Pacific electric ray C;Species: Torpedo californica (Pacific electric ray) C;Decies: Jo-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004 C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004 C;Accession: S00503; S28885; S29880
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                                                                                                                                                                                                                                                    C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; F;96-120/Domain: transmembrane #status predicted <TML>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 228-240;431-438;535-550;671-690;1011-1022 <KAW2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-1022 < KAW1> A; Cross-references: UNIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Kawakami, K.; Noguchi, (
Nature 316, 733-736, 1985
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A; Residues: 1-974 <SO2>
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                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 386-402; 502-512; 671-689; 887-906 < OHT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Primary structure of the alpha-subunit of Torpedo A;Reference number: S00503; MUID:85296307; PMID:2993905
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                                                                                                                                                                                                                                                                                                               Superfamily: Na+/K+-transporting ATPase alpha chain;
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N;Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-j (Species: Homo sapiens (man) (2-Jun-1988 #sequence revision 02-Jun-1988 #text_change 09-Jul-2004 C;Accession: A24414; A27795; A39910; I60116; S09171 R;Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K. J. Biochem. 100, 389-397, 1986 A;Title: Primary structure of the alpha-subunit of human Na,K-ATPase deduced A;Reference number: A24414; MUID:87057096; PMID:2430951
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Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043; 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043; 1987
A;Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit A;Reference number: A94158; MUID:87231946; PMID:3035563
A;Accession: A27795
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A;Residues: 199-942 <CHE>
A;Cross-references: GB:J03007
A;Cross-references: GB:J03007
R;Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
Genomics 6, 451-460, 1990
Genomics 6, 451-460, 1990
A;Title: The human Na, K-ATPase alpha 1 gene: characterization of the
A;Reference number: I60116; MUID:90228961; PMID:1970326
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A;Molecule type: DNA
A;Residues: 168-189;213-214,'X',216-244 <SHU>
A;Residues: 168-189;213-214,'X',216-244 <SHU>
R;Chehab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blostein, R.
R;Chehab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blostein, R.
A;Title: Human placental Na+,K+-ATPase alpha subunit: cDNA cloning, tissue expression, A;Reference number: A39910; MUID:88068506; PMID:2891135
A;Accession: A39910
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                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 1p13-1p11
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Superfamily: heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein; F;6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>F;6-95/Domain: intracellular #status predicted <INT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translation not shown; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-61 <RES>
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                                                                           F;849-874/Domain:
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                                                                                                                                      349-786/Domain:
;587-783/Domain:
                                                                                                                                                                                                                                   150-290/Domain:
291-313/Domain:
                                                                                                              787-810/Domain:
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transmembrane #status predicted <TM4>
intracellular #status predicted <INT3>
ATPase nucleotide-binding domain homology
transmembrane #status predicted <TM5>
transmembrane #status predicted <TM6>
intracellular #status predicted <INT4>
transmembrane #status predicted <INT4>
                                                                                                                                                                                                                            transmembrane #status predicted <TM2>
intracellular #status predicted <TM72>
transmembrane #status predicted <TM3>
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Pred. No. 1.7e+02;
0; Mismatches 3;
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Accession: A89813
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                                                                                                                                                                                                                                                                                                                                                                                                                                              glutamate synthase large subunit [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004 C;Accession: A99813
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A; Molecule type: DNA
A; Residues: 1-376 <OLI>
A; Cross-references: UNIPROT: Q9Y7J0; EMBL: AL049489;
A; Cross-reference: strain 972h-; cosmid c1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T39685
R;Oliver, K.; Harris, D.; Wood, V.; submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein SPBC1778.03c - fissi
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1499 «KUR»
A;Cross-references: UNIFROT:099WD1;
A;Experimental source: strain N315
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7; Conserve
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                                                                                              Score 43.5; DB 2;
Pred. No. 2.8e+02;
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Pred. No. 1.7e+02;
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Pred. No. 79;
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March 1998
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awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Taka DNA Res. 6, 83-101, 1999
A,Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy: A;Reference number: A72450; MUID:99310339; PMID:10382966
A,Accession: D72595
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T15386
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A;Molecule type: DNA
A;Residuss: 1-113 <KAW>
A;Cross-references: UNIPROT:Q9YCM9; DDBJ:AP000061; NID:g5104821; PIDN:BAA80218.1;
A;Experimental source: strain K1
C;Genetics:
C;Genetics:
A;Gene: APE1229
                                                                                                                                                      mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change C;Accession: 148685; S43172 R;Huang, R.; Hellman, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72595
                A;Residues: 1-230 <RES>
A;Cross-references: UNIPROT:P21845; EMBL:X78542; NID:g468809; PIDN:CAA55288.1; PID:g4688
                                                                                     Immunogenetics 40, 397-414, 1994
A;Title: Genes for mast-cell serine protease and their molecular evolution.
A;Reference number: I48684; MUID:95048582; PMID:7959952
A;Accession: I48685
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A; Accession: T15386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C03B1.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep_1999 #sequence_revision 20-Sep_1999 #text_change 09-Jul-2004 C;Accession: T153B6
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Best Local S
Matches 8
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Superfamily: trypsin; trypsin homology
                                                  Molecule type: mRNA
                                                                   Status: preliminary; translated
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A; Introns: 91/3
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                       GPTLREWISFCG 17
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R;Kershaw, J.
submitted to the EMBL Data
A;Reference number: Z19208
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A:Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C47B2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lipoate biosynthesis protein B [imported] - Agrobacterium tumefaciens (strain C58, Dupo: C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: hydrolase; serine proteinase F;32-230/Domain: trypsin homology #status atypical
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-246 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: circular chromosome
C;Superfamily: Escherichia coli lipoate-protein ligase lipB
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A;Cross-references: UNIPROT:Q8UF44; GB:AE008688;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB2768
                                                                                                                                           A; Gene: CESP: C47B2.5
                                                                                                                                                                                   A;Experimental source:
                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                  A; Accession: T19988
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                                                                                                                                                                                   Cross-references: UNIPROT:062106; Experimental source: clone C47B2
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Similarity 5; Conserv
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                        EMBL: Z99709; PIDN: CAB16860.1; GSPDB: GN00019; CESP: C
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59;
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A;Gene: AGK C_4000
A;Map position: circular chromosome
A;Map position: circular chromosome
C;Superfamily: Escherichia coli lipoate-protein ligase lipB
C;Superfamily: Escherichia coli lipoate-protein ligase lipB
                                                                                                                                                                                                                                                                                                                                                                                           R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84821
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A; Residues: 1-247 < ROU>
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A; Accession: T01012
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A;Description: Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence.
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                                                                                                                                                                                                                                                                                                                               A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun A;Reference number: A97359; MUID:21608551; PMID:11743194 A;Accession: D97548
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A; Residues: 1-268 < KUR>
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                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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Best Local
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Superfamily: conserved hypothetical protein YPR016c
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                                                                   Matches
                                                                                                                                                                                                                                            Cross-references: UNIPROT:Q8UF44; GB:AE007869; PIDN:AAK87341.1; PID:g15156641; GSPDB
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GGCAD-----GPTLREWISFCG 17
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                                                                                     Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
                                                                Mismatches
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A;Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509 R;Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990 A;Title: Different mouse mast cell populations express various combinations of A;Reference number: A35646; MUID:90222202; PMID:2326280 A;Accession: D35646
                                                                                                                                                                                                                                           probable membrane protein YMR266w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM8156.08
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-31/Domain: activation peptide #status predicted <ACT>
F;32-276/Product: mast cell proteinase 6 #status experimental <MAT>
F;32-288/Domain: trypsin homology <TRY>
F;75,122,225/Active site: His, Asp, Ser #status predicted
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A;Residues: 32-54 <RE3>
A;Residues: 32-54 <RE3>
R;Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, Scand. J. Immunol. 38, 359-367, 1993
Scand. J. Immunol. 38, 359-367, 1993
A;Title: Expression of a mast cell tryptase in the human monocytic cell la;Reference number: 159478; MUID:94023807; PMID:8210998
A;Accession: 159478
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J. Biol. Chem. 266, 3847-3853, 1991
A;Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription A;Reference number: A38654; MUID:91139682; PMID:1995638
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C;Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A38654; B38654; D35646; I59478
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A; Residues: 1-276 < RES>
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A; Residues: 1-276 < REY>
                                      A; Molecule type: DNA
A; Residues: 1-953 < LYE>
                                                                                                     A;Accession: S54478
                                                                                                                                                                  submitted to the EMBL Data
                                                                                                                                                                                        R; Lye, G.; Churcher, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-276 < RE2 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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A;Cross-references: UNIPROT:Q03516; EMBL:Z49260; NID:g809081; PID:g809089; GSPDB:GN0001
                                                                                                                        A; Reference number: S54014
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 LNYWIHFCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LREWISFCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
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                                                                                                                                                           Library, May 1995
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Pred. No.
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A;Map position: 13R
C;Superfamily: yeast probable membrane protein YOL084w
C;Reywords: transmembrane protein
F;32-48/Domain: transmembrane #status predicted <TM1>
F;106-122/Domain: transmembrane #status predicted <TM2>
F;106-122/Domain: transmembrane #status predicted <TM3>
F;152-168/Domain: transmembrane #status predicted <TM4>
F;35-411/Domain: transmembrane #status predicted <TM4>
F;35-451/Domain: transmembrane #status predicted <TM5>
F;435-451/Domain: transmembrane #status predicted <TM7>
F;545-561/Domain: transmembrane #status predicted <TM7>
F;546-662/Domain: transmembrane #status predicted <TM8>
F;646-662/Domain: transmembrane #status predicted <TM8>
F;668-684/Domain: transmembrane #status predicted <TM9>
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Am. J. Physiol. 259, C619-C630, 1990
A;Title: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.
A;Reference number: A37227; MUID:91023019; PMID:2171348
A;Accession: B37227
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B37227
                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: S00801; S04019; A27397; S02275
R;Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Melkov, A.M.;
dyanov, N.N.; Sverdlov, E.D.
FEBS Lett. 233, 87-94, 1988
A;Title: Family of human Na,K-ATPase genes. Structure of the gene for the catalytic sub A;Reference number: S00801; MUID:88255304; PMID:2838329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-1010 <TA2>
A;Residues: 1-1010 <TA2>
A;Cross-references: UNIPROT:P24798; GB:M59960; NID:g212407; PIDN:AAA48982.1; PID:g212408
A;Cross-references: UNIPROT:P24798; GB:M59960; NID:g212407; PIDN:AAA48982.1; PID:g212408
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - chicken C;Species: Gallus gallus (chicken) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004 C;Accession: B37227; I50395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;202,470/Binding site: carbohydrate (Asn) (covalent) #status predicted F;363/Active site: Asp (aspartylphosphate intermediate) #status predicted F;495/Binding site: ATP (Lys) #status predicted
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A;Cross-references: UNIPROT:P13637; EMBL:M37456 R;Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, ov, N.N.; Ovchinnikov, Y.A.
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                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1013 < OVC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - human
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                                                                                                                                                                                                               Accession: S00801;
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Best Local
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41.2%;
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Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 2;
Pred. No. 2.3e+02;
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                                        N.E.; Ushkarev,
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                                                                                                                                                                                                                                                                                                          gene for the catalytic sub
                                        Y.A.;
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                                                 Melkov,
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                                                 Smirr
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F,865-942/Domain: intracellular #status predicted <TM6>
F,965-942/Domain: intracellular #status predicted <TM74>
F,943-968/Domain: transmembrane #status predicted <TM7>
F,969-1013/Domain: extracellular #status predicted <TM7>
F,366/Active site: Asp (aspartylphosphate intermediate) #
F,498/Binding site: ATP (Lys) #status predicted
F,707,711,716/Active site: Asp, Asp, Lys #status predicted
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F;310-338/Domain: transmembrane #status predicted <TM4>
F;310-776/Domain: intracellular #status predicted <TM4>
F;339-776/Domain: ATPase nucleotide-binding domain homology
F;777-800/Domain: transmembrane #status predicted <TM5>
F;839-864/Domain: transmembrane #status predicted <TM6>
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A;Residues: 1. /EIH', 3-1013 <SVE1>
A;Residues: 1. /EIH', 3-1013 <SVE1>
A;Residues: EMBL:X12910; NID:928963
A;Cross-references: EMBL:X12910; NID:928963
A;Cross-references: EMBL:X12910; NID:928963
A;Note: the authors translated the codon TTC for residue 283 as Ser and TCT for residue A;Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk: A;Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk: R;Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Allikmets, R.L.; Ptina, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchnikov, Y.A.
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Blochemistry 25, 8125-8132, 1986
A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit f A;Reference number: A90512; MUID:87128908; PMID:3028470
A;Accession: C24639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - rat
N;Alternate names: Na+/K+-transporting ATPase alpha(III) chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Unn-1988 #sequence revision 23-Apr-1993 #text_change
C;Accession: C24639; S00514; B27180; A60470
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A; Introns: 2/3; 31/3; 51/3; 119/3; 157/3; 202/3; 242/1; 331/3; 398/1; 435/2; 479/3; C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding don C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding ATPase nucleotide-binding
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A; Residues: 243-434 <
A; Cross-references: GI
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A;Title: The family of human Na+,K+-ATPase genes. No less than five genes and/or pseudo: A;Reference number: A27397; MUID:87247232; PMID:3036582
A;Accession: A27397
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A;Accession: S00514
A;Molecule type: mRNA
A;Residues: 1-907,'C',909-1013 <HAR:
                                                                                                                                         A;Note: In the during O.; Kawakami, K.; Nojamo, O.; Kawakami, K.; Nojamo, O.; R;Hara, Y.; Urayama, O.; Kawakami, K.; Nojamo, O.; R;Hara, Y.; Urayama, 1987
J. Biochem. 102, 43-58, 1987
A;Title: Primary structures of two types of alpha-subunit A;Titl
                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-1013 <SHU>
A;Residues: 1-1013 <SHU>
A;Cross-references: UNIPROT:P06687; EMBL:M14513; NID:g203030; PIDN:AAA40777.1; PID:g203
A;Note: in the authors' translation 405-Ser is shown after residue 409 and, consequentl
A;Note: in the authors' translation 405-Ser is shown after residue 409 and, consequentl
R;Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.;
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Pred. No. 2.3e+02;
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R;Hsu, Y.M.; Guidotti, G.
Blochemistry 28, 569-573, 1989
A;Title: Rat brain has the alpha3 form of the (Na+,K+)ATPase
A;Reference number: A60470; MUID:89229049; PMID:2540801
A;Accession: A60470
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R;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.
J. Cell Biol. 105, 1855-1865, 1987
A;Title: Three differentially expressed Na,K-ATPase alpha subunit isoforms: structural A;Reference number: A92749; MUID:88033255; PMID:2822726
A;Accession: B27180
                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1017 <TAK>
A;Cross-references: UNIPROT:P24797; GB:M59959; NID:g212405; PIDN:AAAA8981.1;
A;Cross-references: UNIPROT:P24797; GB:M59959; NID:g212405; PIDN:AAAA8981.1;
R;Takeyasu, K.; Lemas, V.; Fambrough, D.M.
Am. J. Physiol. 259, C619-C630, 192
Am. J. Physiol. 259, C619-C630, 192
A;Title: Stability of Na(+)-K(+)-192
A;Reference number: A37227; MUID:91023019; PMID:2171348
A;Accession: A37227; MUID:91023019; PMID:2171348
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A;Residues: 117-132;586-595,'X',597-601 <HSU>
C;Comment: The alpha-3 form appears to be highly ouabain-inhibitable, as is alpha-2
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A; Residues: 1,'NL', 4-103,'R',105-113,'E',115-127,'G',129-148,'Q',150-151,'T',153-165,'D'
A; Cross-references: EMBL: M28648; NID: g205633; PIDN: AAA41672.1; PID: g205634
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                                                                                    A; Molecule type: mRNA
A; Residues: 3-1017 <TA2>
C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding
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Am. J. Physiol. 259, 619-630, 1991
A;Title: Stability of the Na+,K+-ATPase alpha-subunit isoforms in
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A; Accession: I50394
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7,339-776/Domain: intracellular #status predicted <TW4>
7,537-773/Domain: AFPase nucleotide-binding domain homology
7,777-800/Domain: transmembrane #status predicted <TW5>
7,839-864/Domain: transmembrane #status predicted <TW6>
7,865-942/Domain: intracellular #status predicted <TW7>
7,943-968/Domain: transmembrane #status predicted <TW7>
7,943-968/Domain: transmem
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;281-303/Domain:
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Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; 581-777/Domain: ATPase nucleotide-binding domain homolo
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Pred. No. 2.3e.
1; Mismatches
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2.3e+02;
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F;94-110/Domain: transmembrane #status predicted <TM1>
F;128-147/Domain: transmembrane #status predicted <TM2>
F;128-286/Domain: intracellular #status predicted <TM2>
F;289-311/Domain: transmembrane #status predicted <TM3>
F;318-346/Domain: transmembrane #status predicted <TM4>
F;318-346/Domain: intracellular #status predicted <TM4>
F;347-783/Domain: intracellular #status predicted <TM4>
F;344-780/Domain: ATPase nucleotide-binding domain homology
F;848-807/Domain: transmembrane #status predicted <TM5>
F;846-807/Domain: transmembrane #status predicted <TM6>
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C;Date: 15-Uun-1990 #sequence revision 15-Jun-1990 #text_C
C;Accession: A34474; B27795; D27397
R;Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
J. Biol. Chem. 264, 17532-17543, 1989
A;Title: Characterization of the human Na,K-ATPase alpha2 A;Reference number: A34474; MUID:90008924; PMID:2477373
A;Accession: A34474
                                                                                                                                                                                                                                        F;950-975/Domain: transmembrane #status predicted <TMT>
F;976-1020/Domain: extracellular #status predicted <EXT>
F;374/Active site: Asp (aspartylphosphate intermediate) i
F;505/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:119712; OMIM:182340
A;Map position: 1q21-1q23
A;Map position: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding C;Superfamily: Na+/K+-transporting ATPase; ion transport; phosphoprotein; potassium C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium F;6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MATF;6-93/Domain: intracellular #status predicted <INTL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Sverdlov, E.D.; Monastyrskaya, G.Š.; Broude, N.E.; Ushkaryov, Y.A.; Allikmets, R.L.; tina, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchnikov, Y.A. FEBS. Lett. 217, 275-278, 1987
A;Title: The family of human Na+, K+-ATPase genes. No less than five genes and/or pseudo A;Reference number: A27397; MUID:87247232; PMID:3036582
A;Accession: D27397
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A;Molecule type: DNA
A;Residues: 211-249 <SH2>
A;Residues: 211-249 <SH2>
A;Cross-references: GB:M16795; NID:g179196; PIDN:AAA51799.1; PID:g553194
A;Cross-references: GB:M16795; PID:g179196; PIDN:AAA51799.1; PID:g553194
A;Cross-references: GB:M16795; PID:g179196; PIDN:AAA51799.1; PID:g553194
A;Cross-references: GB:M16795; PID:g179196; PIDN:g179196; PID:g179196; PIDN:g
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A; Residues: 1-1020 <SHU>
A; Residues: 1-1020 <SHU>
A; Cross-references: UNIPROT: P50993; GB: J05096; NID: g179164; PIDN: AAA51797
A; Shull, M.M.; Lingrel, J.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
A; Title: Multiple genes encode the human Na+, K+-ATPase catalytic subunit.
A; Reference number: A94158; MUID: 87231946; PMID: 3035563
A; Accession: B27795
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N;Alternate names: Na+/K+-exchanging ATPase alpha chain-4; sodium/potassium transportin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;371/Active site: Asp (aspartylphosphate intermediate) #status
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A; Residues: 251-442
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transmembrane #status predicted <TM6>
intracellular #status predicted <INT4
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                                                                                                                                                                                         Asp, Lys #status predicted
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Score 43; DB
Pred. No. 2.4e
1; Mismatches
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Pred. No. 2.3e+02;
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                                                                                               Length 1020;
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reates the electrochemical gradient of sodium and potassium, providing the energy for

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Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep
N;Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chai;
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01074; A35426
C;Accession: A01074; A35426
R;Shull, G.E.; Schwartz, A.; Lingrel, J.B.
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A;Residues: 1-1020 <SHU>
A;Cross-references: UNIPROT:P06686; EMBL:M14512; NID:g203028; PIDN:AAA40776.1; PID:g2030
C;Genetics:
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R;Shull, G.E.; Greeb, J.; Lingrel, J.B.
Biochemistry 25, 8125-8132, 1986
A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit fr A;Reference number: A90512; MUID:87128908; PMID:3028470
A;Accession: B24639
                                                                                                                                                    R;Hinz, H.R.; Kirley, T.L.
J. Biol. Chem. 265, 10260-10265, 1990
A;Title: Lysine 480 is an essential residue in the putative ATP
A;Reference number: A35426; MUID:90285144; PMID:2162343
                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-1021 <SHU>
A;Cross-references: UNIPROT:P04074; GB:X02813; NID:g1205; PIDN:CAA26581.1; PID:g1206
                                                                                                                                                                                                                                                                                                                                                                          A;Title: Amino-acid sequence of the catalytic subunit of the A;Reference number: A01074; MUID:85296299; PMID:2993903 A;Accession: A01074
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N;Alternate names: Na+/K+-transporting ATPase
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;94-119/Domain: transmembrane #status predicted
                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 316, 691-695, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;128-147/Domain:
                                   ;Molecule type: protein
;Residues: 475-492 <HIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;976-1020/Domain: extracellular #status predicted <EXTS;374/Accive site: Asp (aspartylphosphate intermediate) #status predicted;505/Binding site: ATP (Lys) #status predicted;714,718,723/Active site: Asp, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      872-949/Domain: intracellular #status predicted <INT4>
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872-949/Domain: intracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318-346/Domain: transmembrane #status predicted <TM4>;318-346/Domain: intracellular #status predicted <INT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;128-147/Domain: transmembrane
;148-288/Domain: intracellular
;289-311/Domain: transmembrane
Comment: This is the catalytic component of the active enzyme, which catalyzes the
                                                                                                                    Accession: A35426
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6; Conserv
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#status predicted <INT2>
#status predicted <TM3>
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Pred. No.
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F;128-144/Domain: transmembrane #status predicted <TM2>
F;289-311/Domain: transmembrane #status predicted <TM3>
F;389-311/Domain: transmembrane #status predicted <TM3>
F;3818-346/Domain: transmembrane #status predicted <TM4>
F;585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F;785-808/Domain: transmembrane #status predicted <TM5>
F;785-808/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                F;318-346/Domain: transmembrane #status predicted <TM4>
F;347-784/Domain: intracellular #status predicted <TM73>
F;548-781/Domain: ATPase nucleotide-binding domain homology
F;785-808/Domain: transmembrane #status predicted <TM5>
F;847-872/Domain: transmembrane #status predicted <TM6>
F;847-872/Domain: intracellular #status predicted <TM6>
F;847-950/Domain: transmembrane #status predicted <TM7>
F;951-976/Domain: transmembrane #status predicted <TM7>
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                                                                                                                                                                                                                                                                                           F;977-1021/Domain: extracellular #status predicted <EXT>
F;374/Active site: Asp (aspartylphosphate intermediate) #status
F;506/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 4/3; 39/3; 59/3; 127/3; 165/3; 210/3; 250/1; 339/3; 406/1; 442/3; 487/3; 552, C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans F;6-1021/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Kano, I.; Nagai, F.; Satoh, K.; Ushiyama, K.; Nakao, T.; Kano, K. PEBS Lett. 250, 91-98, 1989
A;Title: Structure of the alpha(1) subunit of horse Na,K-ATPase gene A;Reference number: S04630; MUID:89290042; PMID:2544461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - horse C;Species: Equus caballus (domestic horse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004 C;Accession: S04630
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F;128-147/Domain: transmembrane #status predicted <TM2
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A; Residues: 1-1021 < KAN>
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Best Local :
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82
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                                                                                                                                Similarity 6; Conserv
                                                                 PTLREWISFC 16
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(Lys) #status predicted
   91
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Pred. No.
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Pred. No.
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C;Accession: A28199
A;Title: Ouabain-sensitive (Na(+) + K(+))-ATPase activity expressed in mouse L cells by A;Feference number: A28199; MUID:88153759; PMID:2831227
A;Accession: A28199
A;Reference number: A28199; MUID:88153759; PMID:2831227
A;Accession: A28199
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1021 <-TAKs
A;Cross-references: UNIPROT:P09572; GB:J03230; NID:g211219; PIDN:AAA48607.1; PID:g211220
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP, glycoprotein; hydrolase; phosphoprotein; transembrane protein
C;Keywords: ATPase nucleotide-binding domain homology <ATN>
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N;Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text change 09-Jul-2004
C;Accession: B24862; I46572; A35504; S00011; S00502; S02569; S29762
C;Accession: B24862; I46572; A35504; S00011; S00502; S02569; S29762
R;Ovchinnikov, Y.A.; Modyanov, N.N.; Broude, N.E.; Petrukhin, K.E.; Grishin, A.V.; A
FEBS Lett. 201, 237-245, 1986
A;Title: Pig kidney Nat, K-ATPase. Primary structure and spatial organization.
A;Reference number: A91361; MUID:86220813; PMID:2423371
A;Accession: B24862
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A; Molecule type: mRNA
A; Residues: 469-617 < OVCl>
A; Cross-references: GB:M32512; NID:g164385; PIDN:AAA31004.1;
A; Cross-references: Galdshleger, R.; Stein, W.D.
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D,Title: Amino acid sequence of the 17-kilodalton fragment of the cytoplasmic region of A;Reference number: I46572
A;Accession: I46572
                     A;Title: Detailed structural analysis of exposed domains of membrane-bound Na+,K+-ATPase A;Reference number: $00011; MUID:87247231; PMID:3036581
A;Contents: annotation; membrane topology
R;Ovchinnikov, Y.A.; Luneva, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Arzamazova, N.M. FEBS Lett. 227, 230-234, 1988
A;Title: Topology of Na, K-ATPase: identification of the extra- and intracellular hydrop A;Reference number: $02569; MUID:88112252; PMID:2448169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Karlish, S.J.D.; Goldshleger, R.; Stein, W.D. Proc. Natl. Acad. Sci. U.S.A. 87, 4566-4570, 1990
A;Title: A 19-kDa C-terminal tryptic fragment of the alpha chain of Na/K-ATPase A;Reference humber: A35504; MUID:90280416; PMID:2162048
A;Accession: A35504
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A; Residues: 836-845,'R', 847-851 <KAR>
R; Ovchinnikov, Y. A.; Arzamazova, N.M.; Arystarkhova,
FEBS Lett. 217, 269-274, 1987
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A; Residues: 1-1021 < OVC2>
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;213,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
;374/Active site: Asp (aspartylphosphate intermediate) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gevondyan, N.M.;
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A; Molecule type: mRNA
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F;128-147/Domain: transmembrane #status predicted <TM2>
F;148-288/Domain: intracellular #status predicted <TM2>
F;289-311/Domain: transmembrane #status predicted <TM2>
F;289-311/Domain: transmembrane #status predicted <TM4>
F;318-346/Domain: intracellular #status predicted <TM4>
F;318-346/Domain: intracellular #status predicted <TM4>
F;585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F;785-808/Domain: transmembrane #status predicted <TM5>
F;871-972/Domain: transmembrane #status predicted <TM4>
F;873-950/Domain: intracellular #status predicted <TM7>
F;977-1021/Domain: transmembrane #status predicted <TM7>
F;977-1021/Domain: extracellular #status predicted <TM7>
F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted F;706/Binding site: ATP (Lys) #status predicted <TM7>
F;06/Binding site: ATP (Lys) #status predicted <TM7>
F;715,719,724/Active site: Asp, Asp, Lys #status predicted
C;Date: 18-Aug-2000 #sequence revision 18-Aug-2000 #text_change 09-Jul-2004 C;Accession: A24639; S00460; A27180; S11020; A25171; S29877; S10758 R;Shull, G.E.; Greeb, J.; Lingrel, J.B. Biochemistry 25, 8125-8132, 1986 Biochemistry 25, 8125-8132, 1986 A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpl A;Reference number: A90512; MUID:87128908; PMID:3028470 A;Accession: A24639
                                                                                                                                                                                                                                                                                                                                          Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain [validated] N;Alternate names: Na+/K+-transporting ATPase alpha chain kidne N;Contains: Na+/K+-transporting ATPase alpha-S chain C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1022 <CUT>
A;Residues: 1-1022 <CUT>
A;Residues: 1-1022 <CUT>
A;Residues: 1-1022 <CUT>
A;Cross-references: UNIPROT:Q92030; EMBL:X76108; NID:g509405; PIDN:CAA53714.1; PID:g509
A;Cross-references: UNIPROT:Q92030; EMBL:X76108; NID:g509405; PIDN:CAA53714.1; PID:g509
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain homotogy chain
C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; transmem
C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; hydrolase; phosphoprotein; hydrolase; phosphoprotein; hydrolase; phosphoprotein; hydrolase; phosphoprotein; hydrolase; phosphoprotein; hydrolase; 
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Similarity 60.0%;
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Pred. No. 2.4e+02;
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Pred. No. 2.4e+02;
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alpha-subunit

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R;Yagawa, Y.; Kawakami, K.; Nagano, K.
Biochim. Biophys. Acta 1049, 286-292, 1990
A;Title: Cloning and analysis of the 5'-flanking region A;Reference number: S11020; MUID:90344872; PMID:2166579
A;Accession: S11020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 4/3
A;Note: the list of introns may be incomplete
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F;6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status experimental <MAT>
F;6-95/Domain: intracellular #status predicted <TMT1>
F;96-120/Domain: transmembrane #status predicted <TMI>
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A;Residues: 6-19 <LYT>
R;Kurihara, K.; Hosoi, K.; Kodama, A.; Ueha, T.
R;Kurihara, K.; Hosoi, K.; Kodama, D.; Ueha, T.
Biochim. Biophys. Acta 1039, 234-240, 1990
A;Title: A new electrophoretic variant of alpha subunit
A;Reference number: S10758; MUID:90304196; PMID:2163680
A;Accession: S10758
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A;Title: Molecular cloning of rat brain Na,K-ATPase alpha-subunit cDNA. A;Reference number: A25171; MUID:85298352; PMID:2994074
A;Accession: A25171
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A; Residues: 1-41 < YAG>
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J. Cell Biol. 105, 1855-1865, 1987

A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural A; Title: Three differentially expressed Na, K-ATPase alpha subunit i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                          F;320-348/Domain:
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                                                                                           ;953-978/Domain:
                                                                                                                                         ;875-952/Domain:
                                                                                                                                                                                       :849-874/Domain:
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//Residues: 6, 'X', B-10, 'X', 12-16 <KUR>
//Residues: 6, 'X', S-10, 'X', 12-16 <KUR>
//Residues: 6, 'X', S-10, 'X', 12-16 
//Oute: designated alpha-S form; thought to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Molecule type: mRNA
;Residues: 489-533 <SCH>
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,Residues: 1-67,'PV',70-174,'E',176-187,'V',189-334,'V',336-1023 <HER>
,Cross-references: EMBL:M28647; NID:g205631; PIDN:AAA41671.1; PID:g205632
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;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard,
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     ;376/Active site: Asp
                                                                                                                                                                                                                                                ;787-810/Domain:
                                                                                                                                                                                                                                                                                              587-783/Domain:
                                                                                                                                                                                                                                                                                                                                                 :349-786/Domain:
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hem. 102, 43-58, 1987
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                                                                                      transmembrane #status predicted <TM4>
intracellular #status predicted <INT3>
ATPase nucleotide binding domain homology
transmembrane #status predicted <TM5>
transmembrane #status predicted <TM6>
intracellular #status predicted <INT4>
transmembrane #status predicted <INT4>
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                                        extracellular
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#status predicted <TM3>
#status predicted <TM4>
                                        #status predicted <EXT>
     intermediate)
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                                                                                                                                                                                                                                                C;Accession: A60444
R;Verrey, F.; Kairouz, P.; Schaerer, E.;
Am. J. Physiol. 256, F1034-F1043, 1989
A; Molecule type:
                                                   A; Status: not compared with
                                                                                                           A; Accession: A60444
                                                                                                                                         A; Reference number:
                                                                                                                                                         A;Title: Frimary sequence of Xenopus laevis Na(+)-K(+)-ATPase
A;Reference number: A60444; MUID:89285429; PMID:2544104
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1023 <AINI>
A;Residues: 1-1023 <AINI>
A;Residues: 1-1023 <AINI>
A;Cross-references: UNIPROT: P30714; EMBL: Z11798; NID: 962491; PIDN: CAA77842.1; PID: 962491
A;Experimental source: urinary bladder cell line TBM 18-23
A;Mote: submitted to the EMBL Data Library, March 1992
A;Note: sequence extracted from NCBI backbone (NCBIP: 111876)
A;Note: sequence extracted from NCBI backbone (NCBIP: 111876)
C;Superfamily: NA+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transpricts ATP; heterodimer; hydrolase alpha-1 chain #status predicted <MAT>
F;6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;130-149/Domain: transmembrane #status predicted <TM2>
F;150-290/Domain: intracellular #status predicted <TM72>
F;150-290/Domain: intracellular #status predicted <TM72>
F;291-313/Domain: transmembrane #status predicted <TM3>
F;320-348/Domain: transmembrane #status predicted <TM4>
F;349-786/Domain: intracellular #status predicted <TM4>
F;547-783/Domain: ATPase nuclectide-binding domain homology
F;587-810/Domain: transmembrane #status predicted <TM5>
F;849-874/Domain: transmembrane #status predicted <TM6>
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A;Title: Primary sequence and functional expression of a novel ouabain-resistant Na,K-A'A;Reference number: A43451; MUID:92380991; PMID:1380956
A;Accession: A43451
N;Alternate names: sodium pump alpha chain
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change C;Accession: A43451; S24650
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                                                                                   Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain
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Pred. No.
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Pred. No.
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3;
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                                                                                            precursor -
        #text_change 09-Jul-2004
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-1025

conceptual translation

Fuentes, P.;

Geering,

K.; Rossier,

B.C.;

Kraeh 'n

and

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1027 <SCH>
A;Residues: 1-1027 <SCH>
A;Residues: 1-1027 <SCH>
A;Residues: 1-1027 <SCH>
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C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium tr ;589-785/Domain: ATPase nucleotide-binding domain homology cATN- F;217,485/Binding site: carbohydrate (Asan) (covalent) #status predicted F;378/Active site: Asp (aspartylphosphate intermediate) #status predicted F;510/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 41
S03632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Schoenrock, C.; Morley, S.D.; Okawara, Y.; Lederis, K.; Richter, D. Biol. Chem. Hoppe-Seyler 372, 279-286, 1991
A;Title: Sodium and potassium ATPase of the teleost fish Catostomus commersoni. A;Reference number: S14740; MUID:91282983; PMID:1711856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                           Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - N;Alternate names: sodium pump alpha chain C;Species: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                R;Lebovitz, R.M.; Takeyasu, K.; Fambrough, D.M.
BMBO J. 8, 193-202, 1989
A;Title: Molecular characterization and expression of the
A;Reference number: S03632; MUID:89231618; PMID:2540956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
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                                                                           A; Reference number: S03632;
A; Accession: S03632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;791-814/Domain:
F;853-878/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,294-316/Domain: transmembrane #status predicted <TM3>
1,323-351/Domain: transmembrane #status predicted <TM4>
1,323-751/Domain: intracellular #status predicted <TM4>
1,352-790/Domain: ATPase nucleotide-binding domain homology
1,791-814/Domain: transmembrane #status predicted <TM5>
1,853-878/Domain: transmembrane #status predicted <TM6>
1,853-878/Domain: intracellular #status predicted <TM7>
1,853-956/Domain: transmembrane #status predicted <TM7>
1,957-982/Domain: transmembrane #status predicted <TM7>
1,957-982/Domain: transmembrane #status predicted <TM7>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
;Molecule type: mRNA
;Residues: 1-1038 <LEB>
                                                                                                                                                                                                                                                                               Date: 30-Jun-1993 #sequence_revision 30-Jun-1993; Accession: S03632; S07049
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Pred. No. 2.4e+02;
l; Mismatches · 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 1; 1
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                     #text_change 09-Jul-2004
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                                                                                                                                                                   (Na+K)-ATPase alpha-subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Drosophila melanogaster)
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R;Gattung, S.; Holmes, A.
R;Gattung, S.; Holmes, A.
submitted to the EMBL Data Library, December 1997
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F;114-165/Domain: transmembrane #status predicted <TM2>
F;146-165/Domain: transmembrane #status predicted <TM2>
F;166-205/Domain: transmembrane #status predicted <TM2>
F;306-328/Domain: transmembrane #status predicted <TM3>
F;305-363/Domain: intracellular #status predicted <TM4>
F;335-98/Domain: intracellular #status predicted <TM4>
F;602-998/Domain: ATPase nucleotide-binding domain homology
F;802-825/Domain: transmembrane #status predicted <TM6>
F;890-966/Domain: intracellular #status predicted <TM6>
F;890-966/Domain: intracelu
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A;Note: the sequence from Fig. 9 is inconsistent wi
A;Note: it is uncertain whether Met-1 or Met-40 is
A;Note: it is uncertain whether Met-1 or Met-40 is
A; Gilmore-Heber, M.; Benz Jr., E.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F42G8.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;994-1038/Domain: extracellular #status predicted cEXT> F;991/Active site: Asp (asparty)phosphate intermediate) #st F;539/Binding site: ATP (Lys) #status predicted F;732,736,741/Active site: Asp, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 3R 93B
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 258, 203-207, 1989
A;Title: Amplification of the phosphorylation site - ATP-binding site A;Reference number: S07049; MUID:90092469; PMID:2557235
                                                                                                                                                                                                                                                         A; Map position: 4
A; Introns: 31/1; 71/3; 102/2; 225/1; 279/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-353 <GAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T32638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: The sequence A;Reference number: Z21203
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                                                                                                                                                                                                                                                                                                                              A;Gene: CESP:F42G8.6
                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:044510; EMBL:AF038618; PIDN:AAB92067.1; GSPDB:GN00022; A;Experimental source: strain Bristol N2; clone F42G8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 397-521 < VAR>
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;113-135/Domain: transmembrane #status predicted <TMl>
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                                                                                                           Similarity
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CADGPTLR---EWISFCG
                                                                                                                                                                                                                   Porphyra purpurea
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                                                                            Conservative
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                                                                                                           39.0%;
38.9%;
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   17
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                                                                                                                                                                                                                      hypothetical protein
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Pred. No. 2.4e+02;
                                                                                                           Score 42.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon
                                                                            Mismatches
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                                                                                                           5; DB 2;
1e+02;
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                                                                                                                                              Length 353;
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256 CGDNPTITAPIDYVLFCG

Q III

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F:131-271/Domain: intracellular #status predicted <INT2>
F;272-296/Domain: transmembrane #status predicted <ING3>
F;301-329/Domain: transmembrane #status predicted <ING3>
F;301-367/Domain: intracellular #status predicted <INT>
F;308-764/Domain: AlPase nucleotide-binding domain homology
F;768-791/Domain: transmembrane #status predicted <INT5>
F;868-791/Domain: transmembrane #status predicted <ING5>
F;856-936/Domain: intracellular #status predicted <ING4>
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A;Residues: 1-1004 <mAC>
A;Residues: 1-1004 <mAC>
A;Cross-references: VNIPROT:P28774; EMBL:X56650; NID:g10933; PIDN:CAA39972.1; PID:g10934
A;Cross-references: VNIPROT:P28774; EMBL:X56650; NID:g10933; PIDN:CAA39972.1; PID:g10934
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F;2-1004/Product: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Macias, M.T.; Palmero, I.; Sastre, L. Gene 105, 197-204, 1991
A;Title: Cloning of a cDNA encoding an Artemia franciscana Na/K ATPase alpha-subunit. A;Reference number: JH0470; MUID:92039032; PMID:1657719
A;Accession: JH0470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain (clone pArATNa136) - brine C;Species: Artemia franciscana (brine shrimp) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 C;Accession: JH0470; S24196
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-1302 < OHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: Prediction of the coding sequences of unidentified human genes. A;Reference number: Z14073
A;Accession: T00038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Ohara, O.; Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Nomura, N. submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
C;Accession: T00038
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F;357/Active site: Asp (asparty)phosphate intermediate) #status
F;489/Binding site: ATP (Lys) #status predicted
F;698,702,707/Active site: Asp, Asp, Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein KIAAO289 - human (fragment)
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                                                                                                                            Matches
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Best Local :
                                                                                                                                                                                                                                                                                                       Experimental source: brain
                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:AB006627; NID:d1170680; PIDN:BAA22958.1; PID:d1023834
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                                                                                                                            Conservative
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                                                                                                                                                  39.0%;
                                                            ---ADGPTLREWISFCG 17
                                                                                                                     Score 42.5; DB 2;
Pred. No. 3.5e+02;
1; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Pred. No. 2.7e+02;
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Search completed: September Job time : 17.7266 secs

1, 2005,

16:22:47

RESULT 45

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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, lerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel., Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein Atu2063 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AH2829
                                                                                                                                                                                                                                                       A;Residues: 1-141 <KUR>
A;Cross-references: UNIPROT:Q8UDQ8; GB:AE008688; PIDN:AAL43054.1; PID:g17740521; GSPDB:(A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                   A;Gene: Atu2063
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: AH2829
                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                                                                               Query Match
Best Local
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                                                                                                                    Similarity
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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109
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 ,
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Q7V2B2
Q9RKM5
Q7V2K4
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Q77UR5
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(without alignments)
137.677 Million cell updates/sec
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O7uge4 rhodopirell
O9nex6 caenorhabdi
O98a97 rhizobium l
O8kjf9 rhizobium l
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O8kzm3 candida tro
O8kzm4 candida tro
O9kie9 streptomyce
O9rkm5 streptomyce
O6vmh4 streptomyce
O6vmh4 streptomyce
O7ulr5 rhodopirell
O7qc63 anopheles g
O7ulr5 rhodopirell
O82cw2 streptomyce
O6mx73 azoarcus sp
O8dhx7 synechococc
O89pe8 bradyrhizob
O9uaf5 caenorhabdi
O966d4 caenorhabdi
O966d4 caenorhabdi
O966d9 parteriopha
O8clj9 kluyveromyc
O978b3 bradyrhizob
O98fpc4 corynebacte
O7mv49 porphyromon
O81852 homo saplen
O63kh8 burkholderi
O7vwy61 bordetella
O7w9k1 bordetella
O7w9k1 bordetella
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Q6B1Z6
Q8AY57
Q6VYM7
AT1A_TORCA
A1A1_HUMAN
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Q66GJ0
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Q69PA9
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Q7UQE4;
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein Y105E8A.21.
ORFNames=Y105E8A.21;
Caenorhabditia - 2
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NCBI_TaxID=117;
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InterPro; IPR003169; GYF.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
PROSITE; PS50829; GYF; 1.
EMBL; AL132876; CAC48140.1; -.
WormBase; WBGene00013679; Y105E8A.21.
WormPep; Y105E8A.21; CE25162.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003676; F:nucleic acid binding; GO; GO:0008270; F:zinc ion binding; IEA.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=99069613;
                                                                                                                                                                                                              Submitted (AUG-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                  Sulston
                                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: investigating biology."; Science 282:2012-2018(1998).
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Pred. No. 2.2;
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475F670F02C78E9B CRC64;
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Q8KJF9;
01-OCT-2002
01-OCT-2002
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Pfam; PF02515; CoA_transf_3; 1.
Complete proteome.
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MEDLINE=21082930; PubMed=11214968;
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Rhizobium loti (Mesorhizobium
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01-OCT-2001
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HSSP; P77407; 11
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STRAIN=R7A;

MEDLINE=21999272; PubMed=12003951;

DOI=10.1128/JB.184.11.3086-3095.2002;

Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W.,
                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation updat
pUTATIVE RACEMASE/DEHYDRATASE PROTEIN.
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                                                                                                                                                                                                                                                                                   Rhizobium loti (Mesorhizobium loti).
                                                                                                                                                                                                                                                                                                                   Name=msi181;
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Best Local S
Matches 9
                                                   PubMed=12614607; DOI=10.1016/S0022-2836(03)00038-X;
Alrenne T.T., Torkko J.M., Van den plas S., Sormunen R
Kastaniotis A.J., Wiserenga R.K., Hiltunen J.K.;
"Structure-function analysis of encyl thioester reduct mitochondrial maintenance.";
J. Mol. Biol. 327:47-59(203).
-1- FUNCTION: Required for respiration and the mainten mitochondrial compartment. May have a role in the synthesis of fatty acids.
-1- CATALYTIC ACTIVITY: Acyl-(acyl-carrier protein] + 2,3-dehydroacyl-(acyl-carrier protein] + ADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossback Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.T. "Comparative sequence analysis of the symbiosis island of Mesorhizobium loti strain R7A.";

J. Bacteriol. 184;3086-3095(2002).
EMBL; AL672113; CAD31586.1; -.
HSSP; P77407; 1PQY.
GO, GO:0008152; P:metabolism; IEA.
GO, GO:0008152; P:metabolism; IEA.
InterPro; IPR003673; CALB_BAIF.
Pfam; pF02515; COA transf_3; 1.
SEQUENCE 389 AA; 42703 MW; 6678D2C96A7E5204 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8WZM3;
25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Encyl-[acyl-carrier protein] reductase [NADPH mitochondrial precursor (EC 1.3.1.10).
                                                                                                                                                                                                                                                Torkko J.M., Koivuranta K.T., Kastaniotis A.J., Airenne T.T., Glumoff T., Ilves M., Hartig A., Gurvitz A., Hiltunen J.K.; "Candida tropicalis expresses two mitochondrial 2-enoyl thioester reductases that are able to form both homodimers and heterodimers."; J. Biol. Chem. 278:41213-41220(2003).
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                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 20336;
                                                                                                                                                                                                                                                                                                                                                                                 respiratory competence.";
Mol. Cell. Biol. 21:6243-6253(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                        DOI=10.1128/MCB.21.18.6243-6253.2001;
Torkko J.M., Koivuranta K.T., Miinalainen I.J., Yagi A.I., Schn
Kastaniotis A.J., Airenne T.T., Gurvitz A., Hiltunen K.J.;
"Candida tropicalis Etrip and Saccharomyces cerevisiae Ybr026p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION.
STRAIN=ATCC 20336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycetales; mitosporic
               +++
                                                                                                                                                                                                                                                                                                                                                     SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS),
                                                                                                                                                                                                                                                                                                                         PubMed=12890667;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida tropicalis (Yeast).
          SUBUNIT: Homodimer and heterodimer with SUBCELLULAR LOCATION: Mitochondrion. SIMILARITY: Belongs to the zinc-containi
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ilarity 42.9%;
Conservative
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Pred. No. 21;
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                                                                                X-RAY CRYSTALLOGRAPHY (2.11 ANGSTROMS).

Airenne T.T., Torkko J.M., Hiltunen J.K.,

"Crystal structure of enoyl thioester reductase 2."

"Crystal structure of enoyl thioester reductase 2."

"Submitted (JUN-2002) to the PDB data bank.

-!- FUNCTION: Required for respiration and the main mitochondrial compartment. May have a role in the synthesis of fatty acids.

-!- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADPH.

2,3-dehydroacyl-[acyl-carrier protein] + NADPH.

2,3-dehydroacyl-[acyl-carrier with ETR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004
25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                          Torkko J.M., Koivuranta K.T., Kastaniotis A.J., Airenne T.T., Glumoff T., Ilves M., Hartig A., Gurvitz A., Hiltunen J.K.; "Candida tropicalis expresses two mitochondrial 2-enoyl thioester reductases that are able to form both homodimers and heterodimers J. Biol. Chem. 278:41213-41220(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
              This
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
NCBI_TaxID=5482;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=ETR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enoyl-[acyl-carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8WZM4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00107; ADH zinc N; 1.
3D-structure; Direct protein sequencing; Fatty acid Mitochondrion; NADP; Oxidoreductase; Transit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                  PubMed=12890667;
                                                                                                                                                                                                                                                                                                                                                                                                                       Candida tropicalis (Yeast).
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InterPro; IPR011032; GroES_like.
                                                       SUBCELLULAR LOCATION: Mitochondrion (By similarity) SIMILARITY: Belongs to the zinc-containing alcohol
                                        family. Quinone oxidoreductase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1GU7; X-ray; A/B=23-386.
1GUF; X-ray; A/B=23-386.
1GYR; X-ray; A/B/C=23-386
SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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(Rel. 45, Last sequence update)
(Rel. 45, Last annotation update)
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                                                                                                                                                                                                                                                                                                Koivuranta K.T., Kastaniotis A.
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42160
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Pred. No.
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Y->N: 0.1% of catalytic activity.
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                                                        dehydrogenase
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     a collaboration - MBL outstation
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                                                                                                                                                                                                                                                              RESULT 8
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Best Local S
Matches 8
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Q9KIE9;
01-OCT-2000
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01-JUN-2003
                                                                                               Q9M060;
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20323220; PubMed=10863099; DOI=10.1016/S0378-1119(0 Wu K., Chung L., Revill W.P., Katz L., Reeves C.D.;
"The FK520 gene cluster of Streptomyces hygroscopicus var. ascomyceticus (ATCC 14891) contains genes for biosynthesis polyketide extender units.";
Gene 251:81-90(2000)
EMBL; AF235504; AAF86384.1; -...
HSSP; P77407; 1PQY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
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                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Eukaryotic translation initiation factor 6 (EIF-6)-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomycineae; S
NCBI_TaxID=132248;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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TRANSIT 1 22 Mit
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3D_structure; Fatty acid biosynthesis; Mitochondrion; NADP;
                                                                                                                                                                                              Q9M060
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InterPro; IPR003673; CAIB BAII
Pfam; PF02515; COA transf-3; :
SEQUENCE 405 AA; 43696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Last sequence update)
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1; Mismatches
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Emoyl-[acyl-carrier protein] reductase
[NADPH, B-specific] 2.

91ABE00831F0C2E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49.5;
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Matches
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Q7V2B2;
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Q1-OCT-2003 (TrEMBLrel. 25, C
Q1-OCT-2003 (TrEMBLrel. 25, L
Q1-MAR-2004 (TrEMBLrel. 26, L
D1hydroorotase (EC 3.5.2.3).
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Benes V., Wurmbach E., D:
Lemcke K., Mayer K.F.X.,
Submitted (MAR-2000) to 1
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Arabidopsis thaliana (Mouse-ear eres).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Core e Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                         SEQUENCE FROM N.A.
                                                            Prochlorococcus.
NCBI_TaxID=59919;
                                                                                                                  Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
                                                                                                                                                       Name=pyrC;
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Pfam; PF01912; eIF-6; 1.
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  MEDLINE=22825698;
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GO; GO:0006413; P:translational
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bmitted (APR-2000) to the EMBL/GenBank/DDBJ databases
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8; Conserv
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                                                                                                                                                            OrderedLocusNames=PMM0569;
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245 AA;
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    PubMed=12917642;
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57.1%;
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al initiation; IEA.
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    DOI=10.1038/nature01947;
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T., Kamiya A.,
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Chen H.,
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Best Local S
Matches
                                                                                           HSSP; P05020; 1J79.
GO; GO:0004151; F:dihydroorotase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0019856; P:pyrimidine base biosynthesis; IEA.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR004721; DHOdimr.
InterPro; IPR002195; Dihydroorotase.
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MEDLINB-2196410; Pubmed=12000953; DOI=10.1038/417141a;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
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Nature 424.1042-1047(2003).
EMBL; EX572091; CAE19028.1; -.
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TIGRFAMB; TIGR00856; PYCC_dimer; 1.
PROSITE; PS00482; DIHYDROOROTASE 1; UNKNOWN
PROSITE; PS00483; DIHYDROOROTASE_2; 1.
                   PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH MERR; 1.
PROSITE; PS50937; HTH MERR 2; 1.
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putative MerR family transcriptional regulator.
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349 AA; 39958 MW;
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proteome; DNA-binding
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Streptomycetaceae; Streptomyces.
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Pred. No. 32;
2; Mismatches
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06VMH4;
05-JUL-2004
05-JUL-2004
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"Runctional angucycline-like antibiotic gene cluster in the terminal "Punctional angucycline-like antibiotic gene cluster in the terminal inverted repeats of the Streptomyces ambofaciens linear chromosome.";

Antimicrob. Agents Chemother. 48:575-588(2004).

Antimicrob. Agents Chemother. 48:575-588(2004).

EMBL; AY338477; AAR30165.1; -.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0000156; F:two-component response regulator activity; IEA.

GO; GO:0000156; P:two-component signal transduction system (p. . .; I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name-a-p-,
Pacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Li L., Bannantine J., Zhang
Submitted (SEP-2003) to the
EMBL; AE017232; AAS03801.1;
GO; GO:0005506; F:iron ion b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=ATCC 23877; PubMed=14742212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                          Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR009059; bi resp_regltr_C.
InterPro; IPR005158; BTAD.
InterPro; IPR001867; Trans_reg_C.
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NCBI_TaxID=1889;
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                                                                                                                                 STRAIN=k10;
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                Corynebacterineae; Mycobacteriaceae;
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                                                                                                                                                                   FROM N.A
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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46.7%;
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      binding;
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Last annotation updat
                                                                  Q., Amonsin A., Alt D., Kap
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                          Kapur V.;
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                                                                                             01-OCT-2003
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Pfam; PF00
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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InterPro; IPR000719; Prot_kinase.
InterPro; IPR003726; S_methyl_trans.
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GO; GO:0006898; F:homocysteine S-methyltransferase activit
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0006468; F:protein amino acid phosphorylation; IEA
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Name=cpcE;
                                                                  Similar to
                                                                                                                                                                                          Q7ULR5;
                                                                                                                                                                                                                               Q7ULR5
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GO:0006725; P:aromatic compound metabolism;
GO:0006118; P:electron transport; IEA.
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Pro; IPR001663; Ring_hydroxyl_A.
PF00355; Rieske; 1.
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Q82CW2;
01-JUN-2003
                                                                 EMBL; AP005042; BAC72938.1; -.
GO; GO:000567; F:DNA binding; IEA.
GO; GO:006355; P:regulation of transcription,
InterPro; IPR005471; HTH_ICLR.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
                                                                                                                                                                                           "Complete genome sequence and comparative microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
                                                                                                                                                                                                                                                                                                                                                                                                      Proc.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MA-4680;
MEDLING=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative IclR-family transcriptional regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR008938; ARM.
InterPro; IPR004155; PBS; lyase_HEAT
Pfam; PF03130; HEAT PBS; 1.
SMART; SM00567; EZ_HEAT; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Planctomycetes; Pla
Planctomycetaceae; Pirellula.
NCBI_TaxID=117;
                                                                                                                                                                                                                                                                         Ikeda H., Ishikawa J., Hanamoto
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of an avermitilis: deducing t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces avermitilis.
Bacteria; Actinobacteridae; Actinomycetales;
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GO; GO:0016829; F:lyase activity; IEA
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SEQUENCE
                                              Pfam; PF01614; IclR;
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolites.";
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                                                                                                                                                                                                                                                                                                                             MEDLINE=22608306; PubMed=12692562;
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Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
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26142 MW;
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Pred. No. 37
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  F63B1705578EEE67 CRC64;
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                                                                                                                            DNA-dependent;
                                                                                                                                                                                                                                                                                                        Kikuchi H.,
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=BP-1;
MEDLINE=22225144; PubMed=12240834;
MEDLINE=2225144; PubMed=12240834;
MEDLINE=2225144; PubMed=12240834;
MEDLINE=2225144; PubMed=12240834;
MEDLINE=2225144; PubMed=12240834;
MEDLINE=2225144; PubMed=12240834;
MEDLINE=22225144; PubMed=12240834;
MEDLINE=2225444; PubMed=12240834;
MEDLINE=22255444; PubMed=12240834;
MEDLINE=22255444; PubMed=12240834;
MEDLINE=22255444; PubMed=1224084;
MEDLINE=22255444; PubMed=1224084;
MEDLINE=22554464; PubMed=1224084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2003) to the EMBL; BX682953; CAF21985.1; Hypothetical protein. SEQUENCE 94 AA; 9829 MW;
                                                                                Nakamura Y., Kaneko T., Sato S., İkeuchi M., Katoh H., Sasamot Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002)
                                                                                                                                                                                                                                                                                                                                                                            Synechococcus elongatus (
Bacteria; Cyanobacteria;
NCBI_TaxID=32046;
[1]
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01-MAR-2003 (TrEMBLrel.
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Bacteria; Proteobacteria;
Rhodocyclaceae; Azoarcus.
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05-JUL-2004
                                                        EMBL; AP005375; BAC09368.1; -.
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     14644 MW;
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Pred. No. 18;
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     EBB44691E7DD1E12 CRC64;
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., Kishida Y.,
. Nakazaki N.,
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01-JUN-2003
01-OCT-2003
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Q9UAT5;
01-MAY-2000
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                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Cree 01-MAY-2000 (TrEMBLrel. 13, Last 01-OCT-2003 (TrEMBLrel. 25, Last Hypothetical protein C01B4.7, Name=C01B4.7; ORFNames=C01B4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
WormBase Consortium; "Genome sequence of the nematode C. elegans: a platform "Genome sequence of the C. elegans Sequencing Consort
                                                                    SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613;
                                                                                                                                                                                         Caenorhabditis elegans.
Bukaryota; Metazoa; Nem
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HSSP; P19920; 1N62.
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Kaneko T., Nakamura
Sasamoto S., Watanak
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Bacteria; Proteobacteria;
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Name=cutM; OrderedLocusNames=blr3534;
                                                                                                                                                NCBI_TaxID=6239;
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                                                                                                                                                                           Rhabditidae;
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ra Y., Sato S., Minamisawa K., Uci
nabe A., Idesawa K., Iriguchi M.,
oto M., Shimpo S., Tsuruoka H., W
                                                                          PubMed=9851916;
                                                                                                                                                                                           Nematoda;
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4 M., Kawashima k
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Best Local :
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WormBase; WBGene00015271; C01B4.7.
WormBep; C01B4.7; CE20476.
G0; G0:0016021; C:integral to membrane; IE
G0; G0:0005215; F:transporter activity; IE
G0; G0:0006810; P:transport; IEA.
Interpro; IPR007114; MFS.
PROSITE; P850850; MFS; 1.
Hypothetical protein.
SEQUENCE 475 AA; 53094 MW; 79095D45577
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[2]
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Y19D10A.4.
Name=Y19D10A.4; ORFNames=Y19D10A.4;
Caenorhabditis elegans.
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Smith A., Wamsley P., Fronick W.;
Smith A., Wamsley P., Fronick W.;
"The sequence of C. elegans cosmid C01B4.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
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MEDLINE-99069613; PubMed-9851916;

WormBase Consortium;

Wenome sequence of the nematode C.

"Nenome sequence of the C. elegan

investigating biology. The C. elegan

Science 282:2012-2018 (1998).
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  SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                                                                      "The sequence of C.
Submitted (MAR-1999)
                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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                                                                                                                 Johnson D.;
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EMBL; AC006722; AAK68417
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                                                                                                                              Similar to sp|P40825
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InterPro; IPR011013; Gal_mut_like
InterPro; IPR007114; MFS.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004034; F:aldose 1-epimerase activity;
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0005012; P:gdalactose metabolism; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR008183; Ald1_epimerase.
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ORFNames=KLLA0F02431g;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
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25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
Similar to sp|P40825 Saccharomyces cerevisiae YOR
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PROSITE; PS50850; MFS; 1.
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Dujon B., Shern Lafontaine I.,
                    Genolevures;
                               SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                              Saccharomycetales;
NCBI_TaxID=284590;
                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacci
Saccharomycetales; Saccharomycetaceae; Kluyveromyces
                                                                                               Kluyveromyces lactis NRRL Y-1140
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I., de Montigny J.,
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Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souciet J.L.;
"Genome evolution in yeasts.";
Nature 40.75.54.
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Q9Y8B3;
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MEDLINE-20171859; PubMed=10705373;

DOI=10.1002/(SICI)1097-0061(20000330)16:5<451::AID-YEA540>3.0.CO;2-O;

Pereira M., Felipe M.S.S., Brigido M.M., Soares C.M.A., Azevedo M.O.;

"Molecular cloning and characterization of a glucan synthase gene from the human pathogenic fungus Paracoccidioides brasiliensis.";
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Pfam; PF01411; tRNA-synt_2c; 1.
PRINTS; PR00980; TRNASYNTHALA.
the human pathogenic fungus Paracoccidioides brasilie Yeast 16:451-462(2000).

Yeast 16:451-462(2000).

EMBL; AF148715; AAD37783.1; -.

GO; GO:0000148; C:1,3-beta-glucan synthase complex; I GO; GO:0016020; C:membrane; IEA.

GO; GO:0003843; F:1,3-beta-glucan synthase activity; GO; GO:0003675; F:beta-1,3 glucan biosynthesis; IEA.

InterPro; IPR003440; Glyco_trans_48.

InterPro; IPR002114; HPr_SerP_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paracoccidioides brasiliensis.
Eukaryota; Fungi; Ascomycotta; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Paracoccidioides.
NCBI_TaxID=121759;
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01-NOV-1999 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Glucan synthase.
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR00344; alaS; 1.
PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003156; Pesterase_DHHAl.
InterPro; IPR002318; tRNA-synt_2c.
InterPro; IPR006193; tRNA-synt_Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Pb01;
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L; CR382126; CAG97897.1; -.
GO:004813; F:alanine-tRNA ligase activity
GO:0005524; F:ATP binding; IEA.
GO:0003676; F:nucleic acid binding; IEA.
GO:0006419; P:alanyl-tRNA aminoacylation;
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Last sequence
Last anno
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Pred. No.
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ACCOMPANA A REPRESENTATION OF THE PROPERTY OF 
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Q6KG99
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SEQUENCE 166 AA; 19296 MW; 5
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Q6KG99;
05-JUL-2004
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PROSITE;
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SEQUENCE
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Q89HD8;
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Bacteriophage Felix 01.
Viruses; dsDNA viruses,
NCBI_TaxID=77775;
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Blr6053 prot
                                                                                                                                                 "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002). EMBL; AP005957; BAC51318.1; -.
                                                                                                                                                                                                                                                                                               MEDLINE=22484998; Pub
Kaneko T., Nakamura Y.
Sasamoto S., Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
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01-JUN-2003
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                                                                                                                                                                                                                                                     Kohara M., Matsumoto M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=USDA110;
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                                                                                                                              HSSP; P27017; 1Q00
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TE; PS00589; PTS_HPR_SER; I
NCE 1926 AA; 220574 MW;
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426 AA;
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                                                                                                                                                                                                                                                                                                                                                         PubMed=12597275;
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                                                                            47042 MW;
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66.7%;
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. A., Idesawa K., Irıy.
. Phimpo S., Tsuruoka H
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Pred. No. 3
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                                                                            AE20AA1EC6CBE038
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a K., Iriguchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characterization."
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                                                                                                                                                                                                                                                                               H., Wada
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'ada T., Yama'
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Gojobori
                                                                                                                                                                         DOI=10.1128/JB.185.18.5591-5601.2003;

Nelson K.E., Fleischmann R.D., DeBoy R.T., Paul Eisen J.A., Daugherty S.C., Dodson R.J., Durkir Haft D.H., Kolonay J.F., Nelson W.C., Mason T.N. Granger D., Tettelin H., Dong H., Galvin J.L., Dewhirst F.E., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=YS-314;
MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura
Nishio S. Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                    "Complete genome sequence of the oral Porphyromonas gingivalis strain W83.", J. Bacteriol. 185:5591-5601(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=PG1251;
Porphyromonas gingivalis (Bacteroides Bacteria; Bacteroidetes; Bacteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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OrderedLocusNames=CE1858;
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22829867; PubMed=12949112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=837;
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                                                           AE017176; AAQ66334.1;
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10632 MW; 6C
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Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                         bacterium
                                                                                                                                                                                                                                             n I.T., see S., Gwinn M./
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         RESULT 28
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RESULT 27
Q8N85
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                                                                                                                                                                                                                                                                                                                                                RX PubMed=14702039; DOI=10.1038/ng1285;
RA PubMed=14702039; DOI=10.1038/ng1285;
RA Wakamatsu A., Hayashi K., Satto H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Satto H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Abe K., Kanda K., Katsuta N., Sarto K., Tanikawa M., Yamazaki M.,
RA Abe K., Kamihara K., Katsuta N., Sarto K., Tanikawa M., Yamazaki M.,
RA Abe K., Kamihara M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takahashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ono Y., Takahashi-Pujii A., Hara H., Tanase T., Nomura Y.,
RA Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T., Kubano J.,
RA Masashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shinizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai M., Matanabe M., Kawakami G., Ohara O., Isogai T., Sugano S.,
RA Nakai M., Matanabe M., Kawakami A., Matai M., Matanabe M., Kawakami A.,
RA Nakai M., Matanabe M., Ka
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Q8N852;
01-OCT-2002
01-OCT-2002
01-OCT-2002
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01-OCT-2002 (TrEMBLrel. 22, La
01-OCT-2002 (TrEMBLrel. 22, La
Hypothetical protein FLJ40008.
Homo sapiens (Human).
                                                                                                                                                                                                                                           EMBL; AKO
SEQUENCE
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EMBL; AK097327; BAC04999.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                             CDNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Stomach;
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                                     GGCA----DGPTLREWISF
GGCGLIVKHGMTLRNWASF
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           17782
                                                                                                                                                   42.2%;
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Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B4421EB01D186859 CRC64;
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                                                                                                                          Mismatches
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PRELIMINARY;

PRT;

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Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,

RA Bentley S.D., Sebalhia M., Thomson N.R., Bason N., Beacham I.R.,

RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,

RA Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,

RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,

RA Keith K.B., Maddison M., Moule S., Price C., Quail M.A.,

RA Rabbinowitesch E., Rutherford K., Sanders M., Simmonds M.,

RA Rabbinowitesch E., Stevens K., Tumapa S., Vesaratchavest M.,

Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;

RA "Genomic plasticity of the causative agent of melioidosis,

Burkholderia pseudomallei.";

EMBL; BX571966, CAH38855.1;

W Hypothetical protein
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                                                                       SEQUENCE FROM N.A.

STRAINSTONAMMA I / ATCC BAA-589 / NCTC 13251;

WEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

WEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Parkhill J., Sebalhia M., Preston A., Murphy L.D., Thomson N.R.,

A A Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quall N.A.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

AA Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

AF Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

AR Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

AR Abbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

BAAR Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella paragerrussis and Bordetella bronchiseptica.";

Bordetella 53:32-40(2033).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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25-OCT-2004
25-OCT-2004
25-OCT-2004
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
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Burkholderiaceae; Burkholderia.
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Burkholderia; Proteobacteria; Betaproteobacteria; Burkholderiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella pertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative lipoprotein. OrderedLocusNames=BP2072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alcaligenaceae; Bordetella.
                                                      EMBL; BX640417; CAE42350.1; -.
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  proteome; Lipoprotein.
196 AA; 21519 MW;
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162 AA; 1
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88.9%;
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Pred. No. 44;
     FF6E2E86B5EE9968 CRC64
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REDINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Chillingworth T., Collins M., Cromin A., Davis P., Doggett J.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

RT "Comparative analysis of the genome sequences of Bordetella pertussis,

RT Bordetella parapertussis and Bordetella bronchiseptica.";
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Q8GVF5,
Q8GVF5,
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Q1-mar-2004 (TremBlrel. 26, Last annotation factor
                                                                                                                                                                Putative eukaryotic translation initiation factor 6.

Name=001340 C08.131;
Oryza sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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SEQUENCE
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Bacteria; Proteobacteria;
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     Sasaki T., Matsumoto T., Katan
"Oryza sativa nipponbare(GA3)
clone:OJ1340 CO8.";
Submitted (MAY-2002) to the EU
                                                                                                                                         NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BX640428; CAE37057.1; -.
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       to the EMBL/GenBank/DDBJ databases
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                                                                               Katayose Y.;
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Pred. No. 53;
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Gramene; Q8GVF5;...
GO; GO:0003743; F:translation initiation factor activity; IEA.
GO; GO:0006413; P:translational initiation; IEA.
InterPro; IPR002769; eIF6.
InterPro; IPR002769; eIF6.
Pfam; PF01912; eIF-6; 1.
ProDom; PD006880; eIF6; 1.
SMART; SM00554; eIF6; 1.
TIGRPAMB; TIGR00323; eIF-6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99255950; PubMed=10322640;
DOI=10.1002/(SICI)1520-6408(1999)24:3/4<319::AID-DVG15>3.0.CO;2-#;
Nicolas S., Caubit X., Massacrier A., Cau P., Le Parco Y.;
"Two Nkx-3-related genes are expressed in the adult and regenerating central nervous system of the urodele Pleurodeles walti.";
Dev. Genet. 24:319-328(1999).
-i- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pleurodeles waltlii (Iberian ribbed newt)
Eukaryota; Metazoa; Chordata; Craniata; Vo
Amphibia; Batrachia; Caudata; Salamandroi
                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription fractor
GO; GO:006355; F:regulation of transc:
InterPro; IPR001356; Homeobox.
InterPro; IPR000957; Homeodomain_like.
InterPro; IPR000907; HTM lambrepressr.
Pfam; PF00046; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U88714; AACO8704.1; -. HSSP; P22808; INK3. C:nucleus; II GO; GO:0005634; C:nucleus; II GO; GO:0003700; F:transcript:
                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 275 AA; 30341 MW; 4519CD44
                                                                                                                                                                                                                                                                                    PRINTS; PR00024; HOMEOBÓX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=PwNkx-3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP005292;
32
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                                                                                                               Similarity
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CAPGPACGDWRRLCAG
                                            CADGPTLREWISFCGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1G62.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB Pred. No. 66; 3; Mismatches
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                                                                                            1;
                                                                                                                  Score 46; DB
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EB526A7DD103291B CRC64;
                                                                                                                                                                                          4519CD44E3348DE0 CRC64;
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275
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DNA-dependent; IEA.
                                                                                                                                           Length 275;
                                                                                                 Indels
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RESULT

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Q7PPP6
ID Q7PPP6
ID Q7PPP6
AC Q7PPP6
DT 01-MAR-2004
DT 01-MAR-2004
DE ENSANGP000000
GN Name=ENSANGGI
OS Anopheles gar
OC Enkaryota; M
OC Neoptera; En
OC NCGI_TAXID=11
EN [1]
EN 
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Q88NU2
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Best Local S
Matches 8
                               Query Match
Best Local &
   Matches
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Q88NU2;
01-JUN-2003
01-JUN-2003
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                                                                                                                                           "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002). EMBL; AE016778; AAN66737.1; -. TIGR; PP1112; -. Complete proteome; Hypothetical protein. SEQUENCE 403 AA; 42380 MW; 4D71AA1F370C58A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINES 242306; PubMed=12534463;

MEDINES 242306; PubMed=12534463;

Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,

Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,

Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,

Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,

Hance I., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,

Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,

Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim (

Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
-i-CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonadaceae; Pseudomonas.
NCBI TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=PP1112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                               Kiewitz C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
L; AAAB01008944; EAA10075.2;
GO:0008898; F:homocysteine
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PF02574; S-methyl_trans; 1.
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Similarity
8; Conserv
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3 (TrEMBLrel. 24,
3 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           putida (strain KT2440).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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   Conservative
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                               42.2%;
61.5%;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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   1;
                                  Score 46; DB 2;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                             Length 403;
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Q9P858
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Matches 8
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01-OCT-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nawson J.M., Cutler S.B., Ca
Submitted (MAY-2000) to the
EMBL; AJ277966; CAB91876.1;
Hypothetical marris
                                                                                                                                                                        Rabus R., Ruepp A., Frickey T., Rattei T., Fa
Bauer M., Zibat A., Lombardot T., Becker I.,
Teeling H., Leuschner W.D., Gloeckner F.-O.,
                                                                                                                                                                                                                                                                                                                                        Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; SEQUENCE 443 AA; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                           from permanently cold Arctic sedimen
Bnviron. Microbiol. 6:887-902(2004).
BMBL; CR522870; CAG37750.1; -.
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                                                                                                                                                           Klenk H.-P.;
                                                                                                                                                                                                                                       PubMed=15305914;
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                                     Pfam; PF02696; UPF0061; 1.
                                                           InterPro; IPR003846; UPF0061.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                      genome of Desulfotalea
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                                                                                                                                      psychrophila,
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Pred. No. 1
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5F401BE29D89323D CRC64
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, Gellner K.,
N., Amann R.,
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Vanbrunt A., Nguyen C., Du F., Lamar B., Courthey L., Kalicki J.,

Vanbrunt A., Nguyen C., Du F., Lamar B., Courthey L., Kalicki J.,

Vanbrunt A., Nguyen C., Du F., Lamar B., Courthey L., Kalicki J.,

Van Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

Van Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

Van Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

Van Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,

Van Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,

Van Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,

Van Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,

Van Hiller N., Vang S.-P., Schultz B.R., Wallis J.W., Spieth J.,

Van Wendl M.C., Yang S.-P., Schultz B.R., Wohldmann P.E., Cook L.L.,

Van Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,

Van Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,

Van Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,

Van Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,

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Van Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,

Van Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,

Van Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,

Van Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,

Van Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,

Van Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B.,

Van Clifton S.W., Chissoe S.L., Mar
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10775527;
Sacksteder K.A., E
Geisbrecht B.V., (
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HUMAN
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                                                                                                                                               Nature 424: 157-164 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R., Wylle K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.B. Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.B., Cordes M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of the alpha-aminoadipic semialdehyde synthase which is defective in familial hyperlysinemia.";

'm. J. Hum. Genet. 66:1736-1743 (2000).
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Mammalia; Eutheria;
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               FUNCTION: A bifunctional enzyme that catalyzes the first t in lysine degradation. The N-terminal and the C-terminal c lysine ketoglutarate reductase and saccharopine dehydrogen activity, respectively.

CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine NADP(+) + H(2)0 = L-lysine + 2-oxoglutarate + NADPH.

CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine)
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Cox R.P., Gould S.J., Ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=12853948; DOI=10.1038/nature01782;
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n analysis
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Pred. No. 1.3e
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, Green E.D.,
                                                                                                      dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pepin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  к.н.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isak A.,
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RESULT 38
Q9Y87
ID Q9Y87
AC Q9Y87
AC Q9Y87
DT 01-NO
DT 01-JU
DE Gluca
GN Name=
OS Coccii
OC Eukar
OC Onyge
OX NCBI
RN [1]
RN [1]
RP SEQUE
RC STRAI
RA Siege
RL Submi
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Best Local S
Matches 7
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                  Q9Y878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
STRAIN-Silveira;
Siegel E.M., Orsborn
Submitted (MAR-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                            Coccidioides posadasii.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007698; InterPro; IPR007886; InterPro; IPR005097;
                                        SEQUENCE
                                                                                                                       Name=FKS1
                                                                                                                                    GLucan
                                                                                                                                                01-JUN-2003
                                                                                                                                                             01-NOV-1999
                                                                                                                                                                           01-NOV-1999
                                                                                                                                                                                       Q9Y878;
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reactome; Q9UDR5; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:17366; AASS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF229180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Lysine degradation; Saccharopine pathway; first step. PATHWAY: Lysine degradation; Saccharopine pathway; second step. SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Mitochondrial (By similarity).
TISSUE SPECIFICITY: Expressed in all 16 tissues examined with highest expression in the liver.
INDUCTION: Induced by starvation (By similarity).
DISEASE: Defects in AASS are the cause of hyperlysinemia [MIM:238700]. Hyperlysinemia is an autosomal recessive conditionarcherized by hyperlysinemia lysinuria and variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erPro; IPR007698; AlaDh_PNT_C.
erPro; IPR007986; AlaDh_PNT_N.
erPro; IPR005097; Saccharop_dh.
m; PP01262; AlaDh_PNT_C; 1.
m; PP05222; AlaDh_PNT_N; 1.
n; PP03435; Saccharop_dh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dehydrogenase family.
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                                        FROM N.A.
                                                                                                                                                                                                                                                                     GATIESYISYCGG 635
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33
477
589
926 AA;
                                                                                                                                              ) (TrEMBLrel.
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) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                         Conservative
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926
589
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 to the
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12,
24,
 Galgiani J.N.;
e EMBL/GenBank/DDBJ databases
                                                                                                                                               Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion (By similarity).
Alpha-aminoadipic semialdehyde
Lysine-ketoglutarate reductase.
Saccharopine dehydrogenase.
S -> C (in Ref. 2).
                                                                                                                                                                                                                                                                                                                         Pred. No. 2.5); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            CB4194014351A18D CRC64;
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                                                                                                                                                                                                                                                                                                                   DB 1; 1.
2.5e+02;
3;
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                                                                                                                                                                                                     A
                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                   Length 926;
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Q7RUA5; 01-MAR-2004 (TIEM 01-MAR-2004 (TIEM 01-MAR-2004 (TIEM Hypothetical prot Name=NCU03933.1;

(TIENMBLrel. 26, Created)
(TIENMBLrel. 26, Last sequence update)
(TIENMBLrel. 26, Last annotation update)
protein B24B19.30.

Neurospora

crassa.

Fungi; Ascomycota;

Pezizomycotina; Sordariomycetes;

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RESULT
QBXZNS
ID
                                                                                                                                                                                                                      RESULT
Q7RUA5
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Best Local S
Matches
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Best Local S
Matches 9
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OBXZN5;
O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE TRANSCRIPTION REGULATOR PROTEIN.
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GO; GO:0000148; C:1,3-beta-glucan synthase complex; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0003843; F:1,3-beta-glucan synthase activity; IEA.
GO; GO:0006075; P:beta-1,3 glucan biosynthesis; IEA.
InterPro; IPR003440; Glyco_trans_48.
Pfam; PF02364; Glucan synthase; 1.
SEQUENCE 1902 AA; 217552 MW; 66FCC3C60E725F2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21681879; PubMed=11823852; DOI=10.1038/415497a; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Charlat M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Siguier D., Thebault P., Whalen M., Wincker P., Levy M., Siguier D., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0003700; F:transcription
GO; GO:0006355; P:regulation of
Pfam; PF00126; HTH 1; 1.
Pfam; PF03466; LysR_substrate; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the plant
Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=RS04642; OrderedLocusNames=RSc1360;
Ralstonia solanacearum (Pseudomonas sola
                                                                                                                                                                                                 Q7RUA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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ilarity 60.0%;
Conservative
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45.5;
Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathogen Ralstonia solanacearum.";
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transcription, DNA-dependent;
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RESULT Q6ZTT44
ID ZTT44
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1. - CAUDION: The sequence shown here is derived from an Emily Genbank D.D. All There and the sequence shown here is derived from an Emily Genbank D.D. All There and the sequence shown here is derived from an Emily Genbank D.D. All There and the sequence shown here is derived from an Emily Methods and the sequence shown here is derived from an Emily Methods and the sequence shown here is derived from an Emily Methods and the sequence shown here is derived from an Emily Methods and the sequence shown here is derived from an experiment of the sequence shown here is derived from an experiment of the sequence shown here is derived from an experiment of the sequence shown here is derived 
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Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AK12623; BAC86495.1; -
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Mammalia; Eutheria; Primates;
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NCBI_TaxID=5141;
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RESULT

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Hayashida K., Hayateu N., Hiramoto K., Hiraoka T., Harozane T., Hayashida K., Hayateu N., Hiramoto K., Hiraoka T., Hirozane T., Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T. Tomaru A., Toya T., Yasunishi A., Muramatan M.
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Q8C4M6;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                       Shibata K. Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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Carninci P., Shibata Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected
prepare full-length cDNA libraries for rapid discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Head;
STRAIN=C57BL/6J; FubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-JUN-2003
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STRAIN=C57BL/6J; TISSUE=Head;
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STRAIN=C57BL/6J; TISSUE=Head;
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Sciurognathi; Muridae;
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05-JUL-2004 (TrEMBLrel. 27,
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SEQUENCE FROM N.A.

STRAIN-CGA009 / ATCC BAA-98;

PubMedCa14704707; DOI=10.1038/nbt923;

Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti
Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F

Gibson J.L., Hansen T.E., Bobst C., Torres y Torres J.L., P

Harrison F.H., Gibson J., Harwood C.S.;
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Eur. J. Biochem. 250:332-341(1997).
EMBL; Y10500; CAA71527.1; -.
PIR; T44944, T44944.
G0; G0:0003677; F:DNA binding; IEA.
G0; G0:0006355; P:regulation of transcription,
Interpro; IPR010985; Met_repress_like.
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                                                                                                                                                                                                                                                         NCBI_TaxID=1076;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=RPA4277;
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NCBI_TaxID=2257;
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
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SEQUENCE
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EMBL; BX572606; CAE29718.1; -.
InterPro; IPR000338; ARM.
InterPro; IPR000357; HEAT.
Pfam; PF02985; HEAT; 2.
                                                                                                               "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yan
Tabata S.;
                                                                                                                                                                                                                                  Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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Copyright (c) 1993 - 2005 Compugen Ltd
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84.131 Million cell updates/sec
                     Aau 25821
Abb 72997
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RESULT 1
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99
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mum. compound (especially if modified, see features table) can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW09457
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                                                                                                                                                                             thrombocytopenia resulting
                                                                                                                                                                                            Thrombopoietin receptor-binding/activating peptide(s) and pepmimetic(s) - useful in treatment of haematological disorders,
                                                                                                                                                                                                                                                                              WPI; 1997-051883/05.
                                                                                                                                                                                                                                                                                                                            Mattheakis LC,
                                                                                                                                                                                                                                                                                                                                                     Dower WJ,
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                                                                                                                             Claim 18; Page 89; 106pp;
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LC, Schatz
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53
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95US-00476168.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Preferably N-terminus is selected from: -NRR1; . NRC(0)R; -NRC(0)OR; -NRS(0)2R; -NRC(0)MR; succinimide; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Preferably linkages are selected from: -CH2OC(O)NR-; phosphomate; -CH2S(O)2NR-; -CH2NR-; -C(; -NHC(O)NH; where R is hydrogen or lower alkyl and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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268
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                                                                                                                          English.
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9 FC-TMP-TM
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and R6 is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy on marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use biological research, for detecting TPO receptors on living cells
                                                                                  chemotherapy, radiation therapy or bone marrow transfusions. may also be used to maintain the proliferation and growth of dependent cell lines and for use in biological research, for
                                                                                                                      The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from
                                                                                                                                                                                           Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, espthrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                     Dower WJ,
Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haematology; thrombocytop
bone marrow transfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW09492 standard;
                                                Sequence 19
                                                                                                                                                                     Disclosure; Page 26; 106pp; English.
                                                                                                                                                                                                                                              WPI; 1997-051883/05.
                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9640189-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-1997
                                                                                                                                                                                                                                                                                                         (GLAX ) GLAXO
                                                                         receptors on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GNADGPTLROWLEGRRPKN
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               Similarity
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                                                                                                                                                                                                                                                                    Barrett RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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A
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transfusion; chemotherapy; radiation therapy.
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                                                                                                                                                                                                                                                                                                         GROUP LTD
                                                                                                                                                                                                                                                                                                                              95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US008998
                                                                        living cells
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            100.0%; Score 108; DB 2; 100.0%; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                     Cwirla SE, I
PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0%;
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Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
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                                                                                                                                                                                                                                                                     Duffin
m CR, W
                                                                                                                                                                                                                                                                     n DJ, Gates
Wrighton NC;
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                         Length
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The peptide
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S

GNADGPTLRQWLEGRRPKN 19

19;

Conservative

0,

Mismatches

Indels

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Gaps

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ARBSULT 3
ADAY3 661
ADAY3 671
AC ADAY3

RESULT 4
AAW33024
ID AAW3
XX
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AC AAW3
AC AAW3
DT 11-N
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DT 11-N
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and recently activation or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                          AAW33024 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombopoietin dependent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1996;
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                            Thrombopoietin receptor binding peptide
                                                                                    11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNADGPTLROWLEGRRPKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barret RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 27; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (firet
                                                                                    (first entry)
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95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or to maintain the proliferation and growth dent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 108; DB 2; 100.0%; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cwirla SE, Duffir PJ, Wagstrom CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Om CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 5
AAW36643
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microw. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                Synthetic
                                                                                                                     Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dower WJ, Barret RW, Cwirl
Mattheakis LC, Schatz PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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07-JUN-1996;
                           19-DEC-1996.
                                                      WO9640750-A1
                                                                                                          signal transduction;
                                                                                                                                                                             Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                          11-MAR-1998
                                                                                                                                                                                                                                                               AAW36643 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                      19;
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                              A.
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor - useful in treatment thrombocytopenia resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00478128.
95US-00485301.
 96WO-US009623
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                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                           receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wagstrom CR,
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                                                                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                       Score 108; DB 2;
Pred. No. 1.1e-09;
; Mismatches 0;
                                                                                                              activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duffin DJ,
                                                                                                              cell culture
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 19;
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RESULT 6
AAB17021
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XX AAB
AC AAB
AC AAB
AC AAB
AC AAB
AC TPO
XX TPO
XX Mod
KW Mod
KW Linh
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EFO; TFO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19
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Mattheakis
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07-JUN-1995;
  Novel composition of matter comprising an
                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                      23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                     04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                    WO200024782-A2
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                                                                                                                                                                                                                                                                                25-OCT-1999;
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                                                                                                 Feige U,
                                                                                                                                                      (AMGE-) AMGEN
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LC, Schatz PJ, Wagstrom CR, Wrighton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical.
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99US-00428082
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95US-00485301
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                                                                                                       Cheetham
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No. 1.1e-09;
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                                                                                                       TC.
  Fc domain and pharmacologically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rc (x1)a-r1-(x2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-p1, -(L1)c-p1-(L2)d-p2, -(L1)c-p1-(L2)d-p2, -(L1)c-p1-(L2)d-p2, -(L1)c-p1-(L2)d-p2, -(L1)c-p1-(L2)d-p2, -(L1)c-p1-(L2)d-p2-(L3)e-p3, or -(L1)c-p1-(L2)d-p2-(L3)e-p3-(L4)f-p4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently 1 inkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 c, d, e, and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, compositions are useful for treating cancer, asthma, compositions are useful for treating cancer, asthma, a pab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA6943 to AAA6926 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the cempolification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 19
                                                                                                                                                                    07-JUN-1995;
07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                           haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human thrombopoietin receptor (TPO-R) activator peptide #48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) FC domain, pharmacologically active peptides, and linkers.
                                WPI; 2001-564142/63
                                                                                   Balasubramanian
                                                                                                  Dower WJ,
                                                                                                                                                                                                                                                         01-MAR-2000; 2000US-00516704
                                                                                                                                                                                                                                                                                           26-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU25862 standard;
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                                                                                Barrett RW,
anian P, Wa
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                                                                                                                                     GROUP LTD
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96US-00699027.
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                                                                                  RW, Cwirla S
Wagstrom CR,
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Deprince RB,
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Activating thrombopoietin receptors

in cells, used to treat

Disclosure;

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20;

128pp;

English

to and activate the human thrombopoietin

AAU25815-AAU26049

represent

peptides

and peptide mimetics

(TPO-R). Methods

the such

receptor

peptide mimetics attached to

thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.

used to treat

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Matches 19
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07-JUN-1996;
15-AUG-1996;
                                                                                                                                                                                                                                                                                                                              haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in set in praising fluorescences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of activating thrombopoietin receptors in cells comprise contacting to cells with effective amounts of peptides and peptide mimetics attache hydrophilic polymers. The methods are used to treat thrombocytopenia as that due to chemotherapy, radiation therapy or bone-marrow
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                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
                  WPI; 2001-564142/63
                                                              Balasubramanian
                                                                            Dower WJ,
                                                                                                                                                                                                             01-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Human thrombopoietin receptor (TPO-R) activator peptide
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llarity 100.0%;
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                                                                                                         GROUP LTD
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95US-00485301.
96WO-US009623.
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Pred. No. 1.1e-09;
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombocoletin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (BLISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The
                                                                                                                                                                                                                                                                                                                                         Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; EUISA; bone marrow transplantation; hematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                Yin
                                             Dower WJ, Barre
Balasubramanian
                                                                                                                                                                                                          01-MAR-2000;
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                                                                                                                                                                                                                                          26-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human thrombopoietin receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU25821 standard; peptide;
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wanian P, Wao
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                                                                                                                                                                                                            2000US-00516704
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96WO-US009623.
96US-00699027.
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strom CR,
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Pred. No. 1.1e-09;
Mismatches 0;
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WPI; 2001-564142/63

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Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.

Sequences AAU25815-AAU26049 represent peptides and

activate the human

thrombopoietin receptor (TPO-R). Methods

peptide mimetics that

to and

Disclosure; Col 65-66; 128pp; English

of activating thrombopoletin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and plattelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO ceptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in still staining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines

Query Match

Local

Similarity

100.0%;

Length 19

Sequence 19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TMP; TNF-alpha inhibitor; interleukin 1 antagonist; TL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antitheumatic; antiathabetic; ophthalmological; antitianaemic; anorectic; antiinfertility; haemostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective; inflammatory disease; autoimmune disease; tumour cancer; rheumatoid archritis; diabetic retinopathy; infertility; cancer; rheumatoid archritis; diabetic retinopathy; infertility; csleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO mimetic
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                                                                                                                           03-MAY-2000; 2000US-00563286
                                                                                                                                                                                                         02-MAY-2001; 2001WO-US014310
                                                                                                                                                                                                                                                                                   08-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                     (AMGE-)
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Pred. No. 1.1e-09;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lupus erythematosus
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Heavner GA,

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(CENZ) CENTOCOR INC.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cultilities and retrictive activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, for identifying normal or abnormal proteins of interest in a biological sample. Additionally, (I) is useful proteins of interest in a biological sample. Additionally, (I) is useful proteins of interest in a biological sample. Additionally, (I) is useful proteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, infertility, and neurological degenerative diseases. (I), comprising EPO-mimetic compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic comprising compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet to deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic tumour which result in thrombocytopaenia, systemic lupus erythematosus, and Fanconi's syndrome. ABB72403 to ABB73426 and ABJ35655 to ABJ35777 represent amino acid and nucleic acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mimetic; CDR mimetibody; gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO mimetic peptide sequence SeqID 513.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ73059 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                          29-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNADGPTLROWLEGRRPKN
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                                                                                                                                                                          2002US-0368791P
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Pred. No. 1.1e-09;
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RESULT 12
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Best Local
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                                                                                      Heavner GA, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/ or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is a TPO mimetic peptide sequence used to make a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, while the province of the comprises at least one human framework region and at least one justeff comprises at least one human framework region and at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for preparing a composition for treating e.g., cardiovascular or neurologic disease.
                                WPI; 2004-082870/08
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004002417-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis; dementia; Alzheimer's disease; cancerous condition; infectious disease; bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CH1 deleted mimetibody-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 513; 97pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-804237/75
                                                                                                                                                                                                                                                   28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                            27-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                         08-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection;
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19; Conserv
                                                                                                                                                                                      CENTOCOR INC.
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llarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                            2003WO-US020347
                                                                                                                      Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to novel mammalian CDR mimetibodies, specific
                                                                                                                         Ghrayeb J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 108; DB 7;
Pred. No. 1.1e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide SeqID513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                         Scallon BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 19;
                                                                                                                         Nesspor TC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anaemia;
infection;
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RESULT 13
ADJ51655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CH1-deleted minetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                      antiallergic; muscular Gen; cytostatic; antiinflammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder; pophthalmologic disorder; pediatric disorder; psychiatric disorder; renal disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascula or neurodegenerative disease or disorder, anemia, cancer, or infection
                                                    28-JUN-2002;
19-SEP-2002;
                                                                                                         30-JUN-2003;
                                                                                                                                                 08-JAN-2004
                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH1 deleted mimetibody; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH1 deleted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention
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                                                                                                                                                                                                                                                                                renal disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNADGPTLRQWLEGRRPKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNADGPTLROWLEGRRPKN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mimetibody-related peptide SeqID513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                   2002US-0392431P
2002US-0412144P
                                                                                                         2003WO-US020495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relates to CH1 deleted mimetibodies (and
hem) compositions, methods and uses. The
                                                                                                                                                                                                                                                                              pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513; 129pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 108; DB 8;
100.0%; Pred. No. 1.1e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular-Gen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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(CENZ) CENTOCOR INC

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RESULT 14
ABP51687
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiinflammatory, neuroleptic, ophthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-modulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CH1 deleted mimethody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endocrine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, haematologic, immunological, allergic, infectious, musculoskeletal, oncological, neurological, nutritional, ophthalmologic, pediatric, psychiatric, renal or pulmonary disorders. The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New CH1 deleted mimetibody polypeptide and nucleic diagnosing, preventing or treating cardiovascular, endocrine, gastrointestinal, gynecologic, infectiou nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which encode them), compositions, methods and uses. The inventio useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavner GA,
Kutoloski KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gastrointestinal-Gen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to CH1 deleted mimetibodies (and the DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; SEQ ID NO 513; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-082872/08
                                                                                                                                                                                                                                                                                                                                                    TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO mimetic peptide SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
immunomodulator, antiallergic, muscular-Gen, cytostatic,
antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
                                                                                                  05-DEC-2000;
04-MAY-2001;
                                                                                                                                                                                                           13-JUN-2002
                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP51687 standard; peptide; 18
                                                                                                                                                               05-DEC-2001; 2001WO-US047656.
                                                                                                                                                                                                                                                  WO200246238-A2
                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                       ALEXION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNADGPTLROWLEGRRPKN 19
                                                                            ; 2000US-0251448P.
; 2001US-0288889P.
; 2001US-0294068P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                         PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 108;
100.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ghrayeb J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scallon BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; DB 8;
. 1.1e-09;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infectious, neurologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nesspor TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid, useful
dermatologic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Sequence 18

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a stimulator of proliferation, differentiation and maturation of chaematopoietic cells, and a stimulator of haematopoietis. (I) is useful ce for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with ceromegakaryocytes or megakaryocytes, which results in increased platelet promegakaryocytes or megakaryocytes, which results in increased platelet components. (I) with a region where amino acid residues corresponding to component of the CDR is replaced with an EPO mimetic, or which has one or component of the CDR is replaced with an EPO mimetic, or which has one or component of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residues corresponding determining region are thrombopoetin mimetic.
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DB; ABQ73365.
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Matches Query Match Best Local : 1 GNADGPTLROWLEGRRP Similarity GPIEGPTLROWLAARAP 17 Conservative 57.4%; 17 Score 62; DB Pred. No. 0.01 1; Mismatches DB 5; <u>ს</u> Length 18 0 Gaps 0

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Thrombopoietin mimetic peptide (TMP4), seq id 4. 01-JUL-2004 ADN59655 standard; peptide; (first entry) 18

ADNS9655
ADNS9655
ADNS9655
AC ADNS9
AC ADNS9
AC ADNS9
XX Thron
DT O1-JU
XX Haemc
KW trans
KW trans
KW trans
KW lupoi
XX Homo
XX Homo
XX Homo
XX 11-00
PF 11-00
XX 11-00
PR 11-00
XX X 11-0CT-2001; 10-0CT-2002; 11-OCT-2002; 2002WO-US032552 WO2003031589-A2 Homo sapiens TMP; c-mpl receptor; platelet precursor; megakaryocyte; thrombocytopaenia; aplastic anaemia; autoimmune thrombo Haemostatic; antianaemic; 17-APR-2003 autoimmune haemolytic anaemia; ransmembrane signaling; mpl lupoid 2001US-0328666P 2002US-00269806 immunosuppressive; platelet; receptor; thrombopoietin mimetic peptide; Hughe's syndrome;

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Barbas-Frederickson

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Renshaw M;

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RESULT 16
ADQ16617
ID ADQ16
XX ADQ16
AC ADQ16
XX O9-SE
XX Inmur
KW inmur
KW eryt!
KW eryt!
KW inmur
XX Unide
XX Unide
XX Unide
XX INTUI
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production platelet precursors, useful for treating thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represents a preferred TMP of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythropoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO mimetic peptide with random flanking residues SEQ ID NO:37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC
                                                                                                                                                                                  17-NOV-2003; 2003WO-US036894.
                                                                                                                                                                                                                                                                                                                                                           WO2004050017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ16617 standard; peptide;
    (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                         17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGPTLKQWLEYRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementarity determining region; CDR; peptide mimetic; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hartley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.4%;
84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62; DB Pred. No. 0.01:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .016;
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RESULT 17
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Best Local
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                                                                                                                                                                                                                                                                                                transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide; TMP; c-mpl receptor; platelet precursor; megakaryocyte; thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia;
         Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production platelet precursors, useful for treating thrombocytopenia.
                                                                                     Min
                                                                                                                                                                                                                                                                                                                                         Haemostatic; antianaemic; immunosuppressive; platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN59822 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising a region where amino acid residues corresponding portion of a two complementarity determining regions (CDRs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The
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                                                                                                                                    11-OCT-2001;
10-OCT-2002;
                                                                                                                                                                       11-OCT-2002; 2002WO-US032552
                                                                                                                                                                                                   17-APR-2003
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                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                          autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present
                                                                                                            (AMGE-)
                                                                                                                                                                                                                                                                          lupoid thrombocytopaenia; linker.
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                                                             2003-403101/38
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                                                                                   Sitney
                                                                                                              AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; SEQ ID NO 37; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNADGPTLROWLEGRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPIEGPTLROWLAARAP 17
                                                                                                                                                                                                                                                                                        haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                                                                                                                                                                                   TMP4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents a TPO mimetic peptide with flanking
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                                                                                                                                    2001US-0328666P.
2002US-00269806.
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Pred.
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No. 0.016;
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Example 6;

Page 83; 126pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that CC binds to the c-mpl (mpl) receptor, and which stimulates the production of platelet precursors, is new. Further CC disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition of matter (II) that binds to an mpl receptor, CC and a pharmaceutical composition of the invention is useful for treating CC pharmocytopaenia in an animal, and for increasing megakaryocytes or CC platelets in a patient. The TMP of the invention is useful for treating CC conditions involving a megakaryocyte and/or platelet deficiency, e.g. CC disease conditions involving thrombocytopaenia such as aplastic anaemia, CC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, CC autoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for CC maintaining the viability or storage life of platelets and/or cC improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds demonstrate an cimproved ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity and in vivo circulation time. The current sequence represents a TMP peptide of the invention to which a two amino acid "cap" has been added to the carboxy terminal to increase peptide affinity.
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                                                           WPI; 2003-403101/38
                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001;
10-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemostatic; antianaemic; immunosuppressive; platelet;
transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide-vehicle compound, seq id 144.
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                                                                                                                                                                       Min H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lupoid thrombocytopaenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMP; c-mpl receptor; platelet precursor; megakaryocyte;
                                                                                                                                                                                                                                                                                   (AMGE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 84.
                                                                                                                                                                       Sitney KC,
                                                                                                                                                                                                                                                                                         AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0328666P.
2002US-00269806.
                                                                                                                                                                             Hartley C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.4%;
84.6%;
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Pred. No. 0.02
1; Mismatches
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cc thrombocytopaenia in an animal, and for increasing megakaryocytes or platelets in a parient. The TMP of the invention is useful for treating conditions involving a megakaryocyte and/or platelet deficiency, e.g. conditions involving thrombocytopaenia such as aplastic anaemia, cautoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, cautoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for cautoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for camaintaining the viability or storage life of platelets and/or megakaryocytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thrombopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelet properties, such as improved plasma half-life, biological activity and in vivo circulation time. The current sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binds to the c-mpl (mpl) receptor, and which stimulates the production of platelets and/or the production of platelet precursor is new. Further disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The pharmaceutical composition of the invention is useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel thrombopoietin mimetic peptides which bind to mpl receptor, and which stimulate the production of platelets and/or the production of platelet precursors, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 144; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a thrombopoietin mimetic peptide
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                          Matches
                                 Query Match
Best Local
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                                  Similarity
DGPTLKOWLEYER 16
       DGPTLRQWLEGRR 16
                          Conservative
                                 57.4%;
                                  Score
Pred.
                             Mismatches
                                   No :
                                   0
                                         DB 7;
                                   .021;
                            <u>,,</u>
                                         Length
                             Indels
                            <u>.</u>
                            Gaps
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Sequence 23

Ā,

represents a peptide-vehicle compound of the invention.

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ADN59774
                                                                                                                                                                                   thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                        Haemostatic; antianaemic; immunosuppressive; platelet; transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide; TMP; c-mpl receptor; platelet precursor; megakaryocyte;
Min H,
                                            11-OCT-2001; 2001US-0328666P
10-OCT-2002; 2002US-00269806
                                                                                                                                                                                                                                                                               01-JUL-2004
                                                                                                                                                                                                                                                                                                                           ADN59774 standard; protein;
                      (AMGE-)
                                                                                                      17-APR-2003
                                                                                                                             WO2003031589-A2
                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                       Peptide-vehicle compound, seq id 126
                                                                               11-OCT-2002; 2002WO-US032552
                                                                                                                                                                         lupoid thrombocytopaenia.
Sitney KC,
                        AMGEN INC
                                                                                                                                                                                                                                                                               (first entry)
  Hartley
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RESULT 20
ADN59692
ID ADN59692
XX ADN59
AC ADN59
XX D1-JU
DT 01-JU
DX Thron
XX Haemc
KW Haemc
KW trans
KW TMP;
KW autool
XX Homo
OX Homo
OX Homo
XX Ho
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binds to the c-mpl (mpl) receptor, and which stimulates the product platelets and/or the production of platelet precursors, is new. Fur disclosed is a composition of matter (II) that binds to an mpl rece and a pharmaceutical composition comprising (II) and a carrier. The pharmaceutical composition of the invention is useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production platelet precursors, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombocytopaenia in an animal, and for increasing megakaryocytes or platelets in a patient. The TMP of the invention is useful for treating conditions involving a megakaryocyte and/or platelet deficiency, e.g. disease conditions involving thrombocytopaenia such as aplastic anaemia, autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, autoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for
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                                     11-OCT-2001;
10-OCT-2002;
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemostatic; antianaemic; immunosuppressive; platelet;
transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
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                                                                                                                                    11-OCT-2002; 2002WO-US032552.
                                                                                                                                                                                                  17-APR-2003
                                                                                                                                                                                                                                                               WO2003031589-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMP; c-mpl receptor; platelet precursor; megakaryocyte;
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                                     2001US-0328666P
2002US-00269806
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Pred. No. 0.02
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq id 41.
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of
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RESULT 21
ADN59762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ct thrombocytopaenia in an animal, and for increasing megakaryocytes or CC platelets in a patient. The TMP of the invention is useful for treating CC conditions involving a megakaryocyte and/or platelet deficiency, e.g. CC disease conditions involving thrombocytopaenia such as aplastic anaemia, CC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, and in the TMP of the invention is also useful for CC autoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for CC megakaryocytes and its derived cells. The compounds demonstrate an CC improved ability to bind to and/or trigger transmembrane signal through, CC i.e. activating, the mpl receptor the compounds have superior control, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of CC platelet precursors. Further, certain of the compounds also exhibit control therapeutic properties, such as improved plasma half-life, CC biological activity and in vivo circulation time. The current sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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                                                                                                                                                       Haemostatic; antianaemic; immunosuppressive; platelet; transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide; TMP; c-mpl receptor; platelet precursor; megakaryocyte; thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;
11-OCT-2002; 2002WO-US032552
                                                                                                                                                                                                                                                            Peptide-vehicle compound, seq id 114.
                                                                                                                                                                                                                                                                                                  01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel
                                  17-APR-2003
                                                                   WO2003031589-A2
                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                      ADN59762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC
                                                                                                                                     lupoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombopoietin mimetic peptides which bind to mpl receptor, stimulate the production of platelets and/or the production plet precursors, useful for treating thrombocytopenia.
                                                                                                                                         thrombocytopaenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 DGPTLRQWLEGRR 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 36 AA.
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                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.4%;
84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62; DB 7;
Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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RESULT 22
ADN59768
IID ADN59768
XX
AC ADN5
XX
DT 01-0
XX
DT Haem
XX
TWB;
KW Haem
KW TWB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC platelets and/or the production of platelet precursors, is new. Further CC disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The CC pharmaceutical composition of the invention is useful for treating thrombocytopaenia in an animal, and for increasing megakaryocytes or CC platelets in a patient. The TMP of the invention is useful for treating CC conditions involving a megakaryocyte and/or platelet deficiency, e.g. CC disease conditions involving thrombocytopaenia such as aplastic anaemia, CC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, autoimmune thrombocytopaenia, and for syndrome and lupoid conditions involving thrombocytopaenia syndrome and lupoid conditions the viability or storage life of platelets and/or megakaryocytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior chromobopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability of the compounds 
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                                                                                                                                                                                                                        transmembrane signaling; mpl receptor; thrombopoietin mimetic pept TMP; c-mpl receptor; platelet precursor; megakaryocyte; thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36
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10-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                             Haemostatic; antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN59768 standard;
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                                           WO2003031589-A2
                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide-vehicle compound, seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the c-mpl
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the production of platelet precursors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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                                                                                                                                                                                                                                                                                                                                          immunosuppressive; platelet;
mpl receptor; thrombopoietin mimetic peptide;
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Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            id 120.
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Matches
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10-OCT-2002; 2002US-00269806
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Pred. No. 0.03
1; Mismatches
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transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide; TMM; c-mpl receptor; platelet precursor; megakaryocyte; thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;

Haemostatic; antianaemic; immunosuppressive; platelet;

Peptide-vehicle compound, seq id 113.

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RESULT 24
ADN59817
ID ADN55
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AC ADN55
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DT 01-JI
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Best Local
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               Haemostatic; antianaemic; immunosuppressive; platelet; transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide; TMP; c-mpl receptor; platelet precursor; megakaryocyte; thrombocytopaenia; aplastic anaemia; autoimmune thromboovtopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombocytopaenia in an animal, and for increasing megakaryocytes or platelets in a patient. The TMP of the invention is useful for treating conditions involving a megakaryocyte and/or platelet deficiency, e.g. disease conditions involving thrombocytopaenia such as aplastic anaemia, autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia,
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                                                                                                               Peptide- linker compound,
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                                                                                                                                                                                                                               ADN59817 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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10-OCT-2002;
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                                                                                                                                                                                                                                                                                                                               DGPTLKQWLEYRR 16
 haemolytic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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2002US-00269806.
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                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%;
84.6%;
                                                                                                           seq id
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62;
Pred. No.
Hughe's
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                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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RESULT 25 ADN59780

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DGPTLKQWLEYRR

4 DGPTLRQWLEGRR

16

Matches Query Match

Local

Similarity

57.4%; 84.6%;

Score 62; DB 7; Pred. No. 0.042;

7; 1,

Length 44;

Mismatches

<u>..</u>

Gaps

0,

Conservative

Sequence 44

A

(first entry compound,

ADN59780

ADN59780 standard; protein; 46 AA.

Peptide-vehicle 01-JUL-2004

geq

id 132.

Haemostatic; antianaemic; immunosuppressive; platelet; transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;

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cc thrombocytopaenia in an animal, and for increasing megakaryocytes or platelets in a parient. The TMP of the invention is useful for treating conditions involving a megakaryocyte and/or platelet deficiency, e.g. disease conditions involving thrombocytopaenia such as aplastic anaemia, cautoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, and invention is also useful for autoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for megakaryocytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thrombopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of plateletes and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of plateletes and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of plateletes and/or megakaryocytopoietic activity, i.e. the ability and in vitro, the production of plateletes precursors. Further, certain of the compounds also exhibit superior therapeutic properties, such as improved plasma half-life, biological activity and in vivo circulation time. The current sequence corporesents a peptide-linker compound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              platelet precursors, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-403101/38
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10-OCT-2002;
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RESULT 26
ADN59786
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                                                                                                                                                                                                                                                                                                                                                                                         CC thrombocytopaenia in an animal, and for increasing megakaryocytes or conditions involving a megakaryocyte and/or platelet deficiency, e.g. conditions involving a megakaryocyte and/or platelet deficiency, e.g. conditions involving thrombocytopaenia such as aplastic anaemia, disease conditions involving thrombocytopaenia such as aplastic anaemia, condimmune thrombocytopaenia, drug induced immune thrombocytopaenia, and thrombocytopaenia, conditions is also useful for autoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TWP of the invention is also useful for megakaryocytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior chromobopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets properties, such as improved plasma half-life, conjoical activity and in vivo circulation time. The current sequence corporates a peptide-vehicle compound of the invention.
                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production platelet precursors, useful for treating thrombocytopenia.
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10-OCT-2002; 2002US-00269806.
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                                       01-JUL-2004
                                                                            ADN59786;
                                                                                                               ADN59786 standard;
                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 132; 126pp; English.
                                                                                                                                                                                                                                                                                     Conservative
                                       (first entry)
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   compound,
                                                                                                               protein; 46
                                                                                                                                                                                                                                                                                                       57.4%;
84.6%;
                                                                                                                                                                                                             21
   seq id 138.
                                                                                                                                                                                                                                                                                     Score 62; DB
Pred. No. 0.04
1; Mismatches
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The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that CCC binds to the c-mpl (mpl) receptor, and which stimulates the production of platelet precursors, is new. Further CC disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The CC and a pharmaceutical composition comprising (II) and a carrier. The CC pharmaceutical composition of the invention is useful for treating CC platelets in an animal, and for increasing megakaryocytes or CC conditions involving a megakaryocyte and/or platelet deficiency, e.g. CC disease conditions involving thrombocytopaenia such as aplastic anaemia, CC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, Hughe's syndrome and lupoid chrombocytopaenia. The TMP of the invention is also useful for megakaryocytes and its derived cells. The compounds demonstrate an cegakaryocytes and its derived cells. The compounds demonstrate an
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improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thromobopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelet precursors. Further, certain of the compounds also exhibit superior therapeutic properties, such as improved plasma half-life, biological activity and in vivo circulation time. The current sequence represents a peptide-vehicle compound of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production platelet precursors, useful for treating thrombocytopenia.
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10-OCT-2002; 2002US-00269806
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Sequence 46
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RESULT 27
ADN59667
ID ADN59
XX
AC ADN55
XX
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                                                                                                            Query Match
Best Local :
                                                                                                    Matches
         ADN59667
                         ADN59667 standard; peptide; 18
                                                                   4
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                                                                                                    11;
                                                                                                            Similarity
                                                                                    DGPTLRQWLEGRR 16
                                                                   DGPTLKQWLEYRR 16
                                                                                                    Conservative
                                                                                                            57.4%;
                                                                                                    Score 62; DB
Pred. No. 0.04
1; Mismatches
                           B
                                                                                                             DB 7;
0.044;
                                                                                                      1;
                                                                                                                     Length 46;
                                                                                                      Indels
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RESULT 28
ADN59834
ID ADN59
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                                                                                                                                                                                                                                                                                         CC thrombocytopaenia in an animal, and for increasing megakaryocytes or cplatelets in a patient. The TMP of the invention is useful for treating conditions involving a megakaryocyte and/or platelet deficiency, e.g. cdisease conditions involving thrombocytopaenia such as aplastic anaemia, cdisease conditions involving thrombocytopaenia such as aplastic anaemia, cdisease conditions involving thrombocytopaenia such as aplastic anaemia, cdisease conditions involving induced immune thrombocytopaenia, and induced immune thrombocytopaenia, and continuous anaemia, autoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for compounds the viability or storage life of platelets and/or megakaryocytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thrombopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of the compounds also exhibit superior therapeutic properties, such as improved plasma half-life, biological activity and in vivo circulation time. The current sequence of the compounds appears and the production of the compounds also exhibit superior therapeutic properties, such as improved plasma half-life, biological activity and in vivo circulation time. The current sequence
                                                                                                                                                                             Query Match
Best Local S
Matches 10
ADN59834 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binds to the c-mpl (mpl) receptor, and which stimulates the production of platelets and/or the production of platelet precursors, is new. Further disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The pharmaceutical composition of the invention is useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production platelet precursors, useful for treating thrombocytopenia.
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                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a thrombopoietin mimetic peptide (TMP)
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10-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin mimetic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemostatic; antianaemic; immunosuppressive; platelet;
transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC
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                                                                                                                                                                                 Conservative
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2002US-00269806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hartley
                                                                                                                                                                                                  55.6%;
  22
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                                                                                                                                                                             Score 60; DB
Pred. No. 0.03
3; Mismatches
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                                                                                                                                                                                                  DB 7;
0.032;
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                                                                                                                                                                                                                  Length 18;
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ADGPTLRQWLEGRR 16

Matches

Conservative

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Indels

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The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that binds to the c-mpl (mpl) receptor, and which stimulates the production of control of platelet sand/or the production of platelet precursors, is new. Further consistent and/or the production of platelet precursors, is new. Further consistent and composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The conditions involving a megakaryocyte and/or platelet for treating conditions involving a megakaryocyte and/or platelet deficiency, e.g. conditions involving thrombocytopaenia such as aplastic anaemia, conditions involving thrombocytopaenia such as aplastic anaemia, contoinmune thrombocytopaenia, drug induced immune thrombocytopaenia, conditions involving thrombocytopaenia such as aplastic anaemia, contoinmune haemolytic anaemia, drug induced immune thrombocytopaenia, conditions the viability or storage life of platelet and/or megakaryocytes and its derived cells. The compounds demonstrate an continuing the viability or storage life of platelets and/or improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thrombocytopaenia, the mpl receptor trigger transmembrane signal through, i.e. the ability to stimulate, in vivo and in vitro, the production of platelet sand/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelet sand/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelet precursors. Further, certain of the compounds also exhibit superior therapeutic properties, such as improved plasma half-life, considered by the carboxy terminal to increase peptide affinity.
    Query Match
Best Local
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                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane signaling; mpl receptor; thrombopoietin mimetic pept: TMP; c-mpl receptor; platelet precursor; megakaryocyte; thrombooytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JMP
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10-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŧ,
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        Similarity
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2002US-00269806.
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    55.6%;
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Score 60; DB 7;
Pred. No. 0.04;
                                            Length
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RESULT 29
ADN59716
                                                                                           CC binds to the c-mpl (mpl) receptor, and which stimulates the production of comparison of matter (II) that binds to the production of flatelet precursors, is new Further CC and a pharmaceutical composition of matter (II) that binds to an mpl receptor, and sicolosed is a composition of matter (II) that binds to an mpl receptor, and spharmaceutical composition comprising (II) and a carrier. The CC pharmaceutical composition of the invention is useful for treating thrombocytopaenia in an animal, and for increasing megakaryocytes or CC platelets in a patient. The TMP of the invention is useful for treating CC conditions involving a megakaryocyte and/or platelet deficiency, e.g. Cd isease conditions involving thrombocytopaenia such as aplastic anaemia, autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, autoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for cc megakaryocytes and its derived cells. The compounds demonstrate an cc improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds demonstrate an thrombocytopaenic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in
Query Match
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Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production platelet precursors, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a thrombopoietin mimetic peptide binds to the c-mpl (mpl) receptor, and which stimulates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001; 2001US-0328666P.
10-OCT-2002; 2002US-00269806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMP; c-mpl receptor; platelet precursor; megakaryocyte; thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-2004
                                                                                         Sequence 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
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                                                                                                                                         represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMGE-) AMGEN INC
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  l Similarity
10; Conser
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Score 60; DB 7;
Pred. No. 0.046;
3; Mismatches
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                                                DB 7;
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                                     CC A compound which binds to an mpl receptor comprising a thrombopoietin commetic peptide (TMP) dimer joined by a linker [TMP1-1(L1)] nTMP2], is comew. TMP1 and TMP2 are amino acid sequences varying from at least 10 to C14 residues in length comprising x 2-x1 0, x 2-x1 1, x 2-x1 2, x 2-c CC x 1 4. X 1 = 1, A, V, L, F or R, X 2 = E, D, K or V, X 3 = G or A, X 4 = CC x 1 4. X 1 = 1, A, V, L, F or R, X 2 = E, D, K or V, X 3 = G or A, X 4 = CC x 1 4. X 1 = 1, A, V, L, F or R, X 2 = E, D, K or V, X 3 = G or A, X 4 = CC x 7 4. X 1, or E, X 1 2 = A, I, V, A, F, M, or K; X 1 3 = R, I, V, L, F, CC x, Y 0 = W, Y or F; X 1 2 = A, I, V, L, F, G, S, or G; X 1 3 = R, K, T, V, CC x, Q or G; X 1 4 = A, I, V, L, F, T, R, E, or G; L 1 = Inker comprising CC 1 to 20 amino acids, and n = 0 or 1. The compounds bind to and activate the c-Mpl receptor which mediates the activity of endogenous composition. The TMPs are useful for increasing the production of CC is useful for treatment of diseases which involve thombocytopenia, e.g. Caplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency constants.
                                                                                                                                                                                                                                                                                                                          Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment diseases which involve thombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                 Claim 16; Page 64; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
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                             associated
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/label=
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                             ITP, and systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= TMP_1
17. .20
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Query Match Best Local Similarity

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NO;

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RESULT 31
ADN59818
CC binds to the c-mpl (mpl) receptor, and which stimulates the production of platelets and/or the production of platelet precursors, is new. Further CC disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The CC and a pharmaceutical composition comprising (II) and a carrier. The CC platelets in a patient. The TMP of the invention is useful for treating CC conditions involving a megakaryocyte and/or platelet deficiency, e.g. CC disease conditions involving thrombocytopaenia such as aplastic anaemia, CC autoimmune haemolytic anaemia, drug induced immune thrombocytopaenia. The TMP of the invention is also useful for megakaryocytes and its derived cells. The compounds demonstrate an CC improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thrombocytopaenia, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of compounds also exhibit to superior therapeutic properties, such as improved plasma half-life, cc biological activity and in vivo circulation time. The current sequence cc represents a peptide-linker compound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide; TMP; c-mpl receptor; platelet precursor; megakaryocyte; thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-403101/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2001;
10-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide- linker compound, seq id 102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN59818 standard; peptide; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2002; 2002WO-US032552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lupoid thrombocytopaenia; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to a thrombopoietin mimetic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursors, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNADGPTLROWLEGRRPKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-0328666P.
2002US-00269806.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO 102; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hartley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TMP)
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Sequence 42 AA;

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RESULT 32
ABP51670
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        CC (I) comprising a region where amino acid residues corresponding to at cleast a portion of the complementary determining region (CDR) are creplaced or fused with biologically active peptides e.g. a peptide cC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has can be used as stimulator of proliferation, differentiation and maturation of a stimulator of proliferation, differentiation and maturation of can be used as stimulator of proliferation, differentiation or growth of comegakaryocytes or megakaryocytes, where (I) is contacted with production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or cC more of its CDRs fused to an EPO mimetic, is useful for increasing the production of CDR is reproducted. (I) is useful for calls or their progenitors. (I) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, cC disorders or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73377 and ABPS1669 to ABPS1696 represent sequences used in the exemplification of the present invention
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Best Local
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04-MAY-2001;
29-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                       A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or
                                                                                                                                                                                                                                                                                                                                                                                                          thrombopoetin mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP51670
                                                                                                                                                                                                                                                                                                                                                                             Claim 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALEX-)
                                                                                                                                                                                                                                                                                                                                              present invention describes an immunoglobin molecule or its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEGPTLREWLEQRK 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000US-0251448P.
; 2001US-0288889P.
; 2001US-0294068P.
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                                                                                                                                                                                                                                                                                                                                                                         6; 113pp;
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Pred. No. 0.081;
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                                                                                                                                                                                                                                                                                                                                              fragment
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RESULT 33
ADQ16585
RESULT 34
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                                                                                                                                                                                                                 The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                      New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowdish KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2003; 2003WO-US036894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin;
erythropoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO mimetic peptide SEQ ID NO:2
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             ABP51689 standard; peptide; 18
                                                                                                                                                                             Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunotherapy; thrombocytopenia.
                                                                                                                                                                                                     present sequence represents a TPO mimetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                           2004-460973/43
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                                                                                                  DGPTLRQWLEGRRP 17
                                                                           EGPTLRQWLAARAP
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                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementarity determining region; CDR; peptide mimetic;
EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.6%;
                                                                                                                                       54.6%;
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                                                                                                                           Score 59; DB 8;
Pred. No. 0.038;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Renshaw M;
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              B
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commettic such as an erythropic tin (BPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has can stimulator of proliferation, differentiation and maturation of constitutive calls, and a stimulator of proliferation, differentiation and maturation of constitution proliferation, differentiation and maturation of constitution proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or comore of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood calls, where (I) is contacted with has one or therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, considers or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in the exemplification of the present invention
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                                                                   Matches
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO mimetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Fig 5; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombopoetin mimetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowdish
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                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogen molecule comprising a region in which amino acid
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                                                                               Similarity
                                  DGPTLRQWLEGRRP 17
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                                                                   Conservative
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71.4%;
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                                                                                   Score 59; DB 5;
Pred. No. 0.046;
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                                                                                                   Length 18;
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RESULT 35 ABP51688

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CC (I) comprising a region where amino acid residues corresponding to at the frequency of the comprising aregion (CDR) are CC replaced or fused with biologically active peptides e.g. a peptide CC mimetic such as an erythropoietin (EPO) or thrombopoietin (FPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has CC antianaemic, haemostatic and nephrotropic activities, and can be used as CC as timulator of proliferation, differentiation and maturation of CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful CC promegakaryocytes or megakaryocytes, where (I) is contacted with CC promegakaryocytes or megakaryocytes, where (I) is contacted with CC promegakaryocytes or megakaryocytes, which results in increased platelet CC promegakaryocytes or megakaryocytes, which results in increased platelet CC promegakaryocytes or megakaryocytes, which results in increased platelet CC production. (I) with a region where amino acid residues corresponding to CC a portion of CDR is replaced with an EPO mimetic, or which has one or CC more of its CDRs fused to an EPO mimetic, is useful for increasing the CC production of red blood cells, where (I) is contacted with haematopoietic Stem cells or their progenitors. (I) is useful for increasing the CC stem cells or their progenitors. (I) is useful for diagnostics or CC therapeutics, in cell isolation strategies, and for treating patients Suffering from deficiency in cell populations caused by disease, CC AB073288 to AB073377 and ABP51669 to ABP51696 represent sequences used in the exemplification of the present invention
                                                                                                                                  Query Match
Best Local S
Matches 10
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04-MAY-2001;
29-MAY-2001;
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DB; ABQ73366.
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                                                                                                                                                                        Score 59; DB 5;
Pred. No. 0.046;
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The present invention describes an immunoglobin molecule or its fragment CC (I) comprising a region where amino acid residues corresponding to at CC least a portion of the complementary determining region (CDR) are CC replaced or fused with biologically active peptides e.g. a peptide CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has CC antianaemic, haemostatic and nephrotropic activities, and can be used as stimulator of proliferation, differentiation and maturation of CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful CC promegakaryocytes or megakaryocytes, where (I) is contacted with CC promegakaryocytes or megakaryocytes, which results in increased platelet CC production. (I) with a region where amino acid residues corresponding to CC a portion of CDR is replaced with an EPO mimetic, or which has one or CC more of its CDRs fused to an EPO mimetic, is useful for increasing the CC production of red blood cells, where (I) is useful for increasing the CC stem cells or their progenitors. (I) is useful for diagnostics or CC therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, CC disorders or treatments related to the suppression of haematopoiesis. CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in the exemplification of the present invention
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04-MAY-2001;
29-MAY-2001;
                                                                                                   Sequence 18
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Score 59; DB 5; Pred. No. 0.046;
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                 Query Match
Best Local Similarity
Matches
                                                                                                      for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or more of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with haematopoietic stem cells or their progenitors. (I) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, disorders or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                            (1) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (BPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or
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04-MAY-2001; 2001US-0288889P.
29-MAY-2001; 2001US-0294068P.
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                                                                           Sequence 18
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71.4%;
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Matches Best Local Query Match

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Similarity

54.6%; 71.4%;

Score 59; Pred. No.

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                                                           CC (I) comprising a region where amino acid residues corresponding to at the comprising a region where amino acid residues corresponding to at the complementary determining region (CDR) are complementary determining region (CDR) in the complementary termining (I) has complementary determining to complementary determining region of growth of complementary determining region of growth of complementary determining region of complementary determining to complementary determining to complementary determining region where amino acid residues corresponding to complementary determining region where an EPO mimetic, or which has one or compression of CDR is replaced with an EPO mimetic, or which has one or compression of red blood cells, where (I) is contacted with has one or compression of red blood cells, where (I) is contacted with has one or compression of red blood cells, where (I) is useful for increasing the contacted or their progenitors. (I) is useful for diagnostics or compression of the cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, contacted to the suppression of haematopoiesis.

CC disorders or treatments related to the suppression of haematopoiesis.

CC disorders or treatments related to the suppression of haematopoiesis.

CC disorders or treatments related to the suppression of haematopoiesis.

CC disorders or treatments related to the suppression of haematopoiesis.
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Fig 5; 113pp; English
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                                                                                   CC (I) comprising a region where amino acid residues corresponding to at at C least a portion of the complementary determining region (CDR) are CC replaced or fused with biologically active peptides e.g. a peptide CC mimetic such as an erythropoletin (EPO) or thrombopoletin (TPO) mimetic, CC that is flanked with proline at its carboxy terminus. (I) has CC antianaemic, haemostatic and nephrotropic activities, and can be used as Ethmulator of proliferation, differentiation and maturation of CC haematopoletic cells, and a stimulator of haematopoiesis. (I) is useful CC promegakaryocytes or megakaryocytes, where (I) is contacted with CC promegakaryocytes or megakaryocytes, which results in increased platelet CC production. (I) with a region where amino acid residues corresponding to CC a portion of CDR is replaced with an EPO mimetic, or which has one or CC more of its CDRs fused to an EPO mimetic, is useful for increasing the CC production of red blood cells, where (I) is contacted with haematopoietic Stem cells or their progenitors. (I) is useful for diagnostics or CC therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, CC disorders or treatments related to the suppression of haematopoiesis. (C hae73288 to AB073377 and ABP51669 to ABP51696 represent sequences used in
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04-MAY-2001;
29-MAY-2001;
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                           The present invention describes an immunoglobin molecule or its fragment ((1) comprising a region where amino acid residues corresponding to at ((1) comprising a region where amino acid residues corresponding to at ((1) comprising a region where amino acid residues corresponding to at ((1) comprising a population of the complementary determining region (CDR) are ((1) complementary determining region (CDR) are ((1) complementary determining region (CDR) are ((1) complementary determines). ((1) has ((1) has a complementary determines). ((1) has a stimulator of proliferation, differentiation and maturation of ((1) has a complementary determines). ((1) is contacted with ((1) compregakaryocytes or megakaryocytes, where ((1) is contacted with ((1) compregakaryocytes) or megakaryocytes, which results in increased platelet ((1) production. ((1) with a region where amino acid residues corresponding to ((1) complementary determines). ((1) has one or ((2) contacted with has one or ((2) contacted with has one or ((2) contacted with has determined or ((2) contacted with h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
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    present invention
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RESULT 41
ABP51675
The present invention describes an immunoglobin molecule or its fragment (CI) comprising a region where amino acid residues corresponding to at CI least a portion of the complementary determining region (CDR) are CI replaced or fused with biologically active peptides e.g. a peptide CI mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, CI that is flanked with proline at its carboxy terminus. (I) has essential and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of CI as a stimulator of proliferation, differentiation or growth of CI promegakaryocytes or megakaryocytes, where (I) is contacted with CI promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or CI aportion of red blood cells, where (I) is contacted with has one or CI stem cells or their progenitors. (I) is useful for increasing the corresponding to a new collist on their progenitors. (I) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, CI abg73288 to Abg73377 and Abp51669 to Abp51696 represent sequences used in the exemplification of the present invention
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 55; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-566610/60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-2001; 2001WO-US047656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO mimetic antibody related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPO; thrombopoietin; erythropoietin; antibody; CDR region; lementarity determining region; immunoglobin; antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barbas-Frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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71.4%;
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Pred. No. 0.046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Renshaw M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
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RESULT 43 ADQ16619

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RESULT 42
AD016611
ID AD016
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AX AD016
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KW                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Best Local
                                                                                                        Matches
                                                                                                                                      Best
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                          comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoletin (EPO) mimetic and a thrombopoletin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or creating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wit or a TPO mimetic, useful for treating thrombocytopenia.
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                                                                                                                                                                                                           Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel immunoglobulin molecule or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 31; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowdish KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-2002; 2002US-00307724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin; complementarity determining region; CDR; peptide mimetic;
erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO mimetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ16611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapy; thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALEX-) ALEXION PHARM INC
                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-460973/43.
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                                                    4 DGPTLROWLEGRRP 17
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                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
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                                                                                                                                 54.6%;
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                                                                                                           ۳.
                                                                                                                                 Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                           Mismatches
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                                                                                                                                      0.046;
                                                                                                                                                            DB 8;
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                                                                                                                                                               Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 39; 107pp; English.
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                                        immunoglobulin; complementarity determining region; erythropoietin; EPO; thrombopoietin; TPO; immunosup;
                                                                                 TPO mimetic peptide with random flanking residues SEQ ID
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                           lmmunotherapy; thrombocytopenia.
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erythropoietin; EPO; thrombopoietin; TPO; immunosuppressi
immunotherapy; thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with EPO mimetic or a TPO mimetic, useful for treating thrombocytopenia.
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01-OCT-2003
01-OCT-2003
                                                                                                                                                                  STRAIN=A3(2) / M145;

MEDLINE=21956410; PubMed=12000953; DOI=10.1038/417141a;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L.D., O'lver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
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InterPro; IPR003169; GYF.
PROSITE; PS00152; ATPASE_ALPHA_BETA;
PROSITE; PS50829; GYF; 1.
Complete proteome; Hypothetical prote
SEQUENCE 297 AA; 31805 MW; 475F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Planctomycetes; Planctomycetaceae; Pirellula
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                                                                                                 "Complete genome sequence coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomycineae;
NCBI_TaxID=1902;
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Bacteria; Actinobacteridae; Actinomycetales;
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                                                                        Nature 417:141-147 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                              Hopwood D.A.;
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SIMILARITY: Contains 1 HTH merR-
L; AL939118; CAB56383.1; -.
GO:0005622; C:intracellular; IEA
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68.8%;
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475F670F02C78E9B CRC64;
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AC Q7PR
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CC EUKa
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TREMBLREL. 26, Last annotation update)
PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
Name=RS02135; OrderedLocusNames=RSp1579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATRAIN-PEST;
Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-i- CAUTION: The sequence shown here is derived from an
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01-MAR-2004 (TrEMBLrel. 26, Creat
01-MAR-2004 (TrEMBLrel. 26, Last
01-MAR-2004 (TrEMBLrel. 26, Last
ENSANGP00000014364 (Fragment).
Name=ENSANGG00000011875;
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SMART; SM00422; HTH MERR; 1.
PROSITE; PS50937; HTH MERR 2; 1.
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InterPro; IPR009061; Putativ_DNA_bind
Pfam; PF00376; MerR; 1.
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NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mang
                                                                                                                                                                                                            Ralstonia solanacearum (Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                          Q8XPQ9
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                                                  STRAIN-GMI1000
                                                                       SEQUENCE FROM N.A.
                                                                                                                                          Burkholderiaceae;
                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                     Plasmid megaplasmid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 AA;
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                                                                                                                                            Ralstonia.
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                                                                                                                                                                  Betaproteobacteria;
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Last annotation update)
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Pred. No. 4.8;
2; Mismatches
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Best Local S
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InterPro; IPROV. 1; 2.
Pfam; PF00078; RVT 1; 2.
RNA-directed DNA polymerase; T
RNA-directed DNA polymerase; T
RNA-directed DNA polymerase; T
                                                                                                                                                                                                                                                  Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.
Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
OSJNBa0035B13.2 protein.
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GO; GO:000700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-deper
Pfam; PF00196; GerE; 1.
PRINTS; PR01590; HTHFIS.
PRINTS; PR00038; HTHLUXR.
PRODOM; PD000307; HTH LUXR; 1.
SMART; SM00421; HTH LUXR; 1.
Complete proteome; DNA-binding; Plasmid; Transcription;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the plant pathogen Nature 415:497-502(2002).
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                                                                                                                                                                                         Nature 420:316-320(2002).
EMBL; AL662966; CAD40429.1;
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L; AL646085; CAD18730.1; -.
                                                                                                           GO:0003723; F:RNA binding; IEA.
GO:0003964; F:RNA-directed DNA polymerase act
GO:0016740; F:transferase activity; IEA.
GO:0006278; P:RNA-dependent DNA replication;
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                                                                                                                                                                                                                         analysis of rice chromosome 4.";
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 47.2%;
50.0%;
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san A., Robert C., Saurin W., Schiex
Whalen M., Wincker P., Levy M.,
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 51;
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37;
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RA Adams M.D., Cedniker S.E., Holt R.A., Evans C.A., Golayne J.D.,
RA Adams M.D., Cedniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barndon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport J.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraez G., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Degwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D., Scheler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Stupg R., Sunth T.,
RA Wang Z.Y., Wasssarman D.A., Weinstock G.M., Weisenbach J.,
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Q9V492;
01-MAY-2000
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Vente Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                              Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., WooddageT, WoodlageT, Wu D., Yang S., Yao Q.A., Ye Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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NCBI_TaxID=7227;
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                                                                                                                                                                  MEDLINE=22426065; PubMed=12537568;
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T 05-JUL-2004 (TrEMBLrel. 27, Created)

T 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

T 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

T 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Bradykinin.potentiating peptides and C-type natriureti

Bothrops jararaca (Jararaca).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bullepidosauria; Squamata; Scleroglossa; Serpentes; Colubition of the properties of th
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SEQUENCE FROM N.A.

MEDLINE=22426069; PubMed=12537572;

MEDLINE=22426069; M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

""anleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Kaminker J.S., Bergman C.M., Kronmiller
Patel S., Frise E., Wheeler D.A., Lewis
Ashburner M., Celniker S.E.;
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Celniker S.,
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1. 3:RESEARCH0083-RESEARCH0083(2002)
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Q75LM1;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
Hypothetical protein OSJNBa0047824.16.
Name=OSJNBa0047824.16.
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ProDom; PD005617; Natr_peptide; 1.
SMART; SM00183; NAT_PEP; 1.
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-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Belongs to the natriuretic peptide
EMBL, D85843; BAA12879.1; --
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Proc. Natl. Acad. Sci. U.S.A. 94:1189-1193(1997).
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TISSUE=Venom gland;
MEDLINE=97188443; P
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Pfam; PF00212; ANP; 1.
                                                                                                                                                                                      Hypothetical SEQUENCE 2:
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GO; GO:0005179; F:hormone activity;
                                                                                                                                                                                                                                   Submitted (JAN-2004) to the EMBL; AC092556; AAR87260.1;
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DGNTARFWSSAWIDGRRPKD
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SEQUENCE
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Anopheles Genome Sequencing Consortium;
Anopheles Genome Sequence shown here is derived from an anome shotgun (WGS) entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22056115; PubMed=12060762; DOI=10.1073/pnas.082235599; Thomasova D., Ton L.Q., Copley R.R., Zdobnov E.M., Mang X., Hong Y Sim C., Bork P. Kafatos F.C., Collins F.H.; "Comparative genomic analysis in the region of a major Plasmodium-refractoriness locus of Anopheles gambiae."; Proc. Natl. Acad. Sci. U.S.A. 99:8179-8184(2002). EMBL; AJ439353; CAD27931.1; -. GO; GO:0005634; C:nucleus; IEA. GO; GO:0003700; F:transcription factor activity; IEA. GO; GO:0045449; P:regulation of transcription; IEA. InterPro; IPR008895; YL1.
                                                                                                                                                                                                                                                                         Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Ano
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Name=ENSANGG00000015651;
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01-MAR-2004 (TrEMBLrel.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                       preliminary data.
EMBL; AAAB01008987; EAA00898.2;
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                                                                                                                  GO:0005634; C:nucleus; IEA.
GO:0003700; F:transcription
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GNADGPTLRQWLEGRR 16
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                                                                                                          IPR008895;
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ilarity 50.0%;
Conservative
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Last annotation update)
                                     Score 50; DB Pred. No. 30; 3; Mismatches
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Q82AY3;
01-JUN-2003
01-JUN-2003
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Q8EUH8;
01-MAR-2003
01-MAR-2003
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EMBL; AP004174; BAC44735.1;
HSSP; Q22942; 1NW1.
GO; GO:0016301; F:kinase act
                                                                MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667; Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.; "The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans."; Nucleic Acids Res. 30:5293-5300(2002).
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                                                                                                                                                                                                                                                                                                                       Mycoplasma penetrans.
                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=MYPE9480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence and comparative microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
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NCBI_TaxID=33903;
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Streptomyces avermitilis.
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RESULT 14
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ID Q92Z8
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DT 01-DE
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RA Kalm;
RA Kalm;
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Matches 7
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01-JUN-2003
01-JUN-2003
01-JUN-2003
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InterPro; IPR011009; Kinase Tike.
Pfam; PF01633; Choline kinase; 1.
Complete protecme; Kinase.
SEQUENCE 271 AA; 33289 MW; CFI
MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798; Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P., Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J., Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L., Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Neurospora genome project;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ
EMBL; BX284753; CAD70447.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Schulte U., Aign V., H
Schulte G., Mewes H.
Nyakatura G., Mewes H.
Submitted (MAR-2003) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eokaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein SEQUENCE 387 AA; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein
Name=B2G14.020;
                                                                                                                                        STRAIN=1021
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                           Rhizobiaceae; S
NCBI_TaxID=382;
                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                              Plasmid pSymA.
                                                                                                                                                                                                                                                                                                      Rhizobium meliloti
                                                                                                                                                                                                                                                                                                                                 ORFNames=SMa1131;
                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
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8; Conserv
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(TrEMBLrel. 24, Last sequence up
(TrEMBLrel. 24, Last annotation
protein B2G14.020.
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                                                                                                                                                                                                                                   teobacteria; Alphaproteobacteria;
Sinorhizobium/Ensifer group; Sinc
                                                                                                                                                                                                                                                                                                           (Sinorhizobium
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Kinase like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hoheisel J., Brandt P., IH.W., Mannhaupt G.;
to the EMBL/GenBank/DDBJ
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Last annotation updat
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Pred. No.
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4; Mismatches
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Sinorhizobium.
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                                               Q9NDL7
Q9NDL7;
01-OCT-2000
01-OCT-2000
01-MAR-2004
                                                                                                                                                                                                                                                     InterPro; IPR000873; AMP-bind:
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP-BINDING; UNKNOWN_1.
Complete proceeme.
SEQUENCE 551 AA; 60767 MW; B38B9F7A4F;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (Fragment)
Name=GAPDH;
Hydra magnipapillata (Hydra).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6LG99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti pSymA megaplasmid."; Proc. Natl. Acad. Sci. U.S.A. 98:983-9888(2001). EMBL; AE007250; AAK65269.1; -. PIR; C95338; C95338. Blactmase-like. InterPro; IPR0011279; Blactmase-like. InterPro; IPR001108; RMMBL. Pfam; PF00753; Lactamase-B; 1. Pfam; PF00753; Lactamase-B; 1. Pfam; PF07521; RMMBL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TREMBLrel. 27, Last annotation
Putative 2,3-dihydroxybenzoate-AMP ligase.
Name=S0514; OrderedLocusNames=PBPRB1823;
                                                                                                                                                                                                                                                                                                                                                                           high pressure adaptations.";
Submitted (MAR-2004) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Photobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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SEQUENCE 531 AA; 58948 MW; 93BEC7FB167752E1 CRC64;
                                                                                                                                                                                                                                                                                                                 EMBL; CR378680; CAG23681.1; -.
GO; GO:0003824; F:catalytic activity;
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrionaceae; Photobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=74109;
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                                                                                                                                                                                                                                                                                                                                                                                                    "Genome analysis of Photobacterium
                                                                                                                                                                                                                                                                                                                                                    family.
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8; Conserv
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nilarity 71.4%;
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47.1%;
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l; Mismatches
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AMP-binding
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                                                                                                                                                                                                                                 Length 551;
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Hydroida; Anthomedusae;

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QRDHX7
ID QRDHX
AC QRDHX
AC QRDHX
AC QRDHX
DT 01-M2
DT 01-M
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Q8DHX7;
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                                                                                                                                                                                                                                                                                                                                                                        Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamot Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumco M., Matsunco A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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STRAIN=BP-1;
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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; AB044096; BAA96506.1; -.
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                                                                                                                                                                                                                                                                                                                   AP005375; BAC09368.1;
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Vimura T., Kishida
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Q9GSF9;
01-MAR-2001
01-MAR-2001
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NON_TER
NON_TER
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Soderstrom K., De Petrocellis L., Di Marzo V.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + F.
NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
Hydra attenuata (Hydra) (Hydra vulgaris).
Bukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae;
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                                                                                                                                                                                                                                                                                  Propionibacterium acnes.
Bacteria; Actinobacteridae; Actinomycetales; Propionibacterineae; Propionibacteriaceae; Propionibacterium.
NCBI_TaxID=1747;
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Q6A743;
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GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR000173; GAP_dhdrogenase.
Science 305:671-673(2004).
EMBL; AE017283; AAT83422.1;
Complete proteome.
SEQUENCE 161 AA; 17762 MV
                                                                                               of human
                                                                                                              Brueggeman H., Henne A., Hoster F., Liesegang H., Strittmatter A., Hujer S., Duerre P., Gottschalk G. "The complete genome sequence of Propionibacterium
                                                                                                                                                                                  STRAIN=KPA171202 / DSM 16379;
PubMed=15286373; DOI=10.1126/science.1100330;
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Pfam; PF000044; Gp_dh_N; 1.
PRINTS; PR00078; G3PDHDROMASE.
PROSITE; PS00071; GAPDH; 1.
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=PPA1691;
                                                                                                                                                                                                                                                                                                                                                                                                                Conserved protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PANHWAY: Second phase of glycolysis; first step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate
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L; AF307863; AAG29828.1; -.
                                                                                             complete genome uman skin.";
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139 AA;
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  17762 MW;
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Pred. No. 20;
5; Mismatches
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  52D0DF0CE1330F0E CRC64;
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SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633; DOI-10.1093/nar/24.22.4420;
MEDLINE-97105885; Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0SJNBa0027G07.11;
0SJNBa0027G07.11;
0ryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
MCBI TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                    PIR; $73636; $73636; Kinase like. InterPro; IPR011009; Kinase like. Complete proteome; Hypothetical p SEQUENCE 282 AA; 33295 MW; 56
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Nucleic Acids Res. 24:4420-4449(1996).
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
PubMed=12447439; DOI=10
Feng Q., Zhang Y., Hao
Liu Y., Hu X., Jia P.,
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 DOI=10.1038/nature01183;
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Q1-CCT-2003 (TrEMBLrel. 25, L
Q1-MAR-2004 (TrEMBLrel. 26, L
QSJNBaQQQ6AQ1.14 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-F., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
              Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta,
Spermatophyta, Magnoliophyta, Liliopsid
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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EMBL; AL662937; CAD40947.1; -.
Gramene; Q7XUX8; -.
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SEQUENCE :
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RESULT
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GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016778; P:RNA-dependent DNA replication; IEA.

GO; GO:0006278; P:RNA-dependent DNA replication; IEA.

InterPro; IPR0005135; Exo_endo_phos.

InterPro; IPR000477; RVTse.

Pfam; PF00372; Exo_endo_phos; 1.

Pfam; PF00078; RVT_1; 1.

Pfam; PF00078; RVT_1; 1.

Pfam; PF00078; RVT_1; 1.

PRNA-directed DNA polymerase; Transferase.

SEQUENCE 1189 AA; 135959 MW; 441C5E4B0BBF2643 CRC64;
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Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang X.,
Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.
Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Bozym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
OrderedLocusNames=RB5963;
Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7UR10
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Han B.;
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[1]
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                                                                                                                                                                                                                                                                                                      Complete proteome; Hypothetical SEQUENCE 264 AA; 29816 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of strain 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL731579; CAD41559.2;
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   205
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BX294143; CAD74532.1; -.
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   NLDSPKTAAKRIRTWLEEHRPEN 227
                                                                       NADGP----TLRQWLEGRRPKN 19
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ilarity 50.0%;
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Pred. No. 48;
2; Mismatches
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Pred. No. 2e+02;
2; Mismatches
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Q9NDL5
ID Q9NDL5
AC Q9NDL5
AC Q9NDL5
DT 01-CCT-2000
DT 01-CCT-2000
DT 01-MAR-2004
DE GIVCETALdehy
GN Name=GARDH
OS Tima formosa
OC Eutimidae; M
OC Eutimidae; M
OC EUTIMIA
OC EUTIMIA
CC -I-CATALYTIC
CC -I-CATALYTIC
CC -I-SUBUNIT:
CC
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Q9NDL8
CCCCCCEPARNOCCOS DITION
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Best Local
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Q9NDL8;
01-OCT-2000
01-OCT-2000
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GO; GO:0004365
GO; GO:0016491
GO; GO:0006096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - I- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
- I- PATHMAY: Second phase of glycolysis; first step.
- I- SUBUNIT: Homotetramer (By similarity).
- I- SUBCELULAR LOCATION: Cytoplasmic (By similarity).
- I- SIMILARITY: Belongs to the glyceraldehyde-3-phospha dehydrogenase family.
- BENBL; AB044098; BAA96508.1; -
                GO; GO:0004365; F:glyceraldehyde-3-phosphate de GO; GO:0016491; F:cxidorreductase activity; IEA. GO; GO:0006096; P:glycolysis; IEA. InterPro; IPR000173; GAP_dhdrogenase. Pfam; PF02800; Gp_dh C; 1. Pfam; PF02800; Gp_dh C; 1. Pfam; PF02800; Gp_dh C; 1. PRINTS; PR00078; G3PDHDRGNASE. PROSITE; PR00071; GAPDH; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (Fragment)
                                                                                                                                                                                                                                                                     Hydractinia echinata (Snail fur).
Eukaryota; Metazoa; Cnidaria; Hydrozoa;
Hydractiniidae; Hydractinia.
                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Glyceraldehyde-3-phosphate
                                                                                                                                                                                                                                                                                                                                          Name=GAPDH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=128134;
[1]
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Eutimidae; Tima.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=35630;
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(TrEMBLrel. 15,
(TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                               dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
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Pred. No. 16;
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glyceraldehyde-3-phosphate
                     glyceraldehyde-3-phosphate
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                                                                                                                                                                                                                                                                                                                                                             e update)
ion update)
(Fragment).
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Q9NDL9
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R HSSP; P46406; 110X.

RGO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .;

RGO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .;

RGO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; F:oxidoreductase.

R GO; GO:0016491; F:oxidoreductase.

R GO; GO:0016491; F:oxidoreductase.

R Pfam; PF02800; Gp_dh_C; I.

R Pfam; PF02800; Gp_dh_N; I.

R PF1AM; PF02800; Gp_dh_N; I.

R PRINTS; PR00071; GAPDH; I.

R PROSITE; PS00071; GAPDH; I.
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Best Local (
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                                                                     Query Match
Best Local
                                                       Matches
                                                                                                                Glycolysis;
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NON_TER
SEQUENCE 8
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (Fragmen
                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + pho.
NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                 HSSP; P06977; iDC3.
GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR000173; GAP_dhdrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mochizuki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=EML1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryotā; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Campanulinidae; Eirene.
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                                                                                                                                                                       Pfam; PF02800; Gp_dh_C; 1.
Pfam; PF00044; Gp_dh_N; 1.
PRINTS; PR00078; G3PDHDRGMASE.
PROSITE; PS00071; GAPDH; 1.
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                                                       Similarity 6; Conserv
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                           DGPTLRQWLEGR 15
DGPSMKKWRDGR
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                                                                                                                                                           NAD; Oxidoreductase.
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                                                                                                                8521 MW;
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                                                       Score 47; DB
Pred. No. 16;
5; Mismatches
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Pred. No. 16;
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                                                                                                                   D88CCF28614DBF5D CRC64;
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RESULT 28
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Q93KY0
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Q93KY0;
01-DEC-2001
01-DEC-2001
01-OCT-2003
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087645;
01-NOV-1998
01-NOV-1998
01-DEC-2001
                                                                                                                                                                                                                                                                             from the molecular analysis of Streptomyces viridochromogenes antibiotics.";
                                                                                                                                                                                                                                                                                                                         MEDLINE=21303144; PubMed=11410376; DOI=10.1016/S1074-5521(01)00040-0; Weithauer G., Muhlenweg A., Trefzer A., Hoffmeister D., Sussmuth R.D. Weithauer G., Welzel K., Vente A., Girreser U., Bechtbold A.; "Biosynthesis of the orthosomycin antibiotic avilamycin A: deductions from the molecular analysis of the avi biosynthetic gene cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces viridochromogenes.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergmann D.B., Zahn J.A., Hooper A.B., DiSpirito A.A.; submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases EMBL, AF091435; AAD03547.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99069315; PubMed=9851984;
Bergmann D.J., Zahn J.A., Hooper A.B., DiSpirito A.A.;
"Cytochrome P460 genes from the methanotroph Methylococcus capsulatus bath.";
                                                                                      Mosbacher T., Weitnauer G., Bechthold A., Schulz G.E.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF333038; AAK83165.1; - SEQUENCE 181 AA; 19999 MW; 6255D67F625EAE6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methylococcus capsulatus.
Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=aviX5;
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  Similarity 9; Conserv
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                                                                                                                                                                                                                                                            8:569-581 (2001).
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                        43.5%;
45.0%;
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annotation update)
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RESULT 31
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Best Local S
Matches 8
05-JUL-2004 (TrEMBLrel. 27, Created 05-JUL-2004 (TrEMBLrel. 27, Last sc 05-JUL-2004 (TrEMBLrel. 27, Last ar Similar to sp|p34221 Saccharomyces ORFNames=CAGLOA04301g;
                                                                                                                                      Q6FXT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE009786; AAL63037.1; -.
HAMAP; MF_00354; -; 1.
HAMAP; MF_00354; -; 1.
InterPro; IPR003009; PMN enzyme.
InterPro; IPR011179; IPdP_isomerase; 1.
PIRSF; PIRSF003314; IPP isomerase; 1.
Complete proteome; Flavoprotein; PMN; Isomerase;
Isoprene biosynthesis; NADP.
SEQUENCE 352 AA; 37966 MW; 6854253886324C04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
25-OCT-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the aerophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrobaculum aerophilum. Archaea; Crenarchaeota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8ZYF6;
28-FEB-2003
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NCBI_TaxID=13773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Catalyzes the 1,3-allylic rearrangement of the homoallylic substrate isopentenyl (IPP) to its allylic is dimethylallyl diphosphate (DMAPP) (By similarity). CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the IPP isomerase type 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c. Natl. Acad. FUNCTION: Cata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COPACTOR: FWN and NADPH (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRAE
                                                                                                                                                                                                                                                                                                         338
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                                                                                                                                                                                                                                                                                                                                                                                                               8; Conserv
                                                                                                                                                                                                                                                                                                                                              GPTLRQWLEGRR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DADDPSVREWARGPDRTRRP
                                                                                                                                                                                                                                                                                                         GPRLRNWIEQRR
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                  PRELIMINARY;
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45,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               43.5%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoprotei;
                               Last sequence update)
Last annotation update)
romyces cerevisiae YBL05
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB Pred. No. 79; 1; Mismatches
                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6854253886324C04 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                     PTC3.
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SORRED DRAFT
     DR RAP PRANCOCO OR DR RAP PRANCO
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
RA Goffard N., Frangeul L., Algle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykaster C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Boisrame A., Boyer J., Cattolico L., Ferry-Dumazet H., Groppi A.,
RA Boisrame A., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Kerrest A., Koszul R., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Ra Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker D. Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                 Schulte U., Aly...
Schulte U., Aly...
Nyakatura G., Mewes H.
Neurospora crassa.
Eukaryota; Fungi; As
Sordariomycetidae; S
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9P729
Q9P729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida glabrata CBS138.

Bukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
NCBI TaxID=284593;
                                                                                                                                                                                                       Submitted
EMBL; AL35
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Schulte U., Aign V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probable histone acetyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00332; PP2Cc; 1.
PROSITE; PS01032; PP2C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000222; PPInterPro; IPR001932; PPFfam; PF00481; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; CR380947; CAG57847.1; -.
GO; GO:0003824; F:catalytic activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome evolution in yeasts.";
Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genolevures;
                                                                                                                                                                                                                                                                German
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bouchier C., Caudron B.,
Wincker P., Souciet J.L.;
GO:0016469; C:proton-transporting two-sector ATPase complex; IEA. GG:0046933; F:hydrogen-transporting ATP synthase activity. . .; I GO:0046961; F:hydrogen-transporting ATPase activity, rota. . .; I GO:0005506; F:iron ion binding; IEA. GO:0005908; F:N-acetyltransferase activity; IEA. GO:0016740; F:transferase activity; IEA. GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                  T48737;
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                                                                                                                                                                                                             AL353819;
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                                                                                                                                                                                                                                  neurospora genome
ed (OCT-2001) to t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGPTLRQWLEGRRPKN 19
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                                                                                                                                                                                                                                                                                        FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                  ra genome project;
2001) to the EMBL/GenBank/DDBJ databases
CAB88553.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ascomycota; Po
; Sordariales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48881 MW;
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                                                                                                                                                                                                                                                                                                                                      Hoheisel J., Brandt P., I
H.W., Mannhaupt G.;
to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pezizomycotina;
s; Sordariaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BEF9E25621E3315D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ.
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                                                                                                                                                                                                                                                                                                                                                                                               Fartmann B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sordariomycetes;
Neurospora.
                                                                                                                                                                                                                                                                                                                                              databases
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the European Bioinformatics Institute.

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Z445
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                                                                                                                                                                                              RX MEDLINE=22388557; Pubmede=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Westernan K.J., Malek J.A., Gunaratine P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Gazcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Gazcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Gazcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Toushman J.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Generation and initial analysis of more than 15,000 full-length human
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA segmences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Best Local S
Matches 7
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InterPro; IPR006638; Elp3/MiaB/MifB.
InterPro; IPR006530; Elp3/Mirg/MifB.
InterPro; IPR005910; Elp3/Ac trans.
InterPro; IPR007197; Radical SAM.
Pfam; PF00583; Acetyltransf_1; 1.
Pfam; PF04055; Radical SAM; 1.
SMART; SM00729; Elp3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8R2V3; Q8K216;
10-OCT-2003 (Re
10-OCT-2003 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004
Zinc finger I
Name=Znf445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou G., Wang J., Zhang "Cloning of mouse zinc 1 Submitted (JUL-2003) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
-!- FUNCTION: May be involved in transcriptional r
-!- SUBCELLULAR LOCATION: Nuclear (Potential)
-!- SIMILARITY: Belongs to the krueppel C2H2-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 345-98
MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMs; TIGR01211;
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                 -!- SIMILARITY: Contains
-!- SIMILARITY: Contains
-!- SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase
                                                                                                                                                                                         and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGPTLRQWLEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGPYMSKWLDGR 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345-986 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42, Creat
42, Last
44, Last
in 445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang Y.;
zinc finger protein 445.";
zinc the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64684 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                       to the krueppel C2H2-type zinc-finger protein
                                                  ے ب
                                                                                     12 C2H2-type
                                                 KRAB domain.
SCAN box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 2; LC. Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyl_trans
_SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                     zinc
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                                                                                   fingers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 571;
                                                                                                                                                          regulation
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EMBL
                   a collaboration
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 outstation
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                                                                                                                                 01-OCT-2002
01-OCT-2002
01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                DOMAIN
ZN FING
Stapleton M., Brokstein P., Hong L., Agbayani A., Car
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan
George R., Gonzalez M., Guarin H., Kronmiller B., Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00349; KRAB; 1.

SMART; SM00431; LER; 1.

SMART; SM00035; ZDP C2H2; 12.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50804; SCAN_BOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01352; KRAB; 1.
Pfam; PF02023; SCAN; 1.
Pfam; PF00096; zf-C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexa
                                                                                                                                                                         Q8MT33
                              STRAIN=Berkeley;
                                                                      Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae;
                                                                                                              ORFNames=CG7112;
                                                                                                                       RE63030p.
                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY341877; AAQ24161.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                         SEQUENCE FROM N.A.
                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000003; Znf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                          260
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BC034572; AAH34572.1; ALT_INIT.
                                                                                                                                                                                                                                             μ
                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                                                                                                                          GSSPKPALISWLEARKP
                                                                                                                                                                                                                                              GNADGPTLRQWLEGRRP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001909; KRAB.
IPR003309; Treg_SCAN
IPR007087; Znf_C2H2.
                                                                                                                                 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                     52
219
470
498
553
581
662
718
718
824
933
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulation;
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                                                                                                                                                                                                                                                                                                                            Arthropoda; Hexapoda; Insecta; Pterygota; gota; Diptera; Brachycera; Muscomorpha; hilidae; Drosophila.
                                                                                                                                                                                                                                                                          43.5%;
47.1%;
                                                                                                                                                                                                                                                                                                        114774
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_C2H2; 6.
                                                                                                                                  22,
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SCAN box.
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                                                                                                                                                                                                                           276
                                                                                                                                                                                                                                                                                                       KRAB.

C2H2-type 1.
C2H2-type 2.
C2H2-type 3.
C2H2-type 5.
C2H2-type 6.
C2H2-type 6.
C2H2-type 8.
C2H2-type 9.
C2H2-type 10.
C2H2-type 11.
C2H2-type 11.
C2H2-type 12.
V -> Q (in Ref. 2; AA
R -> Q (in Ref. 2; AA
                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                            Score 47;
Pred. No.
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                           2.4e+02;
                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                   2; AAH34572)
2; AAH34572)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat;
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                                                                                                                                                                                                                                                                                     Length 986;
                                                                                                                                                                                                                                                                                                         CRC64;
                     Carlson
  P.,
  Frise E.,
Liao G.,
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                                                                                                                                                                                                                                                                 Gaps
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RESULT 35
Q9VSI2
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                                REPRESENTATION OF THE PROPERTIES OF THE PROPERTIES OF THE PROPERTY OF THE PROP
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                                            RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocarne J.D., RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Randell M.D., Zhang Q., Chen L.X., RA George R.A., Doyle C., Batter E.G., Helt G., Nelson C.R., Gabor G.L., RA Harli J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baddwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Botchier R., Canter J.M., Cawley S., Dahlke C., Davenport L.B., Databakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I., Cadieu E., Center A., Chandra I., Cadieu E., Center A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Cherry J.M., Cawley S., Dahlke C., Ferriaz C., Ferriera S., Fleischmann W., Poslec C., Goorge F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., RA Dutbin K.J., Brangelista C.C., Kravitz S., Kulp D., Harris M., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., RA Harris D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Harris M., Glasser K., Ra Liu X., Maltei B., McIntosh T.C., McLeod M.P., McIntosh J.A., Ketchum K.A., RA Nelson D.R., Nelson D.L., Ra Nelson D.R., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Nelson S.M., Woodager, World W. Strong R., Wang A.H., Wang X., Ra Nelson D.R., Weinstock G.M., Weissenbach J., Na Nelson D.R., Nelson D.R., Nelson D.R., Nelson D.R., Nelson D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
Matches
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Celniker S.;
Submitted (JUN-2002) to the F
EMBL; AY118408; AAM48437.1;
FlyBase; FBgn0035879; CG7112
InterPro; IPR011036; PH relai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VSI2; PRELIMINARY;
Q9VSI2;
01-MAY-2000 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miranda A. Patel S.,
                            Wang Z.Y.
Williams
Yeh R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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ORFNames=CG7112;
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PF00566; TBC; 1.
; SM00164; TBC; 1.
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1005 AA; 113317 MW;
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Barmur, woodageT, woodageT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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PH_related.
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26,
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S., Wan K.,
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Last annotation updat
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                                Zhang G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58C70A8326D2073A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
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Gibbs R.A.,
"The genome
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SMART; SM00164; TBC; 1
PROSITE; PS50086; TBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2004) to the EMBL; AE003555; AAF50437.2; FlyBase; FBgn0035879; CG7112
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MiBra S., Crosby M.A., Mungall C.J
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Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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Kaminker J.S., Bergman C.M., Kronmiller
Patel S., Frise E., Wheeler D.A., Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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8; Conserv
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A; 113287 MV
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Hodgson .
Ison C.R.,
on E.J.,
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Prochnik S.E.
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GO; GC:0005737; C:cytoplasm; IEA.
GO; GC:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008565; F:protein transporter.
GO; GO:0006886; P:intracellular proteil
InterPro; IPR006938; ARM.
InterPro; IPR006938; Wsol_p115_C.
InterPro; IPR006953; Usol_p115_head.
Pfam; PF04871; Usol_p115_head; 1.
Pfam; PF04869; Usol_p115_head; 1.
SEQUENCE 1171 AA; 131632 MW; 33DF5
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01-OCT-2000
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Schulte U., Aign V., Hoheisel J.,
Nyakatura G., Mewes H.W., Mannhauj
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Eukaryota; Fungi; P
Sordariomycetidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hsing Y.C., Chow T., Chen C Submitted (JAN-2000) to the EMBL; AP001111; BAA90509.1;
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GO:0005737; C:cytoplasm; IEA.
GO:001620; C:membrane; IEA.
GO:0008565; F:protein transporter activity;
GO:0006886; P:intracellular protein transpor
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Mannhaupt G.;
he EMBL/GenBank/DDBJ
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EMBL/GenBank/DDBJ
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Hayette S., Morlé L., Bozon M., Ghanem A., Risinger Tanner M.J.A., Fattoum S., Cohen C.W., Delaumay J.; "A point mutation in the protein 4.2 gene (allele 4. associated with hereditary haemolytic anaemia."; Br. J. Haematol. 89:762-770 (1995).

1. FUNCTION: Probably plays an important role in the erythrocyte shape and mechanical properties.
                                                                                                                        "A novel mutation in the erythrocyte protein patients with hereditary spherocytosis (prote Br. J. Haematol. 88:527-533(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 267:5680-5685(1992).
                                                                                                                                                                            VARIANT HS THR-111.
MEDLINE=95118828; PubMed=7819064;
Takaoka Y., Ideguchi H., Matsuda !
Fukumaki Y.;
                                                                                                                                                                                                                                               associated with a Japanese form (protein 4.2 Nippon).";
Blood 79:1846-1854(1992).
                                                                                                                                                                                                                                                                          Bouhassira E.E., Schwartz R.S., Yawata Y., Ata
Qiu J.T.-H., Nagel R.L., Rybicki A.C.
"An alanine-to-threonine substitution in prote
associated with a Japanese form of hereditary
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93271204; PubMed=8499466; DOI=10.1016/0005-2736(93)90156-T; Dotinas E., Speicher D.W., Guptaroy B., Cohen C.M.; Speicher D.W., Guptaroy B., Cohen C.M.; Potential domain mapping and phosphorylation of human erythrocyte pallidin (band 4.2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92184834; PubMed=1544941; Risinger M.A., Dotimas E.M., Cohen C.M. "Human erythrocyte protein 4.2, a high is N-myristylated.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90138995; PubMed=1689063;
Sung L.A., Chien S., Chang L.-S., Lambert K., Bliss S.A.,
Bouhassira E.E., Nagel R.L., Schwartz R.S., Rybicki A.C.;
"Molecular cloning of human protein 4.2: a major componen
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Eukaryota; Metazoa;
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Bouhassira E.E., Schwartz R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythrocyte membrane.";
Proc. Natl. Acad. Sci. U.S.A. 87:955-959(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete amino acid sequence and
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MEDLINE=91271288; PubMed=2052563;
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                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1148:19-29(1993).
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MEDLINE=90138879; PubMed=2300550;
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                                                                                                                                                                                                                                                                                                                                  PubMed=1558976;
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GO; GO:0005856; C:cytoskeleton; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005524; F:ATTP binding; TAS.
GO; GO:0005220; F:structural constituent
InterPro; IPR001102; GlutransfG.
InterPro; IPR008958; Transglut_C.
InterPro; IPR002931; Transglumase_like.
Pfam; PF0087; Transglut_C; 2.
Pfam; PF00864; Transglut_Core; 1.
Pfam; PF00866; Transglut_N; 1.
PROSITE; PS00547; TRANSGLUTAMINASES; 1.
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EMBL; M39346; A
EMBL; M39647; A
PIR; A39707; A3
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                                                                                                                                               Alternative splicing; Cell shape; Cytoskeleto
Direct protein sequencing; Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:3381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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SLC4A1/band
SUBCELLULAR 1
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PTM: Both cAMP-dependent kinase (CAPK) and another kinase pre in the red-blood cells seem to be able to phosphorylate EPB42 in the red-blood cells seem to be able to phosphorylate EPB42 DISEASE: Defects in EPB42 are a cause of hereditary spherocyt (HS) [MIM:177070], a hematologic disorder leading to chronic hemolytic anemia and characterized by numerous abnormally sha erythrocytes which are generally spheroidal. Absence of band associated with spur or target erythrocytes has also been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLC4A1/band 3 anion transport protein.
SUBCELLULAR LOCATION: Membrane-associated
erythrocyte membranes) and cytoplasmic.
ALTERNATIVE PRODUCTS:
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MISCELLANEOUS:
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L06512;
L06513;
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L06519; AAA52385.1;
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license agreement (See http://www.isb-sib.ch/announce,
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By similarity.
Band 3 binding (By similarity).
N-myristoyl glycine.
Phosphoserine (by PKA) (Probable).
Q -> QGEPSQRSTGLAGLYAAPAASPVFIKGSGMD isoform Long).
                                                                                                                              hape; Cytoskeleton; isease mutation; Erythrocyte maturation; Lipoprotein; Myristate; Phosphorylation;
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transglutaminase
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Matches 10
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Q95QV6;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last 01-MAR-2004 (TrEMBLrel. 26, Last Hypothetical protein C18A3.5, Name=C18A3.5; ORFNames=C18A3.5; Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                      Submitted [5]
           WormBase; WBGene00015943; C18A3.5.
WormPep; C18A3.5c; CB27710.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; RRM 1; 1.
PROSITE; PS50102; RRM; 1.
                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N
STRAIN=Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hallsworth K.;
"The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                            EMBL; U28944; AAK68193
                                                                                                                              WormBase Consortium;
Submitted (SEP-2004)
                                                                                                                                                                      STRAIN-Bristol
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                                                                                                                                                                                                                                               Wilson
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                                                                                                                                                                                                                                                                                   SEQUENCE
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Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A. ristol N2;
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EMBL/GenBank/DDBJ databases.
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V -> L (in Ref. 3);
C6E605E69A0A7A8B
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Pred. No. 1.9e+02;
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/FTId=VAR_012268.
TRPALP -> KRGLPC (in Ref.
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A -> T (in HS; Nippon/Fukuoka).
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RESULT 41
Q9RKP9
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RA PubMedia 14702039; DOI:10.1038/ng1285;
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Albe K., Kamihara K., Watsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Albe K., Kamihara M., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Ono Y., Takahashi T., Yamashita H., Tanase T., Nomura Y.,
RA Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Gato Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Tarigami A., Fujiwara T.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Mizushima-Sugano J., Satoh T., Sitai Y., Masuhami Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai K., Watanabe K., Watanabe M., Masuho Y., Yamashita R.,
RA Nakai K., Watanabe Y., Sugaki M., Masuho Y., Yamashita R.,
RA Nakai K., Masuho Y., Mizuno T., Mohal
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01-OCT-2000
01-OCT-2000
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ10043.
Homo sapiens (Human)
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 Q9RKP9
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                       CDNAs.";
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                                                                                                                        PTLROWLEGRRPK 18
                                                                                          PTLRPWVWTRRPR 27
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905; BAA91418.1;
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                                                                                                                                                             Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                    17352 MW;
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Pred. No. 30;
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01-MAR-2002 (TrE
05-JUL-2004 (TrE
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01-MAY-2000
01-MAY-2000
01-JUN-2003
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation updat
Hypothetical protein SCO2279.

ORFNames=SCC75A.25c;
                                                                                                                                           Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartebeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanaken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbur Salzberg S.L., White O., Fraser C.M.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                        Hypothetical protein OSJNBb0076H04.22 (Putative transcriptase).
Name=OSJNBb0076H04.22; ORFNames=OSJNBa0022D10.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 417:141-147(2002).
EMBL; AL939112; CAB61725.1;
PIR; T50588; T50588.
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Bacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                   SEQUENCE FROM N.A.

The Rice Chromosome 10 Seque:
"In-depth view of structure,
chromosome 10 ".
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MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
                                                                                    Submitted
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4 (TremBLrel. 27,
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26559 MW; 13584D7A81A0EF90 CRC64;
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EMBL; AE017082; AAP53273.1; -.
Gramene; Q7XFF3; -.
GC); GO:0003964; F:RNA-directed DNA pc
GO; GO:0003964; F:RNA-directed DN PC
GO:0003964; F:RNA-directed DN PC
GO:0003964; F:RNA-directed DN PC
GO:0003964; F:RNA-directed DN PC
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GO:0003964; F:RNA-directed DN PC
GO:0003964; F:RNA-directed DN PC
GO:0003964; F:RNA-directed DN PC
GO:0003964; F:RNA-directed DN PC
GO:00039
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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Wing R.A., Yu Y., Soderlund C., Chen M., Kim H
Saski C., Henry D., Oates R., Simmons J.;
Saski C., Henry D., Oates R., Simmons J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
EMBL; AC099402; AAL79345.1; -
GO; GO:0003964; F:RNA-directed DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Bhrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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Q7G731;
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STRAIN=A3(2) / M.45;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser
                                                                                                                                                                                                                 Hypothetical protein SC00239. ORFNames=SCJ9A.18c;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                          Streptomycineae;
NCBI_TaxID=1902;
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SEQUENCE 249 AA; 28243 MW
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                                                                                      SEQUENCE
                                                                                                                                                                           Bacteria; Actinobacteria;
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yta; Liliopsida;
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77;
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"Complete genome sequence and comparative analysis microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005023; BAC68182.1; ---
GO; GO:0005022; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IE.
GO; GO:0006355; P:regulation of transcription, DNA-
InterPro; IPR000005; HTHARAC.
Pfam; PP00155; HTH AraC; 1.
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Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., How
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O
Rabbinowitech E., Rajandream M.A., Rutherford K.M., Rutter
Seeger K., Saunders D., Sharp S., Squares R., Squares S., T
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Park
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metabolites.";
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01-JUN-2003 (TrEMBLrel. 24, Last sequence up
01-MAR-2004 (TrEMBLrel. 26, Last annotation
Putative regulatory protein.
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07-JUN-1995;
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  receptor affinity compound
The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mum. compound (especially if modified, see features table) can be used for
                                                                                                                                                                      mimetic(s) - useful in treathrombocytopenia resulting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Preferably C-terminus is -C(0)R2 where R2 is selected from hydroxy, lower alkoxy, and -NR3R4, where R3 and R4 are independently selected from hydrogen and lower alkyl, and where the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide forming a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Preferably linkages are selected from: -
CH2OC(0)NR-; phosphonate; -CH2S(0)2NR-; -CH2NR-; -C!
; -NHC(0)NH; where R is hydrogen or lower alkyl and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lower
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Best Local S
Matches 19
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                                                                                                                                                                                          The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia
                                                                                resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to invesmechanism of thrombopoietin signal transduction and receptor or to maintain the proliferation and growth of thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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     Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                   19; Page 89; 106pp;
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95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide; 19
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PJ, Wagstrom
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Pred. No. 1.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duffin DJ, Gates com CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                            from chemotherapy, etc.
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                                                                                        y, e.g. to investigate the and receptor activation, thrombopoietin dependent
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Query Match Best Local S Matches 19

Similarity

100.0%;

Score 114; DB 2; Pred. No. 1.3e-09;

Length

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Mismatches

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                                                                                                                                                                      of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimerics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological materials. They may also be used for in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; benzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
07-JUN-1996;
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                                                                                                                      Sequence
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l Similarity
19; Conserv
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mnian P, Waq
100.0%; ilarity 100.0%; Conservative
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96WO-US009623.
96US-00699027.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cwirla SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ğ
                            Score 114; DB 4;
Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TPO-R) activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Gates CM,
Hendren RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schatz PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deprince
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                         Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Podduturi S;
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Indels

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Gaps

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patients suffering from haematological disorders

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RESULT 4
AAW09456
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          receptor affinity compound
          The present sequence is a compound which binds to thrombopoietin (TPO receptor (TR). It has a molecular weight of <8000 Da, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mum. compound (especially if modified, see features table) can be used for
                                                                                                          Thrombopoietin receptor-binding/activating peptide(s) mimetic(s) - useful in treatment of haematological dis
                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                 07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW09456;
                                                                        Claim
                                                                                                thrombocytopenia resulting
                                                                                                                                                                          Mattheakis
                                                                                                                                                                                     Dower WJ,
                                                                                                                                                                                                                                                                           07-JUN-1995
                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                     19-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haematology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW09456
                                                                                                                                                                                                             (GLAX )
                                                                                                                                                 1997-051883/05
                                                                        18;
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                                                                                                                                                                                                              GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCADGPTLREWISFCGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCADGPTLREWISFCGGK
                                                                                                                                                                        Ľ,
                                                                                                                                                                                    Barrett RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombocytopenia; TPO; TR; proliferation;
                                                                                                                                                                                                              GROUP
                                                                                                                                                                                                                                    95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
                                                                       89; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor binding compound peptide
                                                                                                                                                                                                                                                                                                                           96WO-US008998
                                                                                                                                                                                                                                                                                                                                                                                                selected from hydroxy, lower alkoxy, and -NR3R4, where R3 and R4 are independently selected from hydrogen and lower alkyl, and where the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide forming a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Preferably N-terminus is selected from: -NRR1; NRC(0)R; -NRC(0)OR; -NRS(0)2R; -NHC(0)MHR; succinimde; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                          Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CH2OC(O)NR-; phosphonate; ; -NHC(O)NH; where R is h; lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Preferably C-terminus is -C(O)R2 where R2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Preferably linkages are selected from: -
'H2OC(0)NR-; phosphonate; -CH2S(0)2NR-; -CH2NR-;
-NHC(0)NH; where R is hydrogen or lower alkyl i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                              GI.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                        ΡJ,
                                                                                                                                                                                     Cwirla SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemotherapy; radiation therapy
                                                                        English
                                                                                              from chemotherapy,
                                                                                                                                                                       Wagstrom
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                                                                                                                                                                                     Duffin
                                                                                                                                                                        CR,
                                                                                                                                                                        Wrighton
                                                                                                                                                                                     'n,
                                                                                                  etc.
                                                                                                                                                                          Gates
ton NC;
                                                                                                             disorders,
                                                                                                                        and peptide
                                                                                                                                                                                     <u>,</u>
                                                                                                                                                                                       Johnson
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RESULT 5
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PPD 19-1
AX O7-0
PP 07-0
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                                                    Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marrow transfusions. proliferation and grobiological research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombocytopenia resulting from chemotherapy, radiation therapy or k marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18
                                                                                                                                                                                                                                                   resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                            The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dower WJ, Barret RW, Mattheakis LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9640750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW33023
                                                                                                                                                                 Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Page 89; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
18; Conserv
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                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCADGPTLREWISFCGG 18
GGCADGPTLREWISFCGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00478128.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.6%;
                                                    95.6%; Score 109; DB 2; 1
100.0%; Pred. No. 6.6e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cwirla SE, Du
PJ, Wagstrom
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duffin DJ, Gate
om CR, Wrighton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18
                                                                                                            Length 18;
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                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                       Gaps
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                                                                                           CC (XI)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(CC (L2))d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, CC (L2)d-P2-(L3)e-P3, and L4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, CC c, d, e, and f = are each independently 0 or 1, provided that at least 1 or f and b is 1. The composition can have cytostatic, antiasthmatic, CC thrombolytic and immunosuppressive activities. DNAs, vectors and host CC cells from the present invention can be used for producing pharmaceutical CC compositions. The compositions are useful for treating cancer, asthma, CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than CC such as Fc receptor binding, protein A binding, complement fixation, and CC spossibly placental transfer. AAA69343 to AAA69326 and AAB16935 to CC AAB18003 represent nucleotide and amino acid sequences used in the
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; Minhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB17020 standard;
                                                               Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                   active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO-mimetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17020;
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-)
                 Local
                                                                                                                                                                                                                                                                                                                                                                    present invention describes composition of matter (I) comprising domain, pharmacologically active peptides, and linkers. Where (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                composition of matter comprising an Fc domain and pharmacologically peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       μ
18;
                 Similarity
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Pred. No.
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                   6.6e-09;
                                  DB 3;
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                               Length 18;
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                                                                                                                                                                CC bind to and activate the human thrombopoletin receptor (TPO-R). Methods (C of activating thrombopoletin receptors in cells comprise contacting the C cells with effective amounts of peptides and peptide mimetics attached to the C that with effective amounts of peptides and peptide mimetics attached to CC as that due to chemotherapy, radiation therapy or bone-marrow CC transplantation and to prevent thrombocytopenia in patients at risk. The c sequences are used to treat and prevent haematological disorders (C including thrombocytopenia and platelet disorders. They are used in vitro CC as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO CC receptor. The peptides can be used to detect TPO receptors on living CC receptor. The peptides can be used to detect TPO receptors of in the peptides can be used to detect TPO receptors of in purified or natural biological materials. They may also be used for in the staining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed committed or in conjunction with additional cytokines
                                                                  Query Match
Best Local S
Matches 18
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07-JUN-1995;
07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombocytopenia and hematological disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 65-66; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human thrombopoietin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU25820 standard; peptide;
                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Activating thrombopoietin receptors in cells, used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-564142/63
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                                                                                    Similarity
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ĠĠĊADĠPTĹŔĔŴĬŚFĊĠĠ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU25815-AAU26049 represent peptides and peptide mimetics nd activate the human thrombopoietin receptor (TPO-R). Meth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrett
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                                                                    Conservative
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95US-00485301.
96WO-US009623.
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Pred. No. 6.6e-09;
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Hendren RW,
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Deprince RB,
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neuroprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for CC diagnosing diseases characterised by dysfunction of their associated CC protein of interest, for identifying normal or abnormal proteins of CC interest, as a part of diagnostic kit to detect the presence of their CC proteins of interest in a biological sample. Additionally, (I) is useful CC for treating inflammatory and autoimmune diseases, tumour growth, cancer, CC refunction darthritis, diabetic retinopathy, obesity, sleep disorders, creating compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPD-mimetic comprising EPO megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic comprise syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 cc exemplification of the present invention
ABB72906

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 39; Page 44; 176pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes a vehicle-peptide molecule (I) or its
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                                                                                                                                                                                                                                                                           ligand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is a TPO mimetic peptide sequence used to make a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one human framework region and at least one light chain variable region, which there is a such that the comprises at least one human framework region and at least one light thinding region of the control of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2002; 2002US-0368791P
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                          GGCADGPTLREWISFCGG 18
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GGCADGPTLREWISFCGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 512;
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                                                                                                                                                                                                       AA;
                                                                                                   Conservative
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                                                                                                                                                                                                                                                        invention.
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                                                                                                                            Score 109; DB 7; 
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Pred. No.
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                                                                                                                                                    Length 18
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                                                                                                                                                                                                                                                                                                                                         This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be consequenced them), compositions, methods and uses. The invention may be consequenced to the development of compounds with an immunosuppressive, cardiant, hypotensive, neuroprotective, nootropic, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, cardiovascular, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, cardiovascular (for example arrhythmia, typertension or heart immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia conflictions, or infectious diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or conditions, or infectious diseases (for example bacterial, viral or conditions, or infectious diseases (for example bacterial, viral or conditions, or infectious diseases (for example bacterial, viral or conditions, or infectious diseases (for example bacterial, viral or conditions, or infectious diseases (for example bacterial, viral or conditions, or infectious diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or conditions, or infectious diseases or disorders, anaemia, cancerous are fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                                                                                           Matches
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fungicide; gene therapy; immune disorder; cardiovascular dise
arrhythmia; hypertension; heart failure; neurodegenerative;
multiple sclerosis; dementia; Alzheimer's disease; anaemia;
cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH1 deleted mimetibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CH1 deleted mimetibody-related peptide SeqID512
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 512; 129pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-082870/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CENZ ) CENTOCOR INC.
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                                                                                                                                                                               Local
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                                                                                                                                           l Similarity
                                                                                                                                                                                                                                                                                      18
                                                                 GGCADGPTLREWISFCGG 18
                                                                                                                                                                                                                                                                                      8
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective; nootropic; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knight DM,
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                                                                                                                                100.0%;
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ctive; nootropic; antibacterial; virucide;
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Pred. No.
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                                                      cc cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, general cological-Gen, auditory, endocrine-Gen, communomodulator, antiallergic, muscular-Gen, epatotropic, haemostatic, cc immunomodulator, antiallergic, muscular-Gen, cytostatic, cc immunomodulator, antiallergic, muscular-Gen, cytostatic, cc immunomodulator, antiallergic, muscular-Gen, cytostatic, cc respiratory-Gen activity acting as a tumour necrosis factor (TNP)-CC modulator or cytosine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or cc present invention are useful for the diagnosis, prevention and/or cc cardiovascular, dental or conditions associated with aberrant expression cc cardiovascular, dental or oral, dermatological, ear, nose or throat, cendocrine, metabolic, gastrointestinal, gynaecological, hepatic, conscentic, haematologic, immunological, allergic, infectious, musculoskeletal, oncological, neurological, nutritional, ophthalmologic, mecalostric, psychiatric, renal or pulmonary disorders. The present cc gedeaters, psychiatric, renal or pulmonary disorders. The present cc mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heavner GA, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ophthalmological; nephrotropic; respiratory Gen; tumour necrosis factor. TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; oncological disorder; neurological disorder; peychiatric disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New CH1 deleted mimetibody polypeptide and nucleic acid, useful f diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2002;
19-SEP-2002;
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gynaecological-Gen; hepatotropic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to CH1 deleted mimetibodies (and the DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CH1 deleted mimetibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encode them),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 512; 123pp; English
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2002US-0412144P.
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Query Match

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07-JUN-1995;
07-JUN-1995;
                                                                                             The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                           Sequence 14
                                                                                                                                                                                           Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
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07-JUN-1995;
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bone marrow
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                                     Conservative
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95US-00484090.
95US-00485301.
                                                                                                                                                                         91; 106pp; English.
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95US-00473604.
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Pred. No.
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om CR, W
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                                                1.7e-05
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Wrighton
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an ICSO of no more than about 100 mum. Th compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
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Mattheakis
                                                                                                                                                                                                                                  thrombocytopenia resulting from chemotherapy, etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995,
                                                                                                                                                                                              Claim 18; Page 89; 106pp;
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LC, Schatz
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95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Preferably C-terminus is -C(O)R2 where R2 is selected from hydroxy, lower alkoxy, and -NR3R4, whe and R4 are independently selected from hydrogen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Preferably linkages are selected from: -
CH2OC(0)NR-; phosphonate; -CH2S(0)2NR-; -CH2NR-; -C(0)NR6
; -NHC(0)NH; where R is hydrogen or lower alkyl and R6 is
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PJ, Wagstrom
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                                                                                                                                                                                                                                                                                          chemotherapy, radiation therapy or work many also be used to maintain the proliferation and growth dependent cell lines and for use in biological research, for receptors on living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
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   CADGPTLREWISFC
                                                            CADGPTLREWISFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                AA
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombocytopenia; TPO; TR; proliferation;
transfusion; chemotherapy; radiation therap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US008998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.6%; 500
100.0%; Pr
                                                                                                                                                                                    74.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cwirla SE, I
PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
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0; Mismatches
                                                                                                                           0;
                                                                                                                                                        Score 85;
Pred. No.
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                                                                                                                           Mismatches
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om CR, W
                                                                                                                                                        DB 2; L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cyclic
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Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 14;
                                                                                                                                                                                    Length 14;
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                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson
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                                                                                                                                                                                                                                                                                                                                               detecting
                                                                                                                                                                                                                                                                                                                                                                                                     The peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  suffering
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                                                                                                                              Gaps
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RESULT 16
AAW33031
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AAW33
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                                                                                                                                                                                    Query Match
Best Local
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07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                               chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting
                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
                                                                                                                                                                                                                  Sequence 14
                                                                                                                                                                                                                                                                             The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from
                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                        Dower WJ,
Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW09482;
                     Thrombopoietin
                                                                                                                                                                                                                                                                                                                                          thrombocytopenia resulting from chemotherapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin receptor binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW09482
 Thrombopoietin receptor; binding peptide; treatment; agonist;
                                         11-MAR-1998
                                                                                  AAW33031 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLAX )
                                                                                                                                                                                                                                       receptors on
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                                                                                                                                                                                      Similarity
                                                                                                                                   CADGPTLREWISFC
                                                                                                                                                      CADGPTLREWISEC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                       Barrett RW,
LC, Schatz
                                                                                                                                                                                                                  AA,
                                                                                                                                                                                                                                                                                                                       Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombocytopenia; TPO; TR;
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                                        (first entry)
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95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                      GROUP LTD
                     receptor
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                                                                                                                                                                                                                                      living
                                                                                peptide;
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                                                                                                                                                                                                                                                                                                                      106pp;
                                                                                                                                                                                                                                                                                                                                                                                                     PJ,
                     binding peptide
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                                                                                                                                                                                    Score 85;
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                                                                                                                                                                                    DB 2; Lo
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                                                                                                                                                                                                                                                                                                                                                                                                       Wrighton
                                                                                                                                                                                              Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                        Gates CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy
                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson
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Best Local
                                                                            Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                          WO9640750-A1
                                                   Synthetic.
                                                                                                                                               Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                          resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 30; Page 91; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
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Mattheakis LC, Schatz PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                         11-MAR-1998
                                                                                                                                                                                                  AAW36633;
                                                                                                                                                                                                                           AAW36633 standard;
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                                                                                                                                                                         (first
                                                                                                                                             receptor binding peptide
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95US-00485301
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                                                                                                                                                                                                                         peptide;
                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                            74.6%;
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                                                                                                                                                                                                                                                                                                                                               Score 85; DB; Pred. No. 1.7
                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                               1.7e-05;
thes 0;
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19-DEC-1996

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RESULT 18
AAW33029
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin signal transduction and the proliferation and growth of the process of t
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor activation, or to maintain the proliferation thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present
                                                                 WPI; 1997-052226/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW33029 standard;
                                                                                                                                Mattheakis
                                                                                                                                                                Dower WJ,
                                                                                                                                                                                                                                                                                             07-JUN-1995;
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                                                                                                                                                                                                                               (GLAX ) GLAXO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CADGPTLREWISFC 16
         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CADGPTLREWISFC
                                                                                                                                   Barret RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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      peptide mimetics which
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                                                                                                                                                                                                                               GROUP LTD.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cwirla SE, Duffin PJ, Wagstrom CR,
                                                                                                                                   Cwirla SE, Du
PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
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om CR, Wrighton
             bind
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J. 1.7e-05;
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             and
                                                                                                                                      Gates CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   culture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 14;
         activate
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                the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 19
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 AA;
                                                         Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                              WPI;
                                                                                                                                      Dower WJ, Barret RW,
Mattheakis LC, Schatz
                                                                                                                                                                                                    07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                           signal transduction; receptor activation; cell
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95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombocytopenia resulting from chemotherapy, etc
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .14
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100.0%; I
tive 0;
                                                                                                                                         ΡJ,
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                                                                                                                                       Wagstrom
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                                                                                                                                         Wrighton
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The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a

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RESULT 20
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                                                                                                                                                                                                                   thrombocytopaenia resulting from chemocytopaenia resulting from transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and growth
                                                                                                                                                                                                                                                                                              The present peptide, which binds the thrombopoietin receptor (TR), cused to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombopotetin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin receptor binding peptide.
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                                                                                                                                                 Sequence
                                                                                                                                                                                                investigate the mechanism of thrombopoietin signal transceptor activation, or to maintain the proliferation thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mattheakis
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                                              74.6%; Score 85; DB llarity 100.0%; Pred. No. 1. Conservative 0; Mismatches
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J. 1.7e-05;
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1.7e-05;
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                                                                                            Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                           The present peptide, which binds the thrombopoietin receptor (TR), cused to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used disgnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
07-JUN-1995;
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Misc-difference
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                                                                                                                         Similarity
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                             CADGPTLREWISFC
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                                                                                          74.6%; Silarity 100.0%; Conservative 0;
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95US-00485301.
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                                                                                            ; Score 85; DB
k; Pred. No. 1.7
0; Mismatches
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                                                                                                                       DB 2; Le
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Wrighton NC;
                                                                                                                                            Length 14;
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RESULT 22
AAW33032
ID AAW33

AAW33032

standard; peptide;

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RESULT 23
AAB17014
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                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                         The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microw. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                         Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
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07-JUN-1995;
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                                                                                                                                                                                                                        Sequence 14
                                                                                                                                                                                                                                                           resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                 Claim 30; Page 91; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-052226/05.
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                                    AAB17014;
              31-OCT-2000
                                                            AAB17014 standard;
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                                                                                                                                                 CADGPTLREWISFC 16
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LC, Schatz
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            (first
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95US-00485301.
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                                                           peptide;
              entry)
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PJ, Wagstrom CR,
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Pred. No.
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17-DEC-2001 AAU25826;

(first entry)

AAU25826 standard; peptide;

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Human thrombopoietin receptor

Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

(TPO-R) activator peptide #12

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                                                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (XI)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-CC (L2)d-P2-(D3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, CC c, d, e, and f = are each independently 0 or 1, provided that at least 1 CC of a and b is 1. The composition can have cytostatic, antiasthmatic, trambolytic and immunosuppressive activities. DNAs, vectors and host CC cells from the present invention can be used for producing pharmaceutical CC compositions. The compositions are useful for treating cancer, asthma, CC a Fab domain or antoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions and
RESULT 24
                                                                                                                        Query Match
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Matches 14
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                                                                                                                                                                                                                                such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
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22-OCT-1999;
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                                                                                                                                             Similarity
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                                                        CADGPTLREWISEC
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                                                                                                                        74.6%; S llarity 100.0%; Conservative 0;
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99US-00428082
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                                                                                                                                             Score 85;
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RESULT 25
AAU25852
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Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods CC of activating thrombopoietin receptors in cells comprise contacting the CC ells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such CC as that due to chemotherapy, radiation therapy or bone-marrow CC transplantation and to prevent thrombocytopenia in patients at risk. The Sequences are used to treat and prevent basentological disorders CC including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin CC receptor. The peptides can be used to detect TPO receptors on living C cells and fixed cells, in biological fluids, in tissue homogenates, and C in purified or natural biological materials. They may also be used for in Situ staining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed committed committed or in conjunction with additional cytokines
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Matches 14
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                                                                                                                                                                                                                                                                                                                 Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cwith peptides and peptide mimetics attached to hydrophilic polymers.
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                Human thrombopoietin
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llarity 100.0%;
Conservative (
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                receptor (TPO-R) activator peptide
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                                                                                                                     RESULT 26
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                                                                                     AAU25866 standard;
                                                                                                                                                                                                                                                                                      Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activating thrombopoietin receptors in cells, thrombocytopenia and hematological disorders, with peptides and peptide mimetics attached to
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Balasubramanian P,
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                                                         AAU25866;
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95US-00485301.
96WO-US009623.
96US-00699027.
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                                                                                     peptide;
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Wagstrom CR, Hendren
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o hydrophilic polymers
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Deprince RB,
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Human thrombopoietin receptor

(TPO-R) activator peptide #52

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17-DEC-2001

(first entry)

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RESULT 27
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                         05-APR-2002
                                                                                                                      ABB72900 standard;
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strom CR, Hendren RW,
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cc neuroprotective activities. (I) can be used as a therapeutic or cycophylactic agent as well as for screening purposes. (I) is useful for cdiagnosing diseases characterised by dysfunction of their associated comprotein of interest, for identifying normal or abnormal proteins of cinterest, as a part of diagnostic kit to detect the presence of their comproteins of interest in a biological sample. Additionally, (I) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, creating their compounds are useful for treating diseases, tumour growth, cancer, creatility, and neurological degenerative diseases, tumour growth, cancer, creatility, and neurological degenerative diseases. (I), comprising EPO-compounds are useful for treating discorders characterised by low cred blood cell levels such as anaemia. The TPO-mimetic comprising compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic cumour which result in thrombocytopaenia, systemic lupus erythematosus, cand Fanconi's syndrome. ABB72403 to ABB73426 and ABI35695 to ABI35777 represent amino acid and nucleic acid sequences used in the
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                                                                                 Matches
                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressicytostatic, antirheumatic, antiarthritic, antidabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological antianaemic, anorectic, antiinfertility, haemostatic, dermatological antianaemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; antianaemic; anorectic; antiinfertility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
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                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPO mimetic peptide SEQ ID NO:70
                                                                                                        Local
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                                      w
                                                                                                        Similarity
                               CADGPTLREWISFC 16
                                                                                                                                                                        14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheetham JC,
                                                                             74.6%; SUL
100.0%; Pr
14
                                                                                                        Score Pred.
                                                                                    red. No. 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boone TC, Gudas JM;
                                                                                 DB 5; Le
, 1.7e-05;
ches 0;
                                                                                                                            Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive, c, ophthalmological
                                                                                      0
                                                                                      Gaps
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RESULT 29
ADJ52686
ID ADJ52
XX
AC ADJ52
XX
AC ADJ52
XX
DT 06-MA
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                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                             This invention relates to novel mammalian CDR mimetibodies, specific CC portions or variants thereof. Specifically, it refers to an antibody CC fragment where a protein has been inserted into, or replaces a portion CC of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one CC ligand binding region (LBR). The present invention describes human framework region and at least one mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic CC plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms CC preparing compositions for modulating, treating or reducing the symptoms CC preparing compositions for modulating, treating or reducing the symptoms CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This controls as a market a series of the corrective activities. This
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mimetic; CDR mimetibody; gene therapy; transgenic; immune;
cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                     Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ73051 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2002; 2002US-0368791P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAR-2003; 2003WO-US009139
                  06-MAY-2004
                                                 ADJ52686;
                                                                             ADJ52686 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                        14;
                                                                                                                                                            μ
                                                                                                                                                                                          w
                                                                                                                                                                                                                                                                                                                                  t, antimicrobial, cytostatic and neuroprotective activities. sequence is a TPO mimetic peptide sequence used to make a
                                                                                                                                                                             CADGPTLREWISFC
                                                                                                                                                           CADGPTLREWISEC 14
                                                                                                                                                                                                                                                                                                                      of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
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                                                                                                                                                                                                                        Conservative
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                  (first entry)
                                                                                                                                                                                                                                                                                                                      invention.
                                                                           peptide;
                                                                                                                                                                                                                 74.6%; LT
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97pp;
                                                                                14
                                                                                                                                                                                                                                       Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SeqID 505
                                                                                ξ
                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ghrayeb J;
                                                                                                                                                                                                                                DB 7; Le
                                                                                                                                                                                                                                                      Length 14;
                                                                                                                                                                                                                         Indels
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RESULT 30
ADJ51647
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                                                                                                                                                                                                                                                                                                                                           which encode them), compositions, methods and uses. The invention may be cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be useful for creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant; hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
                             CH1 deleted
                                                           06-MAY-2004
                                                                                                                    ADJ51647 standard; peptide; 14
                                                                                                                                                                                                                                                                                                                     Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 505; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-082870/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kutoloski KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUN-2003; 2003WO-US020347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JAN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viral infection; fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH1 deleted mimetibody-related peptide SeqID505
                                                                                         ADJ51647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavner GA,
                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                           14;
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                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                              CADGPTLREWISFC 16
                                                                                                                                                                                                                                                                                                                     ₿,
                             mimetibody-related peptide SeqID505
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knight DM,
                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relates to CH1 deleted mimetibodies (and
                                                           entry
                                                                                                                                                                                                                                                           74.6%; Sc
100.0%; E
tive 0;
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                                                                                                                                                                                                                                                           k; Pred. No. 1.7
0; Mismatches
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                                                                                                                                                                                                                                                      DB 8; Luc.
J. 1.7e-05;
                                                                                                                                                                                                                                                                                       Length 14;
                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                            0,
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Query Match
Best Local
                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic, immunomodulator, antiallergic, muscular-Gen, cytostatic, antiinflammatory, neuroleptic, ophthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-modulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CHI deleted mimetibody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, endocrine, metabolic, gastrointestinal, gynaecological, hepatic, betteric, haematologic, immunological, allergic, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; oncological disorder; neurological disorder; nutritional disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder; pulmonary disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to CHI deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an osteopathic, cardiovascular den, dermatological den, auditory, endocrine den,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CH1 deleted mimetibody polypeptide and nucleic acid, useful f diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic nutritional disorders.
                                                                                                                                                                                                                                                                                                   musculoskeletal, oncological, neurological, nutritional, ophthalmologic, pediatric, psychiatric, renal or pulmonary disorders. The present sequence is that of a peptide which may be used during the creation of a
                                                                                                                                                                                                                Sequence 14
                                                                                                                                                                                                                                                                                mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; SEQ ID NO 505; 123pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-082872/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2002; 2002US-0392431P.
19-SEP-2002; 2002US-0412144P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CENZ ) CENTOCOR INC
                                                                                      14;
                                                                                                                    Similarity
CADGPTLREWISFC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $
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                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003WO-US020495
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                                                                                                                    74.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ghrayeb
                                                                                                                    Score 85; Pred. No.
                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                         Mismatches
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                                                                        DB 8; L-
3. 1.7e-05;
0;
                                                                                                                                                 Length 14;
                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                    creation of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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RESULT 31 AAW09467

RESULT 32
AAW35399
ID AAW35
XX
AC AAW35

AAW35399 standard; peptide; 13 AA.

AAW35399;

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Matches
                                                                              Query Match
Best Local 9
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                              chemotherapy, radiation therapy or bone marrow transfusions may also be used to maintain the proliferation and growth of dependent cell lines and for use in biological research, for TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                 The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
07-JUN-1995;
                                                                                                                               Sequence 13
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-051883/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haematology;
bone marrow t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW09467 standard; protein; 13
                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dower WJ,
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                                                                13;
ш
                             4
                                                                                  Similarity
                             ADGPTLREWISFC 16
                                                                                                                                                                                                                                                                                                   Page 91; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Barrett RW,
LC, Schatz
                                                                                                                                 AA;
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombocytopenia; TPO; TR; transfusion; chemotherapy; r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US008998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "S-carboxymethyl-cysteine alpha-carboxamide;
forming a linkage onto the Ala at position one with
delta C of this residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "The Ala is linked with
position 13"
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                                                         66.7%; 50
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                      ΡJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cwirla SE,
                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Wagstrom
                                                                              Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compound cyclic peptide
                                                                  Mismatches
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om CR, W
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                                                                                DB 2; Le
0.00033;
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Wrighton
                                                                                                Length 13,
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ton NC;
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RESULT 33
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XT 11-M
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Matches 13
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                     investigate the mechanism of thrombopoietin signal trareceptor activation, or to maintain the proliferation thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy;
                                                                                             AAW35417 standard;
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07-JUN-1995;
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                              Thrombopoietin
                                                   11-MAR-1998
                                                                                                                                                                                                                                                                                     thrombocytopaenia resulting from chemotherapy, radiation thermarrow transfusions. It can also be used diagnostically, e.g.
                                                                                                                                                                                                                                                                                                          used to treat disorders which are susceptible to treatment with thrombopoietin agonist, preferably haematological disorders and
                                                                                                                                                                                                                                                                                                                                The present peptide, which binds the thrombopoietin receptor (TR),
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13; Conserv
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95US-00485301.
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                              receptor
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100.0%;
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PJ, Wagstrom CR,
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                             binding peptide.
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                                                                                                                                                                                                    Score 76;
Pred. No.
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e.g. to
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Matches 13
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                                    Synthetic
                                                             Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                          AAW33033 standard; peptide; 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dower WJ, Barret
Mattheakis LC, So
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07-JUN-1995;
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Key
Modified-site
                                                                                                                               Thrombopoietin
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                                                                                                                               receptor binding peptide
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95US-00485301.
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13
Location/Qualifiers
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100.0%; Pr
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k; Pred. No. 0.0
0; Mismatches
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RESULT 35
AAW35413
AAW35423
AC AAW35
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CT Thron
CW Thron
KW Thron
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07-JUN-1995;
                                                                                                                                            Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombopoietin receptor - useful in treatmedisorders, esp. thrombocytopenia resulting
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               WO9640750-A1
                                                      Modified-site
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95US-00485301
                                                                                                                                                                                                              receptor binding peptide.
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                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                            peptide; 13
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100.0%;
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PJ, Wagstrom CR, Wrighton NC;
                                                                  "Br-Ala"
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Pred. No.
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RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, et
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07-JUN-1995;
                                                                                                                                                                                                                       Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; haematologic, bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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                    07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                 Synthetic.
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Modified-site
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                                                                                                                                                                                                                                                                                 receptor binding peptide.
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Schatz PJ, Wagstrom CR,
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100.0%; Pr
                                                                                                                             "NH2-cytosine linked via thiol
                                                                                                                                                      "CO-CH(Ph)-alanine linked via
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76; DB; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duffin DJ, Gates Crom CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemotherapy, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                      CH group to Cysl3"
                                                                                                                              group to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson SS;
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                                                                                                                                Alai"
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(GLAX) GLAXO

GROUP LTD

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Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to treat disorders which are susceptible to t
thrombopoietin agonist, preferably haematological
thrombocytopaenia resulting from chemotherapy, rad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dower WJ,
Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-052226/05.
                                                                                                                                      07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                               signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW35422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW35422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                            Dower WJ,
Mattheakis
                                                                                                                                                                                  07-JUN-1996;
                                                                                                                                                                                                                 19-DEC-1996.
                                                                                                                                                                                                                                               WO9640750-A1
                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present
                                                                                                         (GLAX ) GLAXO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADGPTLREWISFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADGPTLREWISFC
                                                           Barret
LC, Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         esp. thrombocytopenia resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barret RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                         GROUP LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor; binding peptide; treatment; agonist;
                                                                                                                                      95US-00478128.
95US-00485301.
                                                                                                                                                                                  96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64; 106pp;
                                                            Schatz
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                            peptide"
                                                                                                                                                                                                                                                                                         /note= "linked via disulfide bond to
                                                                                                                                                                                                                                                                                                                        note=
                                                                           RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which binds the thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cwirla SE, Du
PJ, Wagstrom
                                                           Cwirla SE, Du
PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                        "optionally acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 76;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemotherapy, radiation therapy or
be used diagnostically, e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duffin
                                                           Duffin DJ, Gate
om CR, Wrighton
bind to and activate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Le 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DJ, Gates CM, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from chemotherapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 13;
                                                                           Gates CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment with l disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                              Z,
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h of
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                                                                              ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can
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Peptides and peptide mimetics which

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The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and

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RESULT 38
AAW35397
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                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, et
                                                                  Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                WPI; 1997-052226/05
                                                                                                                                                                                               07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                  07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                    Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW35397 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13
                                            Example
                                                                                                                                                  Dower WJ,
                                                                                                                                                                                                                                                        19-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADGPTLREWISFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 74;
                                            Page 63;
                                                                                                                                      Barret RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                        GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders which
                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor binding
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                                            106pp;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which binds the thrombopoietin receptor (TR), ers which are susceptible to treatment with a
                                                                                                                                      Cwirla SE, Duffin
PJ, Wagstrom CR,
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                                                                                                                                                                                                                                                                                                                             "COCH2-alanine
                                                                                                                                                                                                                                                                                                   "NH2-cytosine linked via thiol group to Alal"
                                              English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 76;
Pred. No.
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                                                                                                                                                                                                                                                                                                                             linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Le 0.00033;
                                                                                                                                       DJ, Gates C
Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from chemotherapy, etc
                                                                                                                                                                                                                                                                                                                             Via
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                                                                                                                                                                                                                                                                                                                             CH2 group to Cys13"
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RESULT 39
ANU25997
ID AAU25977
ID AAU25977
XX AU25
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KW haemc
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07-JUN-1995;
07-JUN-1996;
Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
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                                                                                                                                                                                                                                                                                                                                                                                                                              Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises con with peptides and peptide mimetics attached to hydrophilic:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Balasubramanian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dower WJ,
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                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemostatic; thrombocytopenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-564142/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLAX ) GLAXO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; arrow transplantation; haematological disorder; platelet disorder; linked immunosorbent assay; in situ staining; biological fluid; homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expansion; megakaryocyte; Headpiece Dimer gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
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                                                                                                                                                                                                                                                                                                                                                                            Col 143-144; 128pp;
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95US-00485301.
96WO-US009623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cwirla SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombopoietin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TPO-R) activator peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SE,
                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R CM
                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises contacting hydrophilic polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                radiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schatz PJ;
Deprince RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO-R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       polymers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Podduturi
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Best Local S
Matches 12
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells and fixed cells, in biological fluids, in tissue homogenates, a in purified or natural biological materials. They may also be used for situ staining, fluorescence-activated cell sorting, Western blotting enzyme-linked immunosorbent assay (ELISA). In addition, the peptides be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                         Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understranding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO
                                                                                                                                                                                                                 Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting with peptides and peptide mimetics attached to hydrophilic polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human thrombopoietin receptor (TPO-R)
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                                                                                                                                                                                        Disclosure; Col
                                                                                                                                                                                                                                                                                  WPI; 2001-564142/63.
                                                                                                                                                                                                                                                                                                                                Balasubramanian
                                                                                                                                                                                                                                                                                                                                              Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene
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lanian P,
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95US-00485301.
96WO-US009623.
96US-00699027.
                                                                                                                                                                                      137; 128pp;
                                                                                                                                                                                                                                                                                                             RW, c. Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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                                                                                                                                                                                                                                                                                                                                  Hendren
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Deprince
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                                                                                                                                                                                                                                                                                                                        ۷ PJ;
                                                                                                mimetics attached to 
thrombocytopenia such
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RESULT 41
AAW35398
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
              The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13
                                                                                                                                                                                                                   Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
07-JUN-1995;
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thrombopoietin dependent cell
                                                                                                                                                                                Example 6;
                                                                                                                                                                                                                                                                                                     WPI; 1997-052226/05
                                                                                                                                                                                                                                                                                                                                             Mattheakis
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                                                                                                                                                                                                                                                                                                                                           Barret
LC, Sc
                                                                                                                                                                              Page 63; 106pp; English.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "NH2-Cy8"
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Pred. No.
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Query Match Best Local S Matches 13

l Similarity

Conservative

Score 76; Pred. No.

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Length 14;

Mismatches

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Gaps

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RESULT 42
AAW35396
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Best Local S
Matches 13
                                                                          The present peptide, which binds the thrombopoietin receptor (TR), (used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                             Sequence
                                                                                                                                                                                       Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                    WPI; 1997-052226/05
                                                                                                                                                                                                                                                          Dower WJ,
Mattheakis
                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin receptor; haematological disorder;
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                                                                  thrombopoietin
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                                                                                                                                                                  6; Page 63; 106pp; English.
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gical disorder; thrombocytopaenia; chemotherapy;
therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                          Barret RW,
LC, Schatz
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                                                                  dependent
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95US-00485301.
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100.0%; Pr
66.7%; 5-
100.0%; Pr
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Pred. No.
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Wrighton NC;
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RESULT 43
AAW35402
RESULT 44
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                                                                                                                                                                        The present peptide, which binds the thrombopoietin receptor (TR), consed to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                       Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                        WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                                                               Mattheakis
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07-JUN-1995;
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                                                                   ADGPTLREWISFC
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LC, Schatz
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PJ, Wagstrom
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                                                   sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoletin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                               Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; hematmological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
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                                                                                                                                     Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 139; 128pp;
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anian P, Wagstrom CR,
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95US-00485301.
96WO-US009623.
96US-00699027.
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                                                                   Score 76; DB; Pred. No. 0.0 0; Mismatches
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lendren RW,
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                                                                                                                           Query Match
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Balasubramanian P, Wagstrom CR, Hendren RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human thrombopoietin receptor (TPO-R) activator peptide #169.
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ADGPTLREWISFC 14
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96WO-US009623.
96US-00699027.
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Database

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Searched:

Sequence:

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R;Smith, A.; Wamsley, P.; Fronick, W. submitted to the EMBL Data Library, February 1999 A;Description: The sequence of C. elegans cosmid (A;Reference number: Z21443 A;Accession: T33943
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A; Introns: 4/1;
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A;Experimental source: cultivar Columbia; BAC clo
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A;Molecule type: DNA
A;Residues: 1-245 <BEN>
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A; Accession: T47701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: protein F1I16.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr.2000 #sequence_revision 20-Apr.200
                                                                        testosterone-resistant immunity-associated protein IAP38 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
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A; Title: Novel gene expressed in spleen cells mediating acquired testosterone-resistant
              R;Kruecken, J.; Schmitt-Wrede, H.P.; Markmann-Mulisch, Biochem. Biophys. Res. Commun. 230, 167-170, 1997
                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9UAT5; EMBL:AF125952; PIDN:AAD14699.1; GSPDB:GN00023; CESP.
A;Experimental source: strain Bristol N2; clone C01B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                        A58583
                                                                                                                                                         RESULT 3
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Best Local S
Matches
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;Map position: 5
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                                                     Accession: A58583
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8; Conser
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36/2; 65/1; 80/1; 123/3; 160/3
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Pred. No. 9.
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C;Accession: T49731
R;Schulte, U; Aigm, V; Hoheisel, J; Brand submitted to the Protein Sequence Database, A;Reference number: Z25022
A;Accession: T49731
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A; Molecule type: DNA
A; Residues: 1-108 <SCH>
A; Cross-references: EMBL; AL356192; GSPDB: GN00116; NCSP:B24B19.30
A; Cross-reference: BAC clone B24B19; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P70224; GB:Y08026; NID:g1550784; PIDN:CAA69283.1; PID:g1550 A;Experimental source: spleen cell C;Comment: This protein is a plasma membrane protein with two membrane-spanning domains C;Comment: This protein is a plasma membrane protein with two membrane-spanning domains
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A;Accession: A58583
A;Molecule type: mRNA
A;Residues: 1-346 <KRU>
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F;148-167/Domain:
F;320-335/Domain:
                                                                                                                                                                                                                                                                                                                          hypothetical protein 5 (imported) - Natronobacterium pharaonis
C;Species: Natronobacterium pharaonis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000
                                                                                                               A;Cross-references: UNIPROT:007291;
A;Experimental source: strain SP1/28
                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-180 < MAT>
                                                                                                                                                                                                        A; Accession: T44944
                                                                                                                                                                                                                              A;Title: Cytochrome ba3 from Natronobacterium pharaonis: A;Reference number: Z22876; MUID:98088958; PMID:9428682
                                                                                                                                                                                                                                                                    R; Mattar, S.; Eng
Eur. J. Biochem.
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to the Protein Sequence Database, May 2000
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77.8%;
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Score 45;
Pred. No.
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Pred. No.
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                   Length 180;
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R;Mallet, L.; Bussereau, F.; Jacquet, M.

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C;Date: 15-Oc
C;Accession:
R;Mortimore,
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Yeast 11, 1195-1209, 1995
A;Title: A 43.5 kb segment of yeast chromosome XIV, which contains MFA2, MEP2, CAP/SRV2
A;Reference number: S59241; MUID:96109932; PMID:8619318
A;Accession: S59247
A;Accession: S59247
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A;Accession: T22969
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A;Cross-references: EMBL:Z46843; NID:g861113; PIDN:CAA86884.1; A;Note: the nucleotide sequence was submitted to the EMBL Data R;Mallet, L.; Busscreau, F.; Jacquet, M. submitted to the Protein Sequence Database, April 1996 A;Reference number: S63069 A;Accession: S63087
                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P41948; EMBL:X83608; NID:g619513; PIDN:CAA58587.1; PID:g6195R;Mallet, L.; Bussereau, F.; Jacquet, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Marini, A.M.; Andre, B.
submitted to the EMBL Data Library, December 1994
A;Reference number: S51089
A;Accession: S51089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: NH3 permease; protein JTA499; protein N1207; pr
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A; Introns: 27/1; 116/1;
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                                                                                                                  A; Molecule type: DNA
A; Residues: 1-499 < MAW>
                                                                                                                                                      A;Status: nucleic
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A;Experimental source: clone F59Al
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Best Local
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                                                                                                                                                        acid sequence not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DE
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: Z81557; PIDN: CAB04538.1;
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                                                                                                                                                          shown;
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                                                                                                                                                          translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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                                                                                                                                                          shown
                                                                                                   PID:g854496
                                                                               Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein N1820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,,</u>
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                                                                                   November 1994
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RESULT 8
                                              hypothetical protein C06C6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 5
A; Introns: 109/1; 135/2;
C; Superfamily: Caenorhabo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T19008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, A; Reference number: Z19059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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F;154-170/Domain:
F;228-244/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;35-51/Domain: transmembrane #status predicted <TM1>F;62-78/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: ammonium transport C;Superfamily: ammonium transport
                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-346 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T19008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;397-413/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 14L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: SGD:MEP2
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A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: D75266
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:C06C6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT: O62030; A; Experimental source: clone C06C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references:
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 9
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                                                                                                                                                                                                                                                              183
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9; Conserva
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Similarity 38.5%;
                                                                                                                                                                                                                                                               GLADGSTTINWDSFIG 198
                                                                                                                                                                                                                                                                                              GCADGPTLREWISFCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGSAGNATIRAWYSIMSTNLAAACGG 272
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                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis
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transmembrane #status predicted <TM4>
transmembrane #status predicted <TM5>
transmembrane #status predicted <TM5>
transmembrane #status predicted <TM6>
transmembrane #status predicted <TM7>
transmembrane #status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                  Conservative
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e: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                160/2; 310/1
ditis hypothetical
                                                                                                                                                                                                                                                                                                                                                  38.6%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              March 1997
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ed <TM1>
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                                                                                         J.D.; Dodson,
T.; Zalewski,
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58.5K hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86440
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
A;Authors: Salzberg, S.L.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-371 <WHI>
A;Residues: 1-371 <WHIPAT: Q9RRJ3; GB:AE002079; GB:AE000513; NID:g6460315; PIDN:AAF120:
A;Experimental source: strain R1
A;Experimental source: strain R1
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A;Accession: T09084
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C; Superfamily: rod shape-determining
                                                                               A;Cross-references:
C;Genetics:
                                                                                                                                                                                     A;Reference number: A86141;
A;Accession: A86440
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C;Species: Chlamydomonas reinhardtii
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                                                                                                                        A; Molecule type: DNA
A; Residues: 1-526 <STO>
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                                                                                                                                                                 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Gene: DR2497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT:004270; EMBL:U97663; NID:g2109290; PIDN:AAC50018.1;
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Best Local
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Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSQDSPGVRRWLSIAG 92
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                                                                                                     UNIPROT: Q9C868; GB: AE005172; NID: g11054679; PIDN: AAG27899.1;
38.6%;
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Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB
Pred. No. 73;
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No.
DB 2;
1e+02;
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                                                                                                                                                                                                                                                                                                              S.; Khaykin, E. S.; Maiti, R.;
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C;Accession: S53489; S34189
R;Sonnewald, U.; Basner, A.; Greve, B.; Steup,
Plant Mol. Biol. 27, 567-576, 1995
A;Title: A second L-type isozyme of potato glu
A;Reference number: S53489; MUID:95201249; PMI
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S34189
                                                                     F;130-149/Domain: transmembrane #status predicted <TM2>
F;150-290/Domain: intracellular #status predicted <INT2>
F;251-313/Domain: transmembrane #status predicted <TM3>
F;320-348/Domain: transmembrane #status predicted <TM4>
F;320-348/Domain: intracellular #status predicted <INT3>
F;349-785/Domain: intracellular #status predicted <INT3>
F;586-782/Domain: ATPass nucleotide-binding domain homology
F;786-809/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 228-240;431-438;535-550;671-690;1011-1022 <KAW2> R;Ohta, T.; Nagano, K.; Yoshida, M. Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986 A;Title: The active site structure of Nat+)/K(+)-transporting A;Reference number: S29880; MUID:86177549; PMID:3008150 A;Accession: S29880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - Pacific electric ray C;Species: Torpedo californica (Pacific electric ray) C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-20 C;Accession: S00503; S28885; S29880
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                                                                                                                                                                                                                                                C;Superfamily: Na+/K+-transporting ATPase alpha chain; i
C;Keywords: ATP; heterodimer; hydrolase; ion transport;
F;96-120/Domain: transmembrane #status predicted <TMl>
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F;874-951/Domain: intracellular F;952-977/Domain: transmembrane
                                             F;786-809/Domain: transmembrane #status predicted F;848-873/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 386-402; 502-512; 671-689; 887-906 < OHT >
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A; Residues: 228-240;43:535-550;671-690;1011-1022 <KAW2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Primary structure of the alpha-subunit of Torpedo A; Reference number: S00503; MUID:85296307; PMID:2993905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Kawakami, K.; Noguchi, Nature 316, 733-736, 1985
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A;Cross-references: UNIPROT:P05025; EMBL:X02810; NID:g64399; PIDN:CAA26578.1; PID:g6440
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Superfamily: glucan phosphorylase;
Seywords: glycosyltransferase; hexosyltransferase; phosphoprotein;
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PMID:7894019
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RESULT 14
A24414
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R;Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
Genomics 6, 451-460, 1990
A;Title: The human Na, K-ATPase alpha 1 gene: characterization of the 5'-flanking
A;Reference number: I60116; MUID:90228961; PMID:1970326
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A; Molecule type: DNA
A; Residues: 168-189;213-214,'X',216-244 <SHU>
A; Residues: 168-189;213-214,'X',216-244 <SHU>
R; Chehab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blostein, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7901-7905, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 7901-7905, 1987
A; Title: Human placental Na+,K+-ATPase alpha subunit: cDNA cloning, tissue expression, A; Reference number: A39910, MUID:88068506; PMID:2891135
A; Accession: A39910
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A;Rosidues: 1-1023 «KAM»
A;Residues: 1-1023 «KAM»
A;Cross-references: UNIPROT:P05023; EMBL:X04297; NID:g28926; PIDN:CAA2784
R;Shull, M.M.; Lingrel, J.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
A;Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit.
A;Reference number: A94158; MUID:87231946; PMID:3035563
A;Accession: A27795
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C;Date: 02-Jun-1988 #sequence revision 02-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24414; A27795; A39910; I60116; S09171
R;Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K.
J. Biochem. 100, 389-397, 1986
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C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
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A;Status: translation not shown;
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N;Alternate names: sodium pump; sodium/potassium transporting
                                                            F;849-874/Domain:
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A; Residues: 199-942 < CHE>
                                                                                ;130-149/Domain: transmembrane #status predicted <TM2>;150-290/Domain: intracellular #status predicted <TMT2>;291-313/Domain: transmembrane #status predicted <TM3>;291-313/Domain: transmembrane #status predicted <TM3>;320-348/Domain: transmembrane #status predicted <TM4>;320-348/Domain: intracellular #status predicted <TM4>;349-786/Jomain: ATPase nucleotide-binding domain homology;587-783/Domain: transmembrane #status predicted <TM5>
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;6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
;6-95/Domain: intracellular #status predicted <INT1>
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Pred. No. 1.8e+02
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predicted <TM6>
predicted <TM7>
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A;Status: pre-americal process of the process of th
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
T39685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glutamate synthase large subunit [imported] - Staphylococcus aureus (strain C;Species: Staphylococcus aureus
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Oliver, K.; Harris, D.; Wood, V.; submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein SPBC1778.03c - C;Species: Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q99WD1;
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004 C;Accession: A89813
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A; Introns: 11/2
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A;Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1499 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
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Pred. No. 3.1e+02;
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Pred. No. 87;
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Pred. No. 1.8e+02;
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March 1998
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K;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; l DNA Res. 6, 83-101, 1999
A,Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy: A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72595
A;Accession: D72595
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A;Experimental source: strain Kl
C;Genetics:
                                                                                            A;Title: Murine erythropoietin gene: cloning, expression, A;Reference number: A24902; MUID:87039105; PMID:3773894 A;Accession: A24902
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                                                                                                                                                                             erythropoietin precursor - mouse
(;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: A24902; A24901
R;Shoemaker_C.B.; Mitsock, L.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid C03B1.
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C; Accession: T15386
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C;Species: Caenorhabditis elegans
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             A;Cross-references: UNIPROT:P07321
A;Note: the authors translated the codon R;McDonald, J.D.; Lin, F.K.; Goldwasser,
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                                                                   A; Molecule type: DNA
A; Residues: 1-192 <SHO>
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                       CASGEVHYHWACFCG
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                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              37.7%;
46.7%;
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB:
Pred. No. 35;
0; Mismatches
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Pred. No. 34;
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                 TTA
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                                    43
A;Reference number: AB2577; MA;Accession: AB2768
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                            C;Accession: AB2768
C;Accession: AB2768
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Ferage, G.; Romero, P.; Zhang, S.
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                                                                                                                ster, E.W.
                                                                                                                               A; Authors: Yoo, H.; Tao,
                                                                                                                                                ; Karp, P.; Romero, P.; Zhang, Science 294, 2317-2323, 2001
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C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-192/Product: erythropoietin #status predicted <MAT>
F;33-187,55-165/Disulfide bonds: #status predicted
F;33-187,55-165/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-67,'P',69-192 < MCD>
A; Residues: 1-67,'P',69-192 < MCD>
A; Cross-references: GB:M12930; NID:g193086; PIDN:AAA37570.1; PID:g387152
A; Cromment: Erythropoietin is produced by kidney or liver of adult mammals
C; Genetics:
C; Genetics:
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A;Title: Cloning, sequencing, and evolutionary analysis of the mouse A;Reference number: A24901; MUID:87039104; PMID:3022133
A;Accession: A24901
                                                                   RESULT 21
AB2768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenetics 40, 397-414, 1994
A;Title: Genes for mast-cell serine protease and their A;Reference number: I48684; MUID:95048582; PMID:7959952
A;Accession: I48685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 5/1; 52/3; 81/3; 141/3 C; Function:
                                                                                                                                                                                                                                                                                                                        C;Keywords: hydroiase; serine processes f;32-230/Domain: trypsin homology #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230 <RESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: I48685; S43172
R; Huang, R.; Hellman, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mast cell proteinase 6 (EC 3.4.21.-) precursor - mo C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996
lipoate biosynthesis protein B [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P21845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148685
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                                                                                                                                                                                                                                                                                                                                                 ;Superfamily: trypsin; trypsin homology;Keywords: hydrolase; serine proteinase
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Best Local &
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Best Local
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Y.; Biddle, P.; Jung, M.; Krespan,

W.; Perry, M.; Gordon-Kamm

tumefaciens

C58

D.; Chen, L.; Wood, G.E.; Chen, D.; Kutyavin, T.; Levy, R.; Li, N

Y.; Woo, '

Natural Genetic; MUID:21608550;

Engineer Agrobacterium PMID:11743193

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probable translation initiation factor [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein T5I7.12 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004 C;Accession: T01012; H84821 C;Accession: T01012; H84821 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, November 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T19988
R;Kershaw, J
submitted to the EMBL Data Library,
A;Reference number: Z19208
A;Accession: T19988
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T19988
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A;Map position: circular chromosome
C;Superfamily: Escherichia coli lipoate-protein
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A;Cross-references: UNIPROT:Q8UF44; GB:AE008688; PIDN:AAL42560.1; PID:g17739983; GSPDB:
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                          A;Cross-references: UNIPROT:022290; EMBL:AC003000; NID:g2642152; PIDN:AAB87131.1; PID:g2 A;Experimental source: cultivar Columbia A;Experimental source: cultivar Columbia R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Fraser, C.M.; Venter, J. Russey, D.; Nlerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Russey, D.; Nlerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Russey, D.; Nlerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Russey, D.; Nlerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Russey, D.; Nlerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Russey, D.; Nlerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Russey, D.; Nlerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Russey, D.; Nlerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Russey, D.; Ru
                                                                                                                                                                                                                                                                                                                                                                      A;Description: Arabidopsis thaliana ch. A;Reference number: Z14162
A;Accession: T01012
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-247 <ROUD
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                                                   Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84821
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A; Residues: 1-246 <WIL>
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;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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nilarity 43.5%;
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41.7%;
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                             A;Molecule type: mRNA
A;Residues: 1-276 <REZ;
A;Cross-references: GB:M57626; NID:9200508; PIDN:AAA39988.1; PID:A;Cross-references: GB:M57626; NID:9200508; PIDN:AAA39988.1; PID:A;Cross-references: GB:M57626; NID:9200508; Carr, M.H.; Austen, Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A;Title: Different mouse mast cell populations express various coa;Reference number: A35646; MUJD:90222202; PMID:2326280
A;Accession: D35646
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A; Molecule type:
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A;Residues: 1-247 <STO>
A;Cross-references: GB:AE002093; NID:g2642164; PIDN:AAB87131.1;
C;Genetics:
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A;Introns: 4/1; 38/2; 82/1; 162/3
C;Superfamily: conserved hypothetical
                                                                                                  R;Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W. J. Biol. Chem. 266, 3847-3853, 1991
A;Title: Cloning of the cDNA and gene of mouse mast cell A;Reference number: A38654; MUID:91139682; PMID:1995638
A;Accession: A38654
                                                                                                                                                                                                           mast cell proteinase 6 (BC 3.4.21.) precursor - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house revision 17-Feb-1994 #text_change C;Date: 21-Feb-1992 #sequence revision 17-Feb-1994 #text_change C;Accession: A38654; B38654; D35646; I59478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome Sequence of the Plant Pathogen and Biotechnology A;Reference number: A97359; MUID:21608551; PMID:11743194 A;Accession: D97548 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
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A;Cross-references: UNIPROT:P21845; GB:M57625; NID:g200506; PIDN:AAA39987.1; PID:g20050
A;Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 37
s Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
                                                                A; Molecule type: DNA
A; Residues: 1-276 < REY >
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A; Residues: 1-268 < KUR>
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Pred. No. 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AE007869;
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A;Residues: 32-54 <RE3>
R;Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson, Scand. J. Immunol. 38, 359-367, 1993
A;Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and A;Reference number: I59478; MUID:94023807; PMID:8210998
A;Accession: I59478
                                                                                                                                              hypothetical protein alr7157 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al hypothetical protein slr7157 [imported] - Nostoc sp. (strain PCC 7120) f.,Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C;Accession: AE2497 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana, Reference number: AB1807; MUID:21595285; PMID:11759840
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AE2497
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A;Residues: 1-434 <HUA>
A;Residues: 1-434 <HUA>
A;Cross-references: UNIPROT:Q52748; EMBL:X56082; NID:g46152; PIDN:CAA39560.1;
A;Note: the coding region was assigned by the authors; it does not start with
A;Note: the authors designated this protein as beta-glucosidase
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A; Accession: S21324
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C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
C;Keywords: hydrolase; serine proteinase; zymogen
E;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1990 A;Description: Nucleotide sequence of a cellulase
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C;Species: Ruminococcus flavefaciens
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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A;Molecule type: DNA
A;Residues: 1-629 <KUR>
A;Cross-references: UNIPROT:Q8YKY1; GB:BA000020; PIDN:BAB78241.1; PID:g17135695; GSPDB:
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                                                                                            A;Status: preliminary
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Best Local
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50.0%;
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Pred. No. 1.2e+02;
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Pred. No.
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n ATG and ov
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A;Molecule type: mRNA
A;Residues: 1-1010 <TA2>
A;Residues: 1-1010 <TA2>
A;Cross-references: UNIPROT:P24798; GB:M59960; NID:g212407; PIDN:AAA48982.1; PID:g21240
A;Cross-references: UNIPROT:P24798; GB:M59960; NID:g212407; PIDN:AAA48982.1; PID:g21240
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassaim transport; sodium t F;574-770/Domain: ATPase nucleotide-binding domain homology <ATN>
F;202,470/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;363/Active site: Asp (aspartylphosphate intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                      Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - chicken C;Species: Gallus gallus (chicken) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004 C;Accession: B37227; I50395
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Am. J. Physiol. 259, C619-C630, 1990
A;Title: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms
A;Reference number: A37227; MUID:91023019; PMID:2171348
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F;106-122/Domain: transmembrane #s
F;152-168/Domain: transmembrane #s
F;395-411/Domain: transmembrane #s
F;435-451/Domain: transmembrane #s
F;545-561/Domain: transmembrane #s
F;599-615/Domain: transmembrane #s
F;646-662/Domain: transmembrane #s
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A;Genome: plasmid
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A; Gene: SGD:RSN1; MIPS:YMR266w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S54014
A; Accession: S54478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable membrane protein YMR266w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM8156.08
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                            F;32-48/Domain: transmembrane #status predicted <TMl>
                                                                                                                                                                                                                                                                                             C; Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: strain AB972
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A;Cross-references: UNIPROT:Q03516;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lye, G.; Churcher, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession:
                                                                                                                                                                                                                                                                                                               Superfamily: yeast probable membrane protein YOL084w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
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558
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GAFLDGTVRKKWNRFCG
                                 GGCADGPTLREWISFCG 17
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                                                                Conservative
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                                                                                  37.7%;
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ne #status predicted <TM4>
ne #status predicted <TM5>
ne #status predicted <TM5>
ne #status predicted <TM6>
ne #status predicted <TM7>
ne #status predicted <TM8>
574
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Pred.
                                                                                                   Score 43;
                                                                    Pred. No. 2.40
2; Mismatches
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                                                                                  No. 2.4e+02;
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                                                                                                     Length 953;
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A;Map position: 19q13.2-19q13.2
A;Introns: 2/3; 31/3; 51/3; 119/3; 157/3; 202/3; 242/1; 331/3; 398/1; 435/2; 479/3; 544/
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
E;86-110/Domain: transmembrane #status predicted <TM1>
E;120-139/Domain: intransmembrane #status predicted <TM2>
E;140-280/Domain: intransmembrane #status predicted <TM3>
E;310-338/Domain: transmembrane #status predicted <TM4>
E;310-338
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A;Residues: 1,'EIH',3-1013 <SVE1>
A;Residues: 1,'EIH',3-1013 <SVE1>
A;Residues: 1,'EIH',3-1013 <SVE1>
A;Residues: 1,'EIH',3-1013 <BMBL:X12910; NID:g28963
A;Note: the authors translated the codon TTC for residue 283 as Ser and TCT for residue A;Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk S A;Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk S R;Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N. E.; Whisaryov, Y.A.; Allikmets, R.L.; W Tina, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchnikov, Y.A.
FEBS Lett. 217, 275-278, 1987
A;Title: The family of human Na+,K+-ATPase genes. No less than five genes and/or pseudog A;Reference number: A27397; MUID:87247232; PMID:3036582
A;Accession: A27397
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A;Residues: 1-1013 <CVC>
A;Residues: 1-1013 <CVC>
A;Cross-references: UNIPROT:P13637, EMBL:M37456
A;Cross-references: UNIPROT:P13637, EMBL:M37456
R;Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkarev, Y.A.; Melkov, A.M.; Smirr
ov, N.N.; Ovchinnikov, Y.A.
ov, N.N.; Ovchinnikov, Y.A.
ov, N.N.; Ovchinnikov, Y.A.
ov, N.N.; Ovchinnikov, Y.A.
A;Title: Family of human Ma(+), K(+)-ATPase genes. Structure of the gene of isoform alpha
A;Reference number: S04019
A;Accession: S04019
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A;Title: Family of human Na,K-ATPase genes. Structure of the A;Reference number: S00801; MUID:88255304; PMID:2838329
A;Accession: S00801
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                                                                                                                                                                                                                                       F;366/Active site: Asp (aspartylphosphate intermediate) #status predicted F;498/Binding site: ATP (Lys) #status predicted F;707,711,716/Active site: Asp, Asp, Lys #status predicted
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F;577-773/Domain:
F;777-800/Domain:
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A;Cross-references: GDB:119713; OMIM:182350
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A; Residues: 243-434 <SVE2>
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plate: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004
plate: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004
plate: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004
plate: 30-Jun-1993 #sequence for sequence for seque
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Best Local
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                                Local Similarity
mes 6; Conserv
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ATPase nucleotide-binding domain homology
transmembrane #status predicted <TW6>
transmembrane #status predicted <TW6>
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60.0%;
                                                                                     37.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             #status predicted <INT4>
#status predicted <TM7>
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Pred. No. 2.6e+02;
1; Mismatches 3
                                                                                Score 43;
Pred. No.
                                                Mismatches
                                                                                                                                           DB 1;
                                                                                           6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1010;
                                                                                                                                           Length 1013;
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F;281-303/Domain: transmembrane #status predicted <TM3>
F;281-303/Domain: transmembrane #status predicted <TM3>
F;310-338/Domain: intracellular #status predicted <TM4>
F;339-776/Domain: ATPase nucleotide-binding domain homology
F;577-773/Domain: transmembrane #status predicted <TM5>
F;777-800/Domain: transmembrane #status predicted <TM5>
F;885-864/Domain: transmembrane #status predicted <TM7>
F;865-942/Domain: intracellular #status predicted <TM7>
F;943-968/Domain: transmembrane #status predicted <TM7>
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A; Residues: 1-907, 'C', 909-1013 <HAR>
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N;Alternate names: Na+/K+-transporting ATPase
                                                                                                                                                                                                                                                                                                                                                                                                  F;498/Binding site: ATP (Lys) #8
F;707,711,716/Active site: Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;366/Active site: Asp (aspartylphosphate intermediate) F;498/Binding site: ATP (Lys) #status predicted
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                                                                                                PTLREWISFC 16
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intracellular #status predicted <TM2>
transmembrane #status predicted <TM3>
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                                                                                                                                                                                                      Score 43; DB 2;
Pred. No. 2.6e+02;
1; Mismatches 3
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C;Date: 30-Jun-1988 #sequence revision 23-Apr-1993 #text_change 09-Jul-2004 C;Accession: C24639; S00514; B27180; A60470 R;Shull, G.E.; Greeb, J.; Lingral, J.B. Biochemistry 25, 8125-8132, 1986 Biochemistry 25, 8125-8132, 1986 A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit A;Reference number: A90512; MUID:87128908; PMID:3028470 A;Accession: C24639
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A;Residues: 1, 'NL', 4-103, 'R', 105-113, 'E', 115-127, 'G', 129-148, 'Q', 150-151, 'T', 153-165, A;Residues: 1, 'NL', 4-103, 'R', NID:g205633; PIDN:ARA41672.1; PID:g205634
A;Cross-references: EMBL:M28648; NID:g205633; PIDN:ARA41672.1; PID:g205634
A;Cross-references: EMBL:M28648; NID:g205633; PIDN:ARA41672.1; PID:g205634
A;Note: the authors translated the codon CAG for residue 149 as Glu, GGC for residue:
R;Hsu, Y.M.; Guidotti, G.
Biochemistry 28, 569-573, 1989
Biochemistry 28, 569-573, 1989
A;Title: Rat brain has the alpha3 form of the (Na+,K+)ATPase.
A;Reference number: A60470; MUID:89229049; PMID:2540801
A;Accession: A60470
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A;Title: Primary structures of two types of alpha-subunit of rat brain Na(+),K(+)-ATPas A;Reference number: S00460; MUID:88032933; PMID:2822682
A;Accession: S00514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 117-132;586-595,'X',597-601 <HSU>
C;Comment: The alpha-3 form appears to be highly ouabain-inhibitable, as is alpha-2 but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1013 <SHUS
A; Cross-references: UNIPROT: P06687; EMBL: M14513; NID: g203030; PIDN: AAA40777.1; PID: g203
A; Cross-references: UNIPROT: P06687; EMBL: M14513; NID: g203030; PIDN: AAA40777.1; PID: g203
A; Note: in the authors' translation 405-Ser is shown after residue 409 and, consequentl
A; Note: in the authors' translation 405-Ser is shown after residue 409 and, consequently.
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ATPase alpha(III) chain
                                                                                         Length 1013;
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Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - human
N,Alternate names: Na+/K+-exchanging ATPase alpha chain-4; sodium/potassium transporting
C;Species: Homo sapiens (man)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34474; B27795; D27397
R;Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
J. Biol. Chem. 264, 17532-17543, 1989
A;Reference number: A34474; MUID:90008924; PMID:2477373
A;Accession: A34474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Shull, M.M.; Lingrel, J.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
A;Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit A;Reference number: A94158; MUID:87231946; PMID:3035563
A;Accession: B27795
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A;Residues: 1-1017 <TAK>
A;Cross-references: UNIPROT:P24797; GB:M59959; NID:g212405; PIDN:AAA48981.1; PID:g212400
A;Cross-references: UNIPROT:P24797; GB:M59959; NID:g212405; PIDN:AAA48981.1; PID:g212400
A;Takeyasu, K.; Lemas, V.; Fambrough, D.M.
Am. J. Physiol. 259, C619-C630, 1990
Am. J. Physiol. 259, C619-C630, 1990
A;Title: Stability of Na(+)-K(+)-AFPase alpha-subunit isoforms in evolution.
A;Reference number: A37227; MUID:91023019; PMID:2171348
A;Accession: A37227
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A;Molecule type: mRNA
A;Residues: 1-1017 <TAK>
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R;Takeyasu, K.; Lemas, M.; Fambrough, D.M.
Am. J. Physiol. 259, 619-630, 1991
A;Title: Stability of the Na+,K+-ATPase alpha-subunit
A;Reference number: I50394
A;Accession: I50394
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A;Cross-references:
C;Genetics:
A;Gene: GDB:ATP1A2
                                                                                                                                                                   A;Cross-references: GB:M16795; NID:g179196; PIDN:AAA51799.1; PID:g553194
R;Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Allikmets, tina, M.B.; Sverdlov, E.; Modyanov, N.N.; Ovchnikov, Y.A.
FEBS Lett. 217, 275-278, 1987
A;Title: The family of human Na+,K+-ATPase genes. No less than five genes and/or A;Reference number: A27397; MUID:87247232; PMID:3036582
A;Accession: D27397
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A; Residues: 3-1017 <TA2>
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A;Residues: 1-1020 <SHU>
A;Cross-references: UNIPROT:P50993; GB:J05096; NID:g179164; PIDN:AAA51797.1; PID:g179165
                                                                                                   A; Molecule type: DNA
A; Residues: 251-442 < SVE>
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 211-249 <SH2>
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Best Local
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                                                                          GB:M27571
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Pred. No. 2.6e+02;
1; Mismatches 3;
                                                                                                                                                                                                      genes. No less than five genes and/or pseudog PMID:3036582
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F;128-147/Domain: transmembrane #status predicted <TM2>
F;148-288/Domain: intracellular #status predicted <TM2>
F;289-311/Domain: transmembrane #status predicted <TM2>
F;289-311/Domain: transmembrane #status predicted <TM3>
F;281-3346/Domain: intracellular #status predicted <TM4>
F;318-346/Domain: intracellular #status predicted <TM4>
F;447-783/Domain: ATPase nucleotide-binding domain homology <ATI
F;584-780/Domain: transmembrane #status predicted <TM5>
F;846-871/Domain: transmembrane #status predicted <TM5>
F;872-949/Domain: intracellular #status predicted <TM7>
F;950-975/Domain: transmembrane #status predicted <TM7>
F;976-1020/Domain: extracellular #status predicted <TM7>
F;374/Active site: Asp (aspartylphosphate intermediate) #status
F;505/Binding site: ATP (Lys) #status predicted
F;714,718,723/Active site: Asp, Asp, Lys #status predicted
                                                                                                                                                                                                       F;94-119/Domain: transmembrane #status predicted <TM1>
F;128-147/Domain: transmembrane #status predicted <TM2>
F;128-289/Domain: intracellular #status predicted <TM2>
F;148-289/Domain: intracellular #status predicted <TM3>
F;289-311/Domain: transmembrane #status predicted <TM3>
F;289-318/Domain: transmembrane #status predicted <TM3>
F;347-783/Domain: intracellular #status predicted <TM3>
F;347-783/Domain: intracellular #status predicted <TM5>
F;846-807/Domain: transmembrane #status predicted <TM5>
F;846-807/Domain: transmembrane #status predicted <TM6>
F;846-871/Domain: transmembrane #status predicted <TM7>
F;950-975/Domain: transmembrane #status predicted <TM7>
F;976-1020/Domain: extracellular #status predicted <TM7>
F;976-1020/Domain: extracellular #status predicted <EXT>
F;374/Active site: App (aspartylphosphate intermediate) #status F;505/Binding site: ATP (Lys) #status predicted
F;714,718,723/Active site: Asp, Asp, Lys #status predicted
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C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Superfamily: Na+/K+-transporting ATPase ion transport; phosphoprotein; potassium transp E;6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans; F;6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>
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A;Residues: 1-1020 <SHU>
A;Cross-references: UNIPROT:P06686; EMBL:M14512; NID:g203028; PIDN:AAA40776.1; PID:g203
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Blochemistry 25, 8125-8132, 1986
Blochemistry 25, 8125-8132, 1986
A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit f
A;Reference number: A90512; MUID:87128908; PMID:3028470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Na+/K+ exchanging ATPase (EC 3.6.3.9) alpha-2 chain - rat
N;Alternate names: Na+/K+-transporting ATPase alpha-plus chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
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                                                                                                                 Similarity
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Pred. No.
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                                                                                                                 Score 43; I
Pred. No. 2
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n function.

C;Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin of C;Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin of C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Seywords: ATP; hydrolase; phosphoprotein; potassium transport; sodium transport; transcipert; transporting ATPase alpha chain #status predicted <MAT>

F;6-1021/Product: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>
                                                                                                                                                                                                                     R;Kano, I.; Nagai, F.; Satoh, K.; Ushiyama, K.; Nakao, T.; Kano, FEBS Lett. 250, 91-98, 1989
A;Title: Structure of the alpha(1) subunit of horse Na,K-ATPase (A;Reference number: $04630; MUID:89290042; PMID:2544461
A;Accession: $04630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 36
S04630
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A;Title: Lysine 480 is an essential residue in the putative ATP site of lamb kidney (Na A;Reference number: A35426; MUID:90285144; PMID:2162343
A;Accession: A35426
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep
N;Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01074; A35426
R;Shull, G.E.; Schwartz, A; Lingrel, J.B.
Nature 316, 691-695, 1985
A;Title: Amino-acid sequence of the catalytic subunit of the (Na(+)+K(+)) ATPase ded
A;Reference number: A01074; MUID:85296299; PMID:2993903
                                                                                                                                                                                                                                                                                                                                                                                       Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - horse C;Species: Equus caballus (domestic horse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change C;Accession: S04630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;94-115/Domain: transmembrane #status predicted <TM1>
F;128-144/Domain: transmembrane #status predicted <TM2>
F;289-311/Domain: transmembrane #status predicted <TM3>
F;318-346/Domain: transmembrane #status predicted <TM4>
F;585-781/Domain: ATPase nucleotide-binding domain homology
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                                  A;Introns: 4/3; 39/3; 59/3; 127/3; 165/3; 210/3; 250/1; 339/3; 406/1; 442/3; 487/3; 552
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-1021 < KAN>
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J. Biol. Chem. 265, 10260-
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A;Residues: 1-1021 <SHU>
A;Cross-references: UNIPROT:P04074; GB:X02813; NID:g1205; PIDN:CAA26581.1; PID:g1206
                                                                                                                               A;Cross-references: UNIPROT:P18907; EMBL:X16773; NID:g1010; PIDN:CAA34716.1; PID:g87102
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;506/Binding site: ATP
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Best Local
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ATP; heterodimer; hydrolase;
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Pred. No.
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ion transport; phosphoprotein; potassium transp
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                                     A; Molecule type: mRNA
A; Residues: 1-1021 < OVC2 >
      A;Cross-references: UNIPROT:P05024; EMBL:X03938; NID:g1897; PIDN:CAA27576.1; PID:g1898
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F;6-1021/Product: Na+/K+-transporting ATPase alpha-1 chain #state F;6-93/Domain: intracellular #status predicted <INT1-194-119/Domain: transmembrane #status predicted <INT1-194-119/Domain: transmembrane #status predicted <INT2-148-288/Domain: intracellular #status predicted <INT2-19-289/Domain: transmembrane #status predicted <INT2-19-289-311/Domain: transmembrane #status predicted <INT3-19-289-311/Domain: intracellular #status predicted <INT3-19-289-311/Domain: intracellular #status predicted <INT3-19-289-311/Domain: ATPase nucleotide-binding domain homology <ATP (F)85-781/Domain: transmembrane #status predicted <INT3-19-280/Domain: transmembrane #status predicted <INT4-19-290/Domain: intracellular #status predicted <INT4-19-291-976/Domain: transmembrane #status predicted <INT4-19-291-976/Domain: extracellular #status predicted <INT4-19-291/Domain: extracellular #sta
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - pig
N;Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase (C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B24862; 146572; A35504; S00011; S00502; S02569; S29762
R;Ovchinnikov, Y.A.; Modyanov, N.N.; Broude, N.E.; Petrukhin, K.B.; Grishin, A FEBS Lett. 201, 237-245, 1986
A;Title: Pig kidney Na+,K+ATPase. Primary structure and spatial organization.
A;Reference number: A91361; MUID:86220813; PMID:2423371
A;Accession: B24862
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A;Residues: 1-1021 cTRK>
A;Residues: 1-1021 cTRK>
A;Residues: 1-1021 cTRK>
A;Cross-references: UNIPROT:P09572; GB:J03230; NID:g211219; PIDN:AAA48607.1; PID:
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding
C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein
F;585-781/Domain: ATPase nucleotide-binding domain homology cATN>
F;513,481/Binding site: carbohydrate (Asm) (covalent) #status predicted
F;374/Active site: Asp (asparty)phosphate intermediate) #status predicted
F;506/Binding site: ATP (Lys) #status predicted
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A;Title: Ouabain sensitive (Na(+)) + K(+))-ATPase activity expressed A;Reference number: A28199; MUID:88153759; PMID:2831227
A;Accession: A28199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken C;Species: Gallus gallus (chicken) C;Date: 21-Sep-1988 #sequence_revision 21-Sep-1988 #text_change 09-Jul-2004 C;Accession: A28199
                                                                                                                                                                                                                                                                                                                                                                                                                           B24862
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Best Local :
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6; Conservative
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K.B.; Grishin, A.V.;

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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 836-845, 'R', 847-851 <KAR>
A;Residues: 836-845, 'R', 847-851 <KAR>
A;Residues: 836-845, 'R', 847-851 <KAR>
R;Ovchinnikov, Y.A.; Arzamazova, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Aldanova, N.
FEBS Lett. 217, 269-274, 1987
A;Title: Detailed structural analysis of exposed domains of membrane-bound Na+,K+-ATPase
A;Title: Detailed structural analysis of exposed domains of membrane-bound Na+,K+-ATPase
A;Title: Detailed structural analysis of exposed domains of membrane zova, N.M.;
A;Tocontents: annotation; membrane identification of the extra- and intracellular hydrop
A;Title: Topology of Na, K-ATPase: identification of the extra- and intracellular hydrop
A;Title: Topology of Na, K-ATPase: identification of the extra- and intracellular hydrop
A;Contents: annotation; membrane topology
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transport;
F;6-1021/Product: Na+/K+-transporting ATPase alpha chain #status experimental <MAT>
F;94-118/Domain: transmembrane #status predicted <TMI>
F;94-118/Domain: transmembrane #status predicted <TMI>
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F;148-288/Domain: intracellular #status predicted <TW7>
F;148-288/Domain: intracellular #status predicted <TW7>
F;289-311/Domain: transmembrane #status predicted <TW3>
F;318-346/Domain: transmembrane #status predicted <TW4>
F;347-84/Domain: intracellular #status predicted <TW1>
F;385-781/Domain: ATPase nucleotide-binding domain homology
F;585-781/Domain: transmembrane #status predicted <TW5>
F;847-872/Domain: transmembrane #status predicted <TW6>
F;873-950/Domain: intracellular #status predicted <TW7>
F;951-976/Domain: transmembrane #status predicted <TW7>
F;951-976/Domain: transmemb
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A;Reference number: S45093
A;Accession: S49127
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1022 <CUT>
A;Cross-references: UNIPROT:Q92030; EMBL:X76108; NID:g509405;
C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; pota
                                                                                                                                                                                                                                                                                                                                                                          Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - C;Species: Anguilla anguilla (European eel) C;Date: 01-Feb-1995 #sequence_revision 14-Jul-1995 # C;Accession: 549127 C;Accession: 549127 R;Cutler, C.; Sanders, I.L.; Cramb, G. submitted to the EMBL Data Library, November 1993 submitted to the EMBL Data Library, November 1993
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60.0%;
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Pred. No. 2.6e
1; Mismatches
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              phosphoprotein; potassium
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3;
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                                                               ATPase nucleotide-binding
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                                                                                                                PIDN: CAA53714.1;
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A;Molecule type: mRNA
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A;Residues: 1-1023 <HAR>
A;Residues: 1-1023 <HAR>
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; DID:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; DID:CAA29306.1; PID:g55772
A;Tile: Three differentially expressed Na,K-ATPase alpha subunit isoforms: figure of the process of the proc
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A;Cross-references: UNIPROT:P06685; EMBL:M14511; NID:g2030
A;Cross-references: UNIPROT:P06685; EMBL:M14511; NID:g2030
A;Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamun
J. Biochem. 102, 43-58, 1987
J. Biochem. 102, 43-58, 1987
A;Title: Primary structures of two types of alpha-subunit
A;Reference number: S00460; MUID:88032933; PMID:2822682
A;Accession: S00460
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F;214,482/Binding site: carbohydrate (Asn) (covalent) #status prev
F;375/Active site: Asp (aspartylphosphate intermediate) #status pref;375/Active site: Asp (aspartylphosphate intermediate) #status preficted
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A;Molecule type: protein
A;Residues: 6-19 <LYT>
R;Kurihara, K.; Hosoi, K.; Kodama, A.
Biochim. Biophys. Acta 1039, 234-240,
A;Title: A new electrophoretic varian
                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 132, 764-769, 1985
A; Title: The catalytic subunits of the (Na(+), K(+))-ATPase
A; Reference number: S29877; MUID:86050667; PMID:2998384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Schneider, J.W.; Mercer, R.W.; Caplan, M.; Emanuel, J.R.; Sweadner, K.J.; Proc. Natl. Acad. Sci. U.S.A. 82, 6357-6361, 1985
A;Title: Molecular cloning of rat brain Na,K-ATPase alpha-subunit cDNA.
A;Reference number: A25171; MUID:85298352; PMID:2994074
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Biochim. Biophys. Acta 1049, 286-292, 1990
A;Title: Cloning and analysis of the 5'-flanking region
A;Reference number: S11020, MUID:90344872; PMID:2166579
A;Accession: S11020
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A; Residues: 1-67, 'PV',
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A;Cross-references: EMBL:M28647; NID:g205631; PIDN:AAA41671.1; PID:g205
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A;Residues: 489-533 <SCH>
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                                              A.; Ueha,
40, 1990
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K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.; l
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of Na(+)/K(+)-ATPase from the

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F;291-313/Domain: t
F;320-348/Domain: t
F;349-786/Domain: i
F;587-783/Domain: F
F;787-810/Domain: t
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F;96-120/Domain: tr
F;130-149/Domain: t
F;150-290/Domain: i
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A;Residues: 1-1023 <JAI>
A;Residues: 1-1023 <JAI>
A;Cross-references: UNIPROT:P30714; EMBL:Z11798; NID:g62491; PIDN:CAA77842.1; PID:g62492
A;Note: sequence extracted from NCB1 backbone (NCB1F:111876)
A;Note: sequence extracted from NCB1 backbone (NCB1F:111876)
C;Superfamily: Na+/K+-transporting AFPase alpha-1 chain #status predicted <MAT>
F;6-1023/Product: Na+/K+-transporting AFPase alpha-1 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - giant toad C;Species: Bufo marinus (giant toad) C;Species: Bufo marinus (giant toad) C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004 C;Accession: A43451, S24650 R;Jaisser, F.; Canessa, C.M.; Horisberger, J.D.; Rossier, B.C. J. Biol. Chem. 267, 16895-16903, 1992 J. Biol. Chem. 267, 16895-16903, 1992 A;Title: Primary sequence and functional expression of a novel ouabain-resistant Na,K-ATA;Reference number: A43451; MUID:92380991; PMID:1380956 A;Accession: A43451
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A;Residues: 6,'X',8-10,'X',12-16 <KUR>
A;Experimental source: submandibular gland
A;Note: designated alpha-S form; thought to arise
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                                                            F;150-290/Domain: intracellular #status predicted <INT2>
F;291-313/Domain: transmembrane #status predicted <TM3>
F;291-313/Domain: transmembrane #status predicted <TM3>
F;349-786/Domain: transmembrane #status predicted <INT3>
F;349-783/Domain: ATPase nucleotide-binding domain homology
F;787-810/Domain: transmembrane #status predicted <TM5>
F;849-874/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                       F;130-149/Domain: transmembrane F;150-290/Domain: intracellular
                                                                                                                                                                                                                                                                                                                    F;96-120/Domain: transmembrane #status predicted <TMl>
                                                                                                                                                                                                                                                                                                                                                  F;6-95/Domain: intracellular #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;6-95/Domain: intracellular #status predicted <INT1>
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Best Local
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in: intracellular #scatus predicted <TM72>
in: transmembrane #status predicted <TM3>
in: transmembrane #status predicted <TM3>
in: intracellular #status predicted <TM4>
in: ATPase nucleotide binding domain homology <A
in: transmembrane #status predicted <TM6>
in: transmembrane #status predicted <TM6>
in: transmembrane #status predicted <TM6>
in: intracellular #status predicted <TM6>
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Pred. No.
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R;Schoenrock, C.; Morley, S.D.; Okawara, Y.; Lederis, K.; Richter, I. Biol. Chem. Hoppe-Seyler 372, 279-286, 1991
A;Title: Sodium and potassium ATPase of the teleost fish Catostomus A;Reference number: S14740; MUID:91282983; PMID:1711856
A;Accession: S14740
A;Molecula ****
                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P25489; EMBL:X58629; NID:g62641; PIDN:CAA41483.1; PID:g6264C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; hydrolase; ion transport; phosphoprotein; potassium transport; sodium F;99-124/Domain: transmembrane #status predicted <TM1>F;133-152/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 43

PMCCNM

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - white sucker

C;Species: Catostomus commersoni (white sucker)

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C;Accession: S14740

C;Accession: S14740
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A;Residues: 1-1025 <VER>
A;Residues: 1-1025 <VER>
A;Cross-references: UNIPROT:Q92123; GB:U10108; NID:g499225; PIDN:AAA19022.1; PID:g49922
C;Comment: The alpha chain is the catalytic chain.
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium t
F;589-785/Domain: ATPase nucleotide-binding domain homology <ATN>
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R;Verrey, F.; Kairouz, P.; Schaerer, E.; Fuentes, P.; Geering, K.; Rossier, B.C.; Krael
Am. J. Physiol. 256, F1034-F1043, 1989
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F;133-152/Domain: transmembrane #status predicted <TMY2>
F;153-293/Domain: intracellular #status predicted <TMY2>
F;254-316/Domain: transmembrane #status predicted <TMY3>
F;294-316/Domain: transmembrane #status predicted <TM4>
F;353-790/Domain: intracellular #status predicted <TM4>
F;352-790/Domain: intracellular #status predicted <TMY3>
F;591-787/Domain: ATPase nucleotide-binding domain homology
F;791-814/Domain: transmembrane #status predicted <TM5>
F;853-878/Domain: transmembrane #status predicted <TM5>
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                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type:
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;217,485/Binding site: carbohydrate (Asn) (covalent) #status predicted
;378/Active site: Asp (aspartylphosphate intermediate) #status predicted
;510/Binding site: ATP (Lys) #status predicted
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Pred. No. 2.6e
1; Mismatches
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Pred. No. 2.6e+02;
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A;Map position: 3R 93B

C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp; 113-135/Domain: transmembrane #status predicted <TM1>
F;1146-165/Domain: transmembrane #status predicted <TM2>
F;166-305/Domain: intracellular #status predicted <TM3>
RESULT 45
A42687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Amplification of the phosphorylation site - ATP-binding site cDNA fragment A;Reference number: S07049; MUID:90092469; PMID:2557235
A;Accession: S07049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - fruit fly (Drosophila melanogaster) N;Alternate names: sodium pump alpha chain C;Speciles: Drosophila melanogaster C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004 C;Accession: S03632; S07049 R;Lebovitz, R.M.; Takeyasu, K.; Fambrough, D.M. BMBO J. 8, 193-202, 1989 A;Reference number: S03632; MUID:89231618; PMID:2540956 A;Accession: S03632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 397-521 <VAR>
A;Cross-references: EMBL:X17471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P13607; EMBL:X14476
A;Note: the sequence from Fig. 9 is inconsistent with that from Fig.
A;Note: it is uncertain whether Met-1 or Met-40 is the initiator
A;Note: it is uncertain whether Met-1 or Met-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;983-1027/Domain: extracellular #status predicted <EXT>
F;379/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;512/Binding site: ATP (Lys) #status predicted
F;721,725,730/Active site: Asp, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;166-305/Domain:
F;306-328/Domain:
F;335-363/Domain:
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A; Residues: 1-1038 < LEB >
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F;602-798/Domain:
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Matches 6
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Best Local S
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335-363/Domain: transmembrane #status predicted <TM4>
335-363/Domain: transmembrane #status predicted <TM4>
3602-801/Domain: intracellular #status predicted <TM3>
602-798/Domain: ATPase nucleotide-binding domain homology
802-825/Domain: transmembrane #status predicted <TM5>
804-889/Domain: transmembrane #status predicted <TM5>
809-966/Domain: intracellular #status predicted <TM7>
809-966/Domain: transmembrane #status predicted <TM7>
809-966/Domain: transmembrane #status predicted <TM7>
807-993/Domain: transmembrane #status predicted <TM7>
808-8096/Domain: transmembrane #status predicted <TM7>
809-9096/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                        ;391/Active site: Asp (aspartylphosphate intermediate);523/Binding site: ATP (Lys) #status predicted;732,736,741/Active site: Asp, Asp, Lys #status predict
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                Score 43; DB 1;
Pred. No. 2.6e+02;
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Search completed: September Job time: 15.4892 secs

2005, 16:22:51

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neurotrophin-4 precursor - human
N;Alternate names: neurotrophin-5
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A42687; UHOS03
R;IP, N.Y: | Dancez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, L.R;IP, N.Y: | Dancez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, L.R;C. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
A;Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distribu A;Reference number: A42687; MUID:92212967; PMID:1313578
A;Accession: A42687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-80/Domain: propeptide #status predicted <PRO>
F;81-210/Product: neurotrophin-4 #status predicted <PRO/
E;81-210/Product: neurotrophin-4 #status predicted <PRO/
E;81-210/Production-4 #status predicted <PRO/
E;81-210
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A;Residues: 1-210 <BER>
C;Comment: The neurotrophins stimulate autophosphorylation
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C;Superfamily: nerve growth factor beta chain
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A; Gene: GDB:NTF5
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A;Reference number: JH0503; MUID:92075279; PMID:1742028
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Local Similarity 47.4%;
nes 9; Conservativa
156
                                                                                                             1 GGCADGPTLREWISFCGGK 19
GGCR-GVDRRHWVSECKAK 173
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Pred. No. 71;
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Maximum Match 100%
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Maximum DB
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Perfect score:
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137.677 Million cell updates/sec
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Gapop 10.0 ,
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1: uniprot_sprot:*
2: uniprot_trembl:*
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114
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Copyright (c) 1993 - 2005 Compugen
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Q7UOS4
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ETR2_CANTR
Q98A97
Q98K1E9
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Q9KK1E9
Q9UNTS
Q8DHX7
Q8GHX8
Q9K1E9
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Q8K1E9
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Q9nex6 caenorhabdi
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4 candida tro
7 rhizobium 1
9 rhizobium 1
9 streptomyce
0 arabidopsis
2 prochloroco
5 streptomyce
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7 mycobacteri
3 anopheles 9
5 rhodopirell
2 streptomyce
3 azoarcus sp
7 synechococc
6 bradyrhizob
caenorhabdi
           caenorhabdi
kluyveromyc
paracoccidi
bacteriopha
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corynebacte
porphyromon
homo sapien
burkholderi
bordetella
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QÓSUAI
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ROROR HUMAN
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Q6N1X5
Q88HF5
Q89JR5
Q89ZCX1
Q82CX1
Q64BD6
Q7XWX0
Q7XXV0
Q629V1
Q63HZ6
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AASS H
Q9Y878
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Q6ZTT4
Q8C4M6
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Q7SHC4
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4. THAK-2003 (TrEMBLTel. 23, Last annotation update)
4. Hypothetical protein Y105E8A.21.
6. ORFNames=Y105E8A.21;
6. Caenorhahair.
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01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein
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SEQUENCE
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                                                                                                      Submitted (AUG-2004) to the EMBL/GenB EMBL; AL132876; CAC48140.1; - WormBase; WBGene00013679; Y105E8A.21. WormBep; Y105E8A.21; CE25162.
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Rhodopirellula baltica.
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Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL; BX294144; CAD74759.1; -.
                                                                                                                                                                                                                                                       Sulston J.E.;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode investigating biology.";
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GO:0005634; C:nucleus; IEA.
GO:0003676; F:nucleic acid binding;
GO:0008270; F:zinc ion binding; IEA
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                                                                                                                                                                                                                                             J. Mol.
                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS), AND MUTAGENESIS OF pubMed=12614607; DOI=10.1016/S0022-2836(03)0038-X; Airenne T.T., Torkko J.M., Van den plas S., Sormunen R.T., Kastaniotis A.J., Wierenga R.K., Hiltunen J.K.; "Structure-function analysis of enoyl thioester reductase mitochondrial maintenance.";
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 20336;
PubMed=12890667; DOI=10.1074/jbc.M307664200;
Torkko J.M., Koivuranta K.T., Kastaniotis A.J., Airenne T.T.,
Glumoff T., Ilves M., Hartig A., Gurvitz A., Hiltunen J.K.;
"Candida tropicalis expresses two mitochondrial 2-enoyl thioester reductases that are able to form both homodimers and heterodimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Enoyl-[acyl-carrier protein] reductase [NADPH,
mitochondrial precursor (EC 1.3.1.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 934 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory competence." Mol. Cell. Biol. 21:6243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOI=10.1128/MCB.21.18.6243-6253.2001;
Torkko J.M., Koivuranta K.T., Miinalainen I.J., Yagi A.I., Schr
Kastaniotis A.J., Airenne T.T., Gurvitz A., Hiltunen K.J.;
"Candida tropicalis Etrip and Saccharomyces cerevisiae Ybr026p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida tropicalis (Yeast).
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8WZM3;
                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                  nol. Biol. 327:47-59(2003).

Mol. Biol. 327:47-59(2003).

FUNCTION: Required for respiration and the maint micochondrial compartment. May have a role in th synthesis of fatty acids.

CATALYTIC ACTIVITY: Acyl-(acyl-carrier protein) + NADPH.
                                                                                                                                                                     2,3-dehydroacyl-[acyl-carrier protein] + NAD SUBUNIT: Homodimer and heterodimer with etr2
                                                                                                                                        SUBCELLULAR LOCATION: Mitochondrion. SIMILARITY: Belongs to the zinc-cont
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                                                                                                                                          Belongs to the zinc-containing alcohol
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3; Mismatches
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SEQUENCE
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InterPro; IPR011032; GroEs like.
Pfam; PF00107; ADH zinc_N; 1.
3D-structure; Direct protein sequencing; Fatty acid biosynthesis;
Mitochondrion; NADP; Oxidoreductase; Transit peptide.

    FUNCTION: Required for respiration and the maintenance of the mitochondrial compartment. May have a role in the mitochondrial synthesis of fatty acids.
    CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADP(+) = trans 2,3-dehydroacyl-[acyl-carrier protein] + NADPH.
    SUBURIT: Homodimer and heterodimer with ETR1.
    SUBURITIAUTAR LOCATION: Mitochondrion (By similarity).
    SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase family. Quinone oxidoreductase subfamily.

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PDB; IGUT; X-ray; A/B=23-386.
PDB; 1GUF; X-ray; A/B=23-386.
PDB; 1GYR; X-ray; A/B/C=23-386.
                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.11 ANGSTROMS).
Alrenne T.T., Torkko J.M., Hiltunen J.K.;
"Crystal atructure of enoyl thioester reductase 2.";
Submitted (JUN-2002) to the PDB data bank
                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=12890667; DOI=10.1074/jbc.M307664200;
PubMed=12890667; DOI=10.1074/jbc.M307664200;
Torkko J.M., Koivuranta K.T., Kastaniotis A.J., Airenne T.T.,
Glumoff T., Ilves M., Hartig A., Gurvitz A., Hiltunen J.K.;
"Candida tropicalis expresses two mitochondrial 2-enoyl thioester
reductases that are able to form both homodimers and heterodimers.";
J. Biol. Chem. 278:41213-41220(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enoyl-[acyl-carrier protein] reductase
mitochondrial precursor (EC 1.3.1.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8WZM4;
25-OCT-2004
                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 20336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida tropicalis (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5482;
                                                                                                                                              between
                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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an email to license@isb-sib.ch
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Y->N: 0.1% of catealytic activity.
; FCBC174A240742D8 CRC64;
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Q8KJF9; O1-OCT-2002 (TrEMBLrel. 22, Creatol-OCT-2002 (TrEMBLrel. 22, Lastol-UN-2003 (TrEMBLrel. 24, L
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Q98A97;
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3D-structure; Fatty acid biosynthesis; Mitochondrion; NADP; Oxidoreductase; Transit peptide.
TRANSIT 1 22 Mitochondrion (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003673; CAIB BAIF.
Pfam; PF02515; CoA transf_3; 1.
Complete proteome.
SEQUENCE 387 AA; 42226 MW;
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Rhizobium loti (Mesorhizobium loti)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu B., Kato T., Sasam Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
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Mlr6096 protein
                                       Bacteria; Proteobacteria;
Phyllobacteriaceae; Mesori
                                                                                                                           Rhizobium loti (Mesorhizobium loti)
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MEDLINE=21082930;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Eukaryotic translation initiation factor 6 (EIF-6)-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces hygroscopicus subsp. ascomyceticus. Bacteria; Actinobacteria; Actinobacteria; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                        ed. No. 34;
Mismatches
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RESULT
Q7V2B2
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  RRR COCOCUE D D T AC
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EMBL; AL161667; CAB81587.1; -.

EMBL; BT009656; AAP75806.1; -.

EMBL; BT009656; AAP75806.1; -.

EMBL; BT009656; AAP75806.1; -.

EMBL; BT009656; TAP701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                             Q7V2B2;
01-OCT-2003 (TrEMBLrel. 25, C:
01-OCT-2003 (TrEMBLrel. 25, L:
01-MAR-2004 (TrEMBLrel. 26, L:
01-MAR-2004 (EC 3.5.2.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shīnn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Nar Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Benes V., Wurmbach E., D.
Lemcke K., Mayer K.F.X.,
Submitted (MAR-2000) to 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=F1116_30; Synonyms=At3g55620;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Espermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                Dihydroorotase (EC 3.5.2.3).
Name=pyrC; OrderedLocusNames=PMM0569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   띰
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SEQUENCE FROM N.A. MEDLINE=22825698;
                                                                                                                                Prochlorococcus marinus subsp. pastoris Bacteria; Cyanobacteria; Prochlorales; I
                                                                                                                                                                                                                                                                                                                                        Q7V2B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00654; eIF6; 1.
TIGRFAMB; TIGR00323; eIF-6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002769; (Pfam; PF01912; eIF-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.
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                                                                  NCBI_TaxID=59919;
                                                                                                        Prochlorococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opsis sequencing project;
(APR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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  PubMed=12917642;
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57.1%;
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., Quetier F., Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207
                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                        Created)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    initiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
     DOI=10.1038/nature01947;
                                                                                                                                                                                                                                                                                                                                           349
                                                                                                                                Prochlorococcaceae;
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                                                                                                                                                             (strain CCMP 1378 / MED4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 245;
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Chen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Narusaka
T., Satou
nada K., Yu
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RESULT
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Best Local
           "Complete genome sequence of the model actinomyce coelicolor A3(2).";
Nature 417:141-147(2002).

-!- SIMILARITY: Contains 1 HTH merR-type DNA-bind EMBL; AL999118; CAB56383.1; -.
GO; GO:0005625; C:intracellullar; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0003755; P:regulation of transcription, DN
InterPro; IPR000551; HTH_MerR.
InterPro; IPR000561; Putativ_DNA_bind.
Pfam; PF00376; MerR; 1.
PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH MERR; 1.
PROSITE; PS50937; HTH_MERR, 2; 1.
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GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0019856; P:pyrimidine base biosynthesis; IEJ
InterPro; IPR006680; Anidohydro_1.
InterPro; IPR004721; DHOdimr.
InterPro; IPR002195; Dihydroorotase.
Pfeam; PPF01979; Amidohydro_1; 1.
TIGRPAMs; TIGR00856; DyrC dimer; 1.
PROSITE; PS00482; DIHYDROOROTASE_1; UNKNOWN_1.
PROSITE; PS00483; DIHYDROOROTASE_2; 1.
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                                                                                                                                                                                                                                                        STRAIN=A3(2) / M145;
MEDLINB=2196410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D. Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Tromin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor
Marren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative MerR family transcriptional regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 424:1042-1047(2003).
EMBL; BX572091; CAE19028.1; -.
HSSP; P05020; 1J79.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor. Bacteria, Actinobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORFNames=SCD17.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9RKM5;
01-MAY-2000
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Complete
                                                                                                                                                                                                                                             Hopwood D.A.;
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349 AA; 39958 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCADGPTLREWISFCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pacteria; Actinobacteridae; Actinomycetales;
Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                              factor activity;
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                                                                                                               DNA-dependent;
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                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                         Collins M., Howarth S., O'Neil S.,
                                                                                                                                                                                                                                                                           Taylor K.,
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A Pang X., Aigle B., Control A Pang X., Aigle B., Control A Pang X., Aigle B., Leblond P., If "Functional angucycline-like antibiotic gene cluster II. If "Functional angucycline-like ambofaciens linear chromosome."; If antimicrob. Agents Chemother. 48:575-588(2004).

RE Antimicrob. Agents Chemother. 48:575-588(2004).

RE GO; GO:0003677; FANR30165.1; -.

DR GO; GO:0000156; P:two-component response regulator activity; IEA.

GO; GO:0000156; P:two-component signal transduction system (p. . .; I GO; GO:000160; P:two-component signal transduction system (p. . .; I InterPro; IPR009059; bi_resp_regitr_C.

DR InterPro; IPR0091867; Trans_reg_C.

DR Pfam; PF003704; BTAD.

DR Pfam; PF003704; BTAD.

DR Pfam; PF003704; BTAD; 35639 MW; 945BC929E5A6EE3D CRC64;

SEQUENCE 342 AA; 35639 MW; 945BC929E5A6EE3D CRC64;
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Q6VMH4
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Q73ZW7
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Matches
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Q6VMH4;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                               Q73ZW7
Q73ZW7;
05-JUL-2004
05-JUL-2004
Submitted (SEP-2003) to the EMBL; AB017232; AA503801.1; GO; GO:0005506; F:iron iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=ATCC 23877; Pubmed=14742212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                              SEQUENCE FR
STRAIN=k10;
                                                                                                                                                                           Corynebacterineae;
NCBI_TaxID=1770;
                                                                                                                                                                                                                             OrderedLocusNames=MAP1484c;
Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomycineae;
NCBI_TaxID=1889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces ambofaciens. Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative SARP family pathway
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation updat
(TrEMBLrel. 27, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                        Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB Pred. No. 50; 2; Mismatches
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Pred. No. 46;
2; Mismatches
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Last sequence update)
Last annotation update)
                                                                   Q., Amonsin A., Alt D., Kap
EMBL/GenBank/DDBJ databases
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RESULT 14
Q7ULR5
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R GO; GO:000898; F:homocysteine S-methyltransferase activity; IEA.

R GO; GO:0004672; F:protein kinase activity; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR010109; Kinase like.

DR InterPro; IPR000719; Prot kinase.

DR Pfam; PF000726; S methyl_trans.

Pfam; PF00059; Pkinase; 1.

DR Pfam; PF00051; Prot kinase; 1.

DR Pfam; PF000001; Prot kinase; 1.

DR Pfam; PF000001; Prot kinase; 1.

DR PROSITE; PSS9011; PROTEIN KINASE DOM; 1.

DR PROSITE; PSS9011; PROTEIN KINASE DOM; 1.
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Q7QC63
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InterPro; IPR001663; Ring_hydroxyl_A.
Pfam; PF00355; Rieske; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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01-MAR-2004
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01-MAR-2004
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                                                               01-OCT-2003
01-MAR-2004
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                                                                                                        Q7ULR5;
01-OCT-2003
                                                                                                                                                     Q7ULR5
Name=cpcE; OrderedLocusNames=RB9340,
                                             Similar
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; GO:0006725;
; GO:0006118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0005524; F:ATP binding; IEA.
GO:00056898; F:homocysteine S-methyltransferase activity;
GO:00008898; F:homocystein kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.
L; AAAB01008859; E
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                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:oxidoreductase activity; IEA.
P:aromatic compound metabolism;
P:electron transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52010 MW;
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75.0%;
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                                      Last sequence update)
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a phycocyanobilin lyase CpcE
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Pred. No. 67;
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Pred. No. 1.6e+02;
L; Mismatches 2;
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RESULT 15
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D2 D1-MA
D3 Strep
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InterPro; IPR004155; PBS 1yase HEAT.
Pfam; PF03130; HEAT PBS; 1.
SMART; SM00567; EZ HEAT; 3.
Complete proceome; Lyase.
SHOUENCE 238 AA; 26142 MW; B7CA
Pfam; PF01614; IclR;
Complete proteome.
SEQUENCE 283 AA; 3
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01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
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Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL; BX294149; CAD76204.1; -.
GO; GO:0016829; F:lyase activity; IEA.
                                                                                                                                                                                                                                                                                                Ikeda H., Ishikawa J., Hanamoto A., Shinos
Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative
microorganism Streptomyces avermitilis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces avermitilis.
Bacteria; Actinobacteridae; Actinomycetales;
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Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Planctomycetes; Planctomycetaceae; Pirellula.
                                                                                                                                                                     Nat. Biotechnol. 21:526-531(2003).
EMBL, APO05042; BAC72938.L; -.
GO; GO:0003677; F:NNA binding; IEA
GO; GO:0006355; P:regulation of tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=SAV5226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative IclR-family transcriptional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolites.";
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                                                                                               InterPro; IPR005471; HTH_IclR.
InterPro; IPR009058; Wing_hlx_DNA_bnd
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22608306; PubMed=12692562;
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39.1%;
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       MW;
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                                                                                                                                                                            of transcription,
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          F63B1705578EEE67 CRC64;
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RESULT 17
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05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2:
Hypothetical protein
ORFNamora
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EMBL; BX682953; CAF219
Hypothetical protein.
SEQUENCE 94 AA; 982
                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8DHX7
Complete
SEQUENCE
                                                                Nakamura Y., Kaneko T., Sato S., İkeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.: "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
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Reinhardt
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01-MAR-2003
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Bacteria; Proteobacteria; B
                                                                                                                                                                                                                                                                                   Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                   Synechococcus elongatus
                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=tll1816;
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                                     EMBL;
                                                        DNA Res.
                                                                                                                                                                                       MEDLINE=22225144;
                                                                                                                                                                                                         STRAIN-BP-1
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                        Tll1816 protein.
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L-MAR-2003 (TrEMBLrel.
L-MAR-2003 (TrEMBLrel.
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                                   es. 9:123-130(2002).
AP005375; BAC09368.1;
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129 AA;
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Rabus
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                                                                                                                                                    PubMed=12240834;
Sato S., Ikeuchi M., Katoh H.,
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14644 MW;
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R.;
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72.7%;
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Pred. No.
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Pred. No. 49;
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 EBB44691E7DD1E12 CRC64;
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RESULT 19
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Best Local S
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Q9UAT5;
01-MAY-2000
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01-JUN-2003
01-JUN-2003
                                                                            Q89PE8
WormBase Consortium;
WormBase Consortium;
"Genome sequence of the nematode C. elegans: a "Genome sequence of the C. elegans Sequencir"
                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Creat 01-MAY-2000 (TrEMBLrel. 13, Last 01-OCT-2003 (TrEMBLrel. 25, Last Hypothetical protein C0184.7, Name=C0184.7;
                                                                                                                                                                                                                                                                                                          Pfam; PF00941; FAD_binding_5;
Complete proteome.
SEQUENCE 271 AA; 29422 MW;
                                    SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP005948; BAC48799.1; HSSP; P19920; 1N62.
                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genomic sequence of nitro Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=cutM; OrderedLocusNames=blr3534; Bradyrhizobium japonicum.
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CutM protein.
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                                                                         NCBI_TaxID=6239;
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GO; GO:0006118; P:electron transport;
InterPro; IPR005107; CO deh flav C.
InterPro; IPR002346; dehydrog molyb.
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Sasamoto S., Watanabe A.,
                                                                                                                                                                                                                              211
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9; Conser
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8; Conser
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                                                                                                                                                                              PRELIMINARY;
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                                      PubMed=9851916;
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56.2%;
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1., Idesawa K., Iriguch
, Shimpo S., Tsuruoka
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Last seq
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Pred. No.
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., Minamisawa K., u...
----a K., Iriguchi M., Kawar
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                                                                                               Rhabditida; Rhabditoidea;
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i M., Kawashima ,
i M., Yar
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         Consortium
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Best Local
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WormBase; WBGene00015271; C01B4.7.
WormPep; C01B4.7; CE30476.
G0:00016021; C:integral to membrane; II
G0; G0:0005215; F:transporter activity; II
G0; G0:0006810; P:transport; IEA.
InterPro; IPR007114; MFS.
PROSITE; P850850; MFS; 1.
Hypothetical protein.
SEQUENCE 475 AA; 53094 MW; 79095D45577
                                                                                                                                                                                                                                                                                                                                                                                                                      Q966D4;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Y19D10A.4.
Name=Y19D10A.4; ORFNames=Y19D10A.4;
Caenorhabditis elegans.
Caenorhabditis elegans, Nematoda, Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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[2]
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"The sequence of C. elegans
Submitted (FEB-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormBase Consortium;
Submitted (SEP-2004) to the
EMBL; AF125952; AAD14699.1;
PIR; T33943; T33943.
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                                                                                                                                                                                                                 STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
Worned sequence of the nematode
investigating biology. The C. ele
Science 282:2012-2018(1998).
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                                                                         Johnson D.;
"The sequence of C.
Submitted (MAR-1999)
                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Bristol N2;
    SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
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8; Conserv
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larity 50.0%;
Conservative
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                                                                                                                                                                                                                                          e nematode C. elegans: a platform The C. elegans Sequencing Consort
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EMBL/GenBank/DDBJ
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                                                                            cosmid Y19D10A.";
EMBL/GenBank/DDBJ databases.
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L; Mismatches
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Matches 8
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GO; GO:0004034; F:aldose l-epimerase activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006012; P:galactose metabolism; IEA.
GO; GO:0006012; P:galactose metabolism; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR008183; Aldl epimerase.
InterPro; IPR011013; Gal_mut_like.
InterPro; IPR007114; MFS.
pfam; PF01263; Aldose_epim; 1.
pROSITE; PS50850; MFS; 1.
                                                                                                                                                                 Q6CLJ9
Q6CLJ9;
25-OCT-2004
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Submitted
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GO; GO:00
GO; GO:00
GO; GO:00
GO; GO:00
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                                                                          OFFNames=Autov. Co. 1. 1140.
Kluyveromyces lactis NRRL Y-1140.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Eukaryota; Fungi; Ascomycotaceae; Kluyveromyces
                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
similar to sp|P40825 Saccharomyces cerevisiae YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                              synthetase.
ORFNames=KLLA0F02431g;
                                                                                                                                                                                                                                                                                                                                   Hypothetical
SEQUENCE 8:
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Dujon B., Sherman D., Fischer G., Durrens
Lafontaine I., de Montigny J., Marck C., N
                    STRAIN=NRRL
Genolevures;
                                                                  NCBI
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                                            SEQUENCE
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                                                               [_TaxID=284590;
                                                                                                                                                                                                                                              268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC006722; AAK68417
                                                                                                                                                                                                                                                                                        Similarity
8; Conserv
                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y19D10A.4; CE21450.
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Pred. No.
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cerevisiae YOR335c
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1.7e+02;
  s P., Casaregola
Neuveglise C.,
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                                                                                                                                                                                                                                                                                                             Length 821;
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Best Local
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GG: GG:0004813; F:alanine-trah ligase activity; l GG: GG:0005524; F:ATP binding; IEA.
GG: GG:0005524; F:ATP binding; IEA.
GG: GG:00056419; P:alanyl-tRNA aminoacylation; IEA.
GG: GG:0006419; P:alanyl-tRNA aminoacylation; IEJ.
InterPro; IPR003156; Pesterase_DHHA1.
InterPro; IPR003156; Pesterase_DHHA1.
InterPro; IPR006193; tRNA-synt_2c.
InterPro; IPR006193; tRNA-synt_Ala.
Pfam; PF01411; tRNA-synt_2c; 1.
Pfam; PF01411; tRNA-synt_Ala.
TIGRPAMS; TIGR00344; alaS; 1.
PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
Aminoacyl-tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                               Q9Y8B3;
Q9Y8B3;
01-NOV-1999
                                                                                                                      MEDINE-20171859; PubMed=10705373;
MEDINE-20171859; PubMed=10705373;
DOI=10.1002/(SICI)1097-0061(20000330)16:5<451::AID-YEA540>3.0.CO;2-O;
Pereira M., Felipe M.S.S., Brigido M.M., Soares C.M.A., Azevedo M.O.;
"Molecular cloning and characterization of a glucan synthase gene from the human pathogenic fungus Paracoccidioides brasiliensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Seniou-Meyer M., Zivanovic I., Bolotin-Fukhhara M., Thierry A.,
the human pathogenic fungus Paracoccidioides brasilie Yeast 16:451-462 (2000).

Yeast 16:451-462 (2000).

EMBL; AP148715; AAD37783.1; -.

GO; GO:000148; C:1,3-beta-glucan synthase complex; I GO; GO:0016020; C:membrane; IEA.

GO; GO:0003843; F:1,3-beta-glucan synthase activity; GO; GO:0006075; P:beta-1,3 glucan biosynthesis; IEA.

InterPro; IPR003440; Glyco_trans_48.

InterPro; IPR002114; HPr_Serp_S.
                                                                                                                                                                                                                                                                      Paracoccidioides brasiliensis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Paracoccidioides.
NCBI_TaxID=121759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope;
Submitted
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01-NOV-1999 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 430:35-44(2004)
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STRAIN=NRRL Y-1140;
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Pred. No.
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2e+02;
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Query Match
Best Local
                                                                                        MEDLINE=22484998; PubMed=12
Kaneko T., Nakamura Y., Sat
Sasamoto S., Watanabe A., I
Kohara M., Matsumoto M., Sh
Tabata S.;
                           Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02364; Glucan_synthase; PROSITE; PS00589; PTS_HPR_SER; USEQUENCE 1926 AA; 220574 MW;
                                                             "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
                                                                                                                                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                        01-JUN-2003
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF320576; AAQ14824.1; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Sriranganathan N., Whichard
"Bacteriophage Felix O1: Gen
Submitted (NOV-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage Felix 01.
Viruses; dsDNA viruses,
NCBI_TaxID=77775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q6KG99;
05-JUL-2004
                                              HSSP; P27017; 1Q00
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID=375;
                                                                                                                                                                                                      OrderedLocusNames=blr6053;
                                                                                                                                                                                                                                                   Q89HD8;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                  Match
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                                                      AP005957; BAC51318.1;
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426 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   166 AA;
                                                                                                                                                                                                                        (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                            PTYCHWISLCG
                                                                                                 PubMed=12597275;
ra Y., Sato S., Minamisawa K., Uci
nabe A., Idesawa K., Iriguchi M.,
oto M., Shimpo S., Tsuruoka H., W
                                                                                                                                                                                                                                                                                                                                                                                    19296 MW;
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46.7%;
                            47042 MW;
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40.8%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 2;
Pred. No. 3.9e+02;
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNKNOWN 1.
                            AE20AA1EC6CBE038
                                                                                                                                                                                                                                                                                                                                                                                    5AAB33E39DC3C989
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46.5;
No. 1.
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DB 2;
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                                                                                                    Wada
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        Length
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ada T., Yamada
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01-MAR-2003
                                                                                                                                   DOI=10.1128/JB.185.18.5591-5601.2003;
Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T.,
Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwi
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J
Dewhirst F.E., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=PG1251;
Porphyromonas gingivalis (Bacteroides
Bacteria; Bacteroidetes; Bacteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7MV49;
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EMBL; AP005220; BAC18668.1; -.
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Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                    "Complete genome sequence of the oral Porphyromonas gingivalis strain W83."; J. Bacteriol. 185:5591-5601(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein
                        EMBL; AE017176; AAQ66334.1; TIGR; PG1251; -.
                                                                                                                                                                                                                                                                              MEDLINE=22829867; PubMed=12949112;
                                                                                                                                                                                                                                                                                                         STRAIN=W83;
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                                                                                                                                                                                                                                                                                                                                                                                                   Porphyromonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                             TaxID=837;
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proteome; Hypothetical protein
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Bacteroides
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Pred. No. 29;
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6CF1DA566EB3004C
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                                                                                                                                                                                                                                                                                                                                                                                                                        gingivalis).
(class); Bacteroidales;
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                                                                                                               pathogenic bacterium
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                                                                                                                                                                Duncan M.J.,
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                                                                                                                                                                                         Gray J.
                                                                                                                                                                                                                                  D.E.,
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,
RA Ninomiya K., Katsuta N., Sato K., Tohiba Y., Ishida S.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Hoututa T., Kusano J.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takamoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takamoto M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nishima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
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Q8N852;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ40008.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
    Q63KH8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                            Nat. Genet.
                                                                                                                                                                                                                                                                                                                                                                                  cDNAs.";
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NCE 159 AA; 17782 M
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       PRELIMINARY;
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52.9%;
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Pred. No.
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Pred. No. 48;
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RESULT Q7MV49

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RESULT 29
Q7VWW5
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                                                                    RP SEQUENCE FROM N.A.

RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

RX Parkhill J., Sebaiha M., Preston A., Murphy L.D., Thomson N.R.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall M.A.,

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Chillingworth T., Collins M., Hauser H., Holroyd S., Jagels K.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Heather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

Bordetella parapertussis and Bordetella bronchiseptica.";

RAI RAYA(A471-Chaz)350 1. -
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Best Local
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25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
Hypothetical protein.
ORFNames=BPSS1383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella pertussis.
Bacteria; Proteobacteria; B
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R., Browk K., Brown K.A., Brown N.F., Challis G.L., Cherevach I., Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D., Peltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K., Keith K.E., Maddison M., Moule S., Price C., Quail M.A., Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M., Songsivilai S., Stevens K., Tumapa S., Vesarachavest M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2003 (TrEMBLrel. 2:
01-OCT-2003 (TrEMBLrel. 2:
Putative lipoprotein.
OrderedLocusNames=BP2072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkh "Genomic plasticity of the causative agent of melioidosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. EMBL; BX571966; CAH38855.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burkholderia pseudomallei."
Proc. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15377794;
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SEQUENCE
                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7VWWS;
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                                                        BX640417; CAE42350.1; -.
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8; Conserv
                       proteome;
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  196
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  Lipoprotein.
21519 MW;
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88.9%;
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28,
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MW;
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Pred. No. 48;
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  FF6E2E86B5EE9968 CRC64;
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MEDLINB-22827954, PubMed=12910271; DOI=10.1038/ng1227;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis
                                                                SEQUENCE FR
Sasaki T.,
                                                                                                                          Putative eukaryotic translation initiation factor 6.
Name=0J1340_C08.131;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete
SEQUENCE
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Nat. Genet. 35:32-40(2003).
EMBL; BX640429.
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Bacteria; Proteobacteria;
                   "Oryza sativa nipponbare(GA3) clone:OJ1340_C08.";
                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
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OrderedLocusNames=BPP1756;
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0003700; F:transcription of transcription, DN
InterPro; IPR001356; Homeobox.
R InterPro; IPR001356; Homeodomain_like.
R InterPro; IPR0009057; Homeodomain_like.
R InterPro; IPR0009057; Homeodomain_like.
R Ffam; PF00046; Homeobox; 1.
R PRINTS; PR00031; HTHREPRESSR.
PRINTS; PR00031; HTHREPRESSR.
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Lev. Genet. 24:319-328(1999).

EMBL; U88714; AACO8704.1; -...

HSSP; P22808; 1NK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0003743; F:translation initiation fac
GO; GO:0006413; P:translational initiation;
InterPro; IPR002769; eIF6.
Pfam; PF01912; eIF-6; 1.
ProDom; PD006880; eIF6; 1.
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                                                                                                                                                                                                       PROSITE; PS00027; HOMEOBOX_1; 1. 1. PROSITE; PS50071; HOMEOBOX_2; 1. DNA-binding; Homeobox; Nuclear p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99255950; PubMed=10322640;
DOI=10.1002/(SICI)1520-6408(1999)24:3/4<319::AID-DVG15>3.0.CO;2-#;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=PwNkx-3.2;
Pleurodeles waltlii (Iberian ribbed newt)
Eukaryota; Metazoa; Chordata; Craniata; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGRO0323; eIF-6; 1.
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Q12522; 10
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Last annotation update)
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Pred.
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4519CD44E3348DE0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/10; TISSUE=Spleen; MEDLINE=97148595; PubMed=9020038; DOI=10.1006/bbrc.1996.5876; Kruecken J., Scmitt-Wrede H.P., Markmann-Mulisch U., Wunderlich F.; "Novel gene expressed in spleen cells mediating acquired testosterone-resistant immunity to Plasmodium chabaudi malaria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human ortholog to mouse gene imap38 encoding protein belongs to a gene family clustered on Gene 282:159-167(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat Immunity-associated protein 1 (Immune associated protein)
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                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21673999; PubMed=11814688;
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                                                                                                                                                                                                Pfam; PF04548; AIG1;
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AJ133125; CAB53101.1; ALT_SEQ.
                         . Similarity 7; Conserv
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 CADGPTLREWISFCGGK 19
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130
277 ;
                            Conservative
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Rodentia;
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Ref.2 sequences were
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                           4.
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Extracellular (Potential).

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GTP (Potential).

GTP (Potential).
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Anchor for type IV memb
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                                                                                  F192E438A7579C5C
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                                                                                                                                                                                     Transmembrane
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R EMBL; AF164116; AAF80492.1; --

R EMBL; AF274060; AAK58697.1; --

R HSSP; Q06486; ICKI.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R InterPro; IPR00109; Kinase like.

R InterPro; IPR001019; Kinase like.

R InterPro; IPR00171; Ser thr pkin_AS.

R Pfam; PF00069; Pkinase; I.
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Eukaryota; Euglenozoa;
NCBI_TaxID=5693;
                                                                                                                                                                             Q7PPP6;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGP00000020769 (Fragment).
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MEDLINE=22276527; PubMed=12387847; DOI=10.1016/S0166-6851(02)00156-1;
Spadafora C., Repetto Y., Torres C., Pino L., Robello C., Morello A.,
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05-JUL-2004 (TrEMBLrel.
Casein kinase 1 homolog
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01-OCT-2000
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; SEQUENCE 312 AA; 35770 MW; 471E0BC2B0546321 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypanosoma cruzi.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spadafora C., Gamarro F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
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                                                                  Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI TaxID=180454;
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                           SEQUENCE FROM N.A.
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nilarity 57.1%;
Conservative
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Best Local
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                                  O9P858 PRELIMINARY;
O9P858;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
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01-JUN-2003
01-JUN-2003
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Nelson K.E., Weinel C., Paulsen I.T., Dodsom R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.B., Gill S.R., Pop M., Holmes M.,
Brinkac L. M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.P.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
Frager C. M.
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Q88NU2;
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted: Requence shown here is derived from an
-i- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
           Hypothetical protein. Phaeosphaeria nodorum
                                                                                                                                                                                                                                                    Complete proteome; SEQUENCE 403 AA;
                                                                                                                                                                                                                                                                             EMBL; AE016778; AAN66737.1; TIGR; PP1112; -.
                                                                                                                                                                                                                                                                                                     "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=PP1112;
Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                           Kiewitz C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=160488;
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Plasmid
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; AAAB01008944; EAA10075.2; -.
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42380 MW; 4D71AA1F370C58A7 CRC64;
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             (Septoria nodorum)
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Last sequence update)
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Last
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Pred. No.
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                                    sequence update) annotation updat
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RESULT
Q6AITO
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Q82LI0
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Q82LI0
Q82LI0;
01-JUN-2003
01-JUN-2003
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Submitted (MAY-2000) to the
EMBL; AJ277966; CAB91876.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M., Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K., Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q6AIT0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Plasmid. SEQUENCE 443 AA; 49466 MW;
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                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=15305914;
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EMBL; CR522870; CAG37750.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klenk H.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                            interPro; IPR003846; UPF0061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome of Desulfotalea psychrophila,
permanently cold Arctic sediments.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             redLocusNames=DP3021;
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AY-2000) to the EMBL/GenBank/DDBJ
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Sacksteder X.7., Biery B.J., Morrell J.C., Goodman B.K., Geisbrecht B.V., Cox R.P., Gould S.J., Geraghty M.T.; "Identification of the alpha-aminoadipic semialdehyde synthase which is defective in familial hyperlysinemia."; Am. J. Hum. Genet. 66:1736-1743 (2000).
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05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 45, Last annotation update)
25-QCT-2004 (Rel. 45, Last annotation update)
Alpha-aminoadipic semialdehyde synthase, mitochondrial precursor (LKR/SDH) [Includes: Lysine ketoglutarate reductase (EC 1.5.1.8) (LKR); Saccharopine dehydrogenase (EC 1.5.1.9) (SDH)].
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-i- SIMILARITY: Belongs to the ATP-dependent
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Putative long chain-fatty acid CoA ligase.
OrderedLocusNames=SAV2030;
Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinom Bacteria; Actinobacteria; Actinobacter
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Sakaki Y., Hattori M.,
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Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takah
Shinose M., Takahashi Y., Horikawa H., Nakazawa H.,
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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Catarrhini;
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anamoto A., Takahashi C.,
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RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Mauphin R., Strowmatt C.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Hatreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Materston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RI Nature 424:157-164 (2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papes F., "Cloning a
                                                                                                                                                                                   EMBL; AF229180; AAF44328.1;
EMBL; AJ007714; CAA07619.2;
EMBL; AC006020; AAF03526.1;
                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed: entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                            Genew; HGNC:17366;
                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                           Reactome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + NADPH.

NADP(+) + H(2)O = L-lysine + 2-oxoglutarate + NADPH.

CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + NAD(+) + H(2)O = L-glutamate + 2-aminoadipate 6-semialdehyde + NADH.

PATHWAY: Lysine degradation; Saccharopine pathway; first step.

PATHWAY: Lysine degradation; Saccharopine pathway; second step.

SUBUNIT: Homodimer (By similarity).

SUBCELLULAR LOCATION: Mitochondrial (By similarity).

TISSUE SPECIFICITY: Expressed in all 16 tissues examined with
                                                                                                                                                                                                                                                                                                                                                                                                S SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest European Bioinformatics Institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [MLM:238700]. Hyperlysinemia is an autosomal recessive characterized by hyperlysinemia lysinuria and variable saccharopinuria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: In the C-dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: A bifunctional enzyme that catalyzes the first two steps in lysine degradation. The N-terminal and the C-terminal contain lysine-ketoglutarate reductase and saccharopine dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: In the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           highest expression in the liver. INDUCTION: Induced by starvation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
IPR007698; AlaDh_PNT_C.IPR007886; AlaDh_PNT_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kemper E.L., Cord-Neto G., Langone F., Arruand expression analysis of the LKR/SDH gene
                                                                                                                           Q9UDR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Defects in AASS are the cause of hyperlysinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-terminal section; belongs to the AlaDH/PNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-terminal
                                                                                                                                                                                         111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    section;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is produced through a commercies and the EMBL
                                                                                                                                                                                                                                                                                                                                            . Usage by and for http://www.isb-sib.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the saccharopine
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Q9Y878;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                             Q8XZN5
Q8XZN5;
Q8XZN5;
Q1-MAR-2002
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CONFLICT
SEQUENCE
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Pfam; PF01502; Alabh_PNT_C; 1.
Pfam; PF05222; Alabh_PNT_N; 1.
Pfam; PF05423; Saccharop_dh; 1.
Mitochondrion; Multifunctional en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Siegel E.M., Orsborn K.I., Galgiani J.N.;
Siegel E.M., Orsborn K.I., Galgiani J.N.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF15953; AAD45326.2; -.
GO; GO:0000148; C:1,3-beta-glucan synthase complex; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000843; F:1,3-beta-glucan synthase activity; IEA.
GO; GO:0006075; P:beta-1,3 glucan biosynthesis; IEA.
InterPro; IFR003440; Glyco trans_48.
Pfam; PF02364; Glucan synthase; 1.
SEQUENCE 1902 AA; 217552 MW; 66FCC3C60E725F2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coccidioides posadasii.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
MCBI_TaxID=199306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
DOMAIN
                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last samotation update)
01-MAR-2004 (TREMBLORICATION REGULATOR PROTEIN.
Name=RS04642; OrderedLocusNames=RSC1360;
SEQUENCE
                                                                                              Burkholderiaceae;
                                                                                                                             Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; Betaproteobacteria; Bur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=FKS1
                                                       NCBI_TaxID=305;
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FROM N.A
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                                                                                                     Raistonia.
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MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.
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Nature 415:497-502(2002).
REMBL, AL646064; CAD15062.1; -.
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MEDLINE=21886396; PubMed=11889111;

DOI=10.1128/JB.184.7.2030-2033.2002;

Chopin M.C., Rouault A., Ehrlich S.D., Gautier
"Filamentous phage active on the gram-positive
Propionibacterium freudentreichi.";

J. Bacteriol. 184:2030-2033(2002).
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Pfam; PF03466; LysR substrate; 1.
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Viruses; ssDNA viruses; Inoviridae;
NCBI_TaxID=189836;
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Eukaryota; Fungi; i
Sordariomycetidae;
NCBI_TaxID=5141;
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01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                       Neurospora crassa.
                                                                                                                                                                 Hypothetical protein
                                                                                                                                         Name=NCU03933.1
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                                  Ascomycota; Pezizomycotina; Sordariales; Sordariaceae;
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RN SEQUENCE FROM N.A.

RSTRAIN=OR74A;

RC STRAIN=OR74A;

RC Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

RA Elkins T., Engels R., Wang S., Nielsen C.B., Washburne M.,

RA Elkins T., Janakiev P., Pedersen D., Nelson M., Washburne M.,

RA Elkins T., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

RA Kothe G.O., Jedd G., Mewes W., Staben C., Rarcotte E., Greenberg D.,

RA Kothe G.O., Jedd G., Mewes W., Staben C., Rudd S., Frishman D.,

RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,

RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,

RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

RA Cogoni C., Maccino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

Ba Esouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

RA Varden O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

RA Varden I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;

"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";

RI Nature O.0-0(2003).
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AABX01000719; E
Hypothetical protein.
SEQUENCE 108 AA; 1
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Mammalia; Eutheria;
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Homo sapiens (Human).
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AAU25868
AAU258824
AAU25871
ABB72912
      ABP51670
ABR62904
ADM72485
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Aab17026 TPO mimet
Aau25868 Human thr
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Aau25874 Human thr
Abb72912 TPO mimet
Adj73064 TPO mimet
Adj51660 CH1 delet
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Aaw36779 Thrombopo
Aaw30304 Thrombopo
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                                                                                                                            The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                            Thrombopoietin receptor-binding/activating peptide(s) and pepmimetic(s) - useful in treatment of haematological disorders,
                                                                                                                                                                                       Disclosure;
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                    AAW09459 standard;
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18; Conserv
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ilarity 100.0%;
Conservative
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95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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                   protein; 18
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                                                                                                                                   The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an ICSO of no more than about 100 mum. I compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The paptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1996;
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                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                            thrombocytopenia resulting from chemotherapy,
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LC, Schatz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Preferably N-terminus is selected from: -NRR1; NRC(0)R; -NRC(0)OR; -NRS(0)2R; -NRC(0)MHR; succinimde; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Preferably linkages are selected from: -
CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6
; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is
lower alkyl"
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S-00485301.
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PJ, Wagstrom
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       Mismatches
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m CR, W
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Wrighton NC;
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                                                                                                                                                                                                                                                           investigate the mechanism of thrombopoietin receptor activation, or to maintain the prol thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                           Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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                                                                                                                                                                                                                                      Sequence
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            Thrombopoietin
                                                                                 AAW33026 standard;
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           receptor binding peptide
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PJ, Wagstrom CR, Wrighton NC;
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                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; TAN4; mimetic; IL-1; TNF; antagonist; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma
                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID
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Pred. No. 1.7e-08;
Mismatches 0;
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Wrighton NC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes composition of matter (I) comprising an CC (XI)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (XI)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(C2)d-P2-(L3)e-P3', or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, CC p3, and P4 = are each independently sequences of pharmacologically active CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, CC c, d, e, and f = are each independently 0 or 1, provided that at least 1 CC of a and b is 1. The composition can have cytostatic, antiasthmatic, CC thrombolytic and immunosuppressive activities. NNAs, vectors and host CC cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than CC such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the
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                                                                                                                                                                     Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; BLISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
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22-OCT-1999;
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                 01-MAR-2000; 2000US-00516704
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                                                                                                                                                      expansion; megakaryocyte; Headpiece Dimer
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bind to and activate the human thrombopoletin receptor (TPO-R). Methods co factivating thrombopoletin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoletin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ scaining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed correspondent alone or in conjunction with additional cytokines
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
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Sequence 18
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96WO-US009623.
96US-00699027.
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standard; peptide; 18
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haemostatic; thrombocytopenia; Chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; Peptide mimetic; human; thrombopoietin receptor; in vitro expansion; megakaryocyte; Headpiece Dimer gene; TPO-R; TPO; cytokine; gene

Human thrombopoietin receptor (TPO-R) activator peptide

17-DEC-2001

(first entry)

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Homo sapiens
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US6251864-B1

26-JUN-2001

01-MAR-2000; 2000US-00516704.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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07-JUN-1995;
07-JUN-1996;
                                                                            erythropoletin; TPO; tumour necrosis factor alpha inhibitor; TWF-alpha inhibitor; interleukin 1 antagonist; II-1 antagonist; TMP; TPO mimetric peptide; EPO mimetric peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; antianaemic; anorectic; antiinfertility; heamostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; bleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting c with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-564142/63.
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                                 thrombocytopaenia;
Fanconi's syndrome
                                                                                                                                                                                                                                                                                                                                                          Modified
                                                                                                                                                                                                                                                                                                                                                                                                                     TPO mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB72910
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                                                                                                                                                                                                                                                                                                                                                    peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIKGPTLRQWLKSREHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIKGPTLROWLKSREHTS
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anian P, Wag
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nilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                  peptide SEQ ID NO:80.
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95US-00485301.
96WO-US009623.
96US-00699027.
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                                                                                                                                                                                                                                                                                                                                                          mimetic; Fc domain;
                                                             metastatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wagstrom CR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB 4;
Pred. No. 1.7e-08;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SE,
                                                             tumour; systemic lupus
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Hendren
                                                                                                                                                                                                                                                                                                                                                          fusion; immunoglobulin G;
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Deprince RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                             IgG;
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ADJ73062
ID ADJ7
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OF TPO
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TPO
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OS Syni

TPO mimetic 06-MAY-2004 ADJ73062; ADJ73062

peptide sequence SeqID

516

(first

entry.

mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; immunomodulator; cardiant; antimicrobial; cytostatic; neuro

neuroprotective; anaemia;

Synthetic

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18

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standard;

peptide;

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                                                                                                                                               Completings: (I) can have antiinflammatory, antidabetic, ophthalmological, cortostatic, antirheumatic, antiarthritic, antidabetic, ophthalmological, comprised antianaemic, anorectic, antiinfertiility, haemostatic, ophthalmological and comprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for composition of interest, for identifying normal or abnormal proteins of their associated protein of interest, for identifying normal or abnormal proteins of their composition of interest in a biological sample. Additionally, (I) is useful correcting inflammatory and autoimmune diseases, tumour growth, cancer, compounds are useful for treating disporters (I), comprising EPO-compounds are useful for treating disorders tharacterised by low red blood cell levels such as anaemia. The TPO-mimetic compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing conditions that involve an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet conditions. ABB73426 and ABBJ35695 to ABBJ35777 conditions and autoided and nucleic acid sequences used in the exemplification of the present invention.
                                        Matches
                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                 Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 39; Page 44; 176pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-130313/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAY-2000; 2000US-00563286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2001; 2001WO-US014310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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μ
                                      l Similarity
18; Conserv
TIKGPTLROWLKSREHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention describes a vehicle-peptide molecule (I) or
                                                                                                                   ₽,
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheetham
                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n,
  18
                                        0
                                      Score 97; DB 5; L
Pred. No. 1.7e-08;
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                                                                                 Length 18;
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RESULT 10
ADJ52697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to novel mammalian CDR mimetibodies, specific CC portions or variants thereof. Specifically, it refers to an antibody CC fragment where a protein has been inserted into, or replaces a portion CC of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which CC itself comprises at least one human framework region and at least one CC itself comprises at least one human framework region and at least one CC ligand binding region (LBR). The present invention describes human CC mimetibodies, including modified immunoglobulins and cleavage products CC that can be useful in gene therapy and the generation of transgenic CC plants and animals. Furthermore, the CDR mimetibody is useful for CC preparing compositions for modulating, treating or reducing the symptoms CC of immune, cardiovascular, infectious, malignant and/ or neurologic CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This composite equence is a TPO mimetic peptide sequence used to make a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variable region comprising human framework or ligand binding useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region,
                                                                                                                    multiple sclerosis; dementia; Alzheimer's disease; cancerous condition; infectious disease; bacterial
                                                                                                                                                                                                                                                                                06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 516; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2002; 2002US-0368791P
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                                                                                                                                                       hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative;
                                                                                                                                                                                                          CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                                                                                                                                                                                     ADJ52697
                WO2004002417-A2
                                                                   Unidentified
                                                                                                                                                                                                                                             CH1 deleted mimetibody-related peptide SeqID516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-804237/75
                                                                                                    infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                                  standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIKGPTLRQWLKSREHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                           TIKGPTLROWLKSREHTS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                (first entry)
                                                                                                    fungal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 97; DB 7;
Pred. No. 1.7e-08;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                        infection;
                                                                                                                                                                           disease;
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RESULT 11
ADJ51658
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Matches
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                                                                                          CH1 deleted mimetibody; osteopathic; cardiovascular-Gen; dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic; aphthalmological, nephrotropic; respiratory-Gen; tumour necrosis factor; ophthalmological, nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; point disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; oral disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; bastetic disorder; haematologic disorder; immunological disorder; ballergic disorder; infectious disorder; musculoskeletal disorder; infectious disorder; musculoskeletal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, cantibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2002; 2002US-0392431P
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                                                         oncological disorder; neurological disorder; ophthalmologic disorder; pediatric disorder;
                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ51658 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-2003; 2003WO-US020347
                                                                                                                                                                                                                                                                                                                                        CH1 deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to CH1 deleted mimetibodies (and the DNA sequences h encode them), compositions, methods and uses. The invention may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; SEQ ID NO 516; 129pp; English
                                       disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TIKGPTLRQWLKSREHTS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                        mimetibody-related peptide SeqID516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knight DM,
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                       pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 97; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ghrayeb J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scallon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             핂,
                                                                                nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nesspor
                                                               disorder;
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Unidentified

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RESULT 12
AAW09491
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                                                                                                                                                                                                                                                                                                                                                                                                         cc gastrointestinal-Gen, gynaccological-Gen, hepatotropic, haemostatic, cc immunomodulator, antiallergic, muscular-Gen, cytostatic, cc antiinflammatory, neuroleptic, ophthalmological, nephrotropic or cc respiratory-Gen activity acting as a tumour necrosis factor (TNF)-Cc modulator or cytokine-agonist. The methods and compositions of the cc present invention are useful for the diagnosis, prevention and/or cc treatment of diseases or conditions associated with aberrant expression cc or activity of the CH1 deleted mimetibody, such as a bone or joint, cc cardiovascular, dental or oral, dermatological, ear, nose or throat, cc endocrine, metabolic, gastrointestinal, gynaecological, hepatic, cobstetric, haematologic, immunological, allergic, infectious, cc pediatric, psychiatric, renal or pulmonary disorders. The present cc mimetibody of the invention.
밁
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which encode them), compositions, methods and uses. The invention mauseful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New CH1 deleted mimetibody polypeptide and nucleic acid, useful diagnosing, preventing or treating cardiovascular, dermatologic, endorrine, gastrointestinal, gynecologic, infectious, neurologic nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-2002;
19-SEP-2002;
                                        Synthetic
                                                                                                              Thrombopoietin
                                                                                                                                          10-SEP-1997
                                                                                                                                                                                                AAW09491 standard;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to CH1 deleted mimetibodies (and the DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-082872/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kutologki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004002424-A2
                                                                  Haematology;
bone marrow t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; SEQ ID NO 516; 123pp; English
                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                      μ
                                                                                                                                                                                                                                                                                    1 TIKGPTLRQWLKSREHTS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-0392431P.
2002US-0412144P.
                                                                 thrombocytopenia; TPO; TR; proliferation chemotherapy; radiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003WO-US020495
                                                                                                                                        (first entry)
                                                                                                            receptor binding peptide
                                                                                                                                                                                              protein; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M,
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 97;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                          DB 8;
1.7e-08;
                                                                                proliferation;
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                                                                                                                                                                                                                                                                                                                                                       Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention may
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RESULT 13
AAW35418
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                          Synthetic.
                                                                                                                                                                                Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                     AAW35418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 26; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor-binding/activating peptide(s) and peptimentic(s) - useful in treatment of haematological disorders, thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dower WJ, Barrett RW, Cwirla SE,
Mattheakis LC, Schatz PJ, Wagstro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dower WJ,
                                                                                         Modified-site
                                                                                                                          Cross-links
                                                                                                                                     Кeу
                                                                                                                                                                                                                                         Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                               11-MAR-1998
                                                                                                                                                                                                                                                                                                             AAW35418 standard;
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                                                       WO9640750-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                           GPTLROWLKSREHTS
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                               (first entry)
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95US-00484090.
95US-00485301.
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95US-00473604
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                                                                                        peptide"
19
                                                                                                                                    Location/Qualifiers
                                                                             note= "NH2-Ser"
                                                                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                           64.9%;
73.3%;
                                                                                                               "linked via
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 63; DB 2;
Pred. No. 0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                 disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in DJ, Gates
Wrighton NC;
                                                                                                                 bond
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                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                 CY83
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                                                                                                                  of identical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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07-JUN-1996;

96WO-US009623

19-DEC-1996.

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RESULT 14
AAW36642
ID AAW36
XX AAW36
XX Thron
XX Thron
XX Thron
XX Thron
XX Synth
XX Synth
XX O7-JI
PR 07-JI
PR
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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07-JUN-1995;
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombopoietin dependent cell lines
                                         Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematologic
                                                                                                           WPI; 1997-052226/05
                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                        WO9640750-A1
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                                                                                                                                                       Mattheakis
                                                                                                                                                                              Dower WJ,
                                                                                                                                                                                                                     (GLAX )
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                                                                                                                                                                                                                       GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPTLRQWLKSREHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
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                                                                                                                                                  Barret RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 73; 106pp;
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LC, Schatz
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                                                                                                                                                                                                                       GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor; binding peptide; treatment; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00478128.
95US-00485301.
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95US-00485301
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                         thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
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73.3%;
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PJ, Wagstrom
                                                                                                                                                                              Cwirla
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                                                                                                                                                     Wagstrom
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Pred. No. 0.
                                                                                                                                                                              SE,
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                         resulting
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                                                                                                                                     1 DJ, Garry
Wrighton NC;
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                         from
                                           of haematological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 19;
                      chemotherapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ź
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                                                                                                                                                                              Johnson
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                         etc.
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RESULT 15
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                                                                                                                                                                                                                                                                    07-JUN-1995;
07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
      Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                           haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                      Activating thrombopoietin receptors thrombocytopenia and hematological d with peptides and peptide mimetics a
                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                   01-MAR-2000; 2000US-00516704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present peptide,
                                                                                                                    thrombocytopenia with peptides and
                                                                                                                                                                                               Yin
                                                                                                                                                                                                          Balasubramanian
                                                                                                                                                                                                                      Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                  US6251864-B1
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide mimetic; human; thrombopoietin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
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                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                          26-JUN-2001.
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                                                                                                                                                                      2001-564142/63.
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                                                                                                                                                                                                                                              GROUP LID
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95US-00485301.
96WO-US009623.
96US-00699027.
                                                                                              20; 128pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  megakaryocyte;
                                                                                                                                                                                                          Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.9%;
73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which binds the thrombopoietin receptor
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TPO-R) activator peptide
                                                                                                                                                                                                                      SE,
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                                                                                                                                                                                                            Hendren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N 63;
                                                                                                                      s in cells, used to treat disorders, comprises contacting attached to hydrophilic polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                  Headpiece
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                                                                                                                                                                                                            RW CM
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Deprince R
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RESULT 16
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Matches
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07-JUN-1995;
07-JUN-1996;
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Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin reals comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                      Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide mimetic; human; thrombopoietin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human thrombopoietin receptor (TPO-R) activator peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU25998
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                                                                                                                                                             Disclosure; Col 143-144; 128pp; English.
                                                                                                                                                                                                                                                                                                     WPI; 2001-564142/63.
                                                                                                                                                                                                                                                                                                                                                Balasubramanian Yin Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPTLRQWLKSREHTS:
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                                                                                                                                                                                                                                                                                                                                                                                             Barrett
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95US-00485301.
96WO-US009623.
96US-00699027.
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Hendren
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                                                                                                                                                                                                                                                                                                                                                                     Schatz PJ
Deprince
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                                                                                                                                                                                                                                                                                                                                                                          Podduturi
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The present invention describes an immunoglobin molecule or its fra (I) comprising a region where amino acid residues corresponding to least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) min that is flanked with proline at its carboxy terminus (I) has antianaemic, haemostatic and nephrotropic activities, and can be used to the contraction of the complex of the carboxy terminus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-2000;
04-MAY-2001;
29-MAY-2001;
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                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                             thrombopoetin mimetic.
                                                                                                                                                                                                                                                                                                                   determining region are
                                                                                                                                                                                                                                                                                                                                                                          A novel
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                                                                                                                                                                                                                                                                                                                   immunogen molecule comprising a region in which amino acions corresponding to at least a portion of the complementary ning region are replaced or fused with an erythropoietin or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALEXION PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPTLRQWLAARNHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombopoietin; erythropoietin; antibody; CDR region; tarity determining region; immunoglobin; antianaemic; ic; nephrotropic; haematopoietic cell; haematopoiesis.
                                                                                                                                                                                                                                      Fig
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; 2001US-0288889P.
; 2001US-0294068P.
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                                                                                                                                                                                                                                            113pp;
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73.3%;
                                                                                                                                                                                                                                            English
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Pred. No. 0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 18
ABP51691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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04-MAY-2001;
29-MAY-2001;
                                                 The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide
                                                                                                                                                                                                                                               A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
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                                                                                                                                                                                        Claim 20; Fig 5; 113pp; English.
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; 2001US-0288889P.
; 2001US-0294068P.
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an erythropoietin (EPO) or thrombopoid with proline at its carboxy terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARM
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78.6%;
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Pred. No. 0.007;
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                            ly active peptides e.g. a peptide (EPO) or thrombopoietin (TPO) min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Renshaw
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immunotherapy. The immunos treating thrombocytopenia

invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing

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Best Local S
Matches 11
                                                               comprising a region where amino acid residues corresponding portion of a two complementarity determining regions (CDRs) with a peptide mimetic selected from an erythropoietin (EPO) a thrombopoletin (TPO) mimetic. An immunoglobulin molecule of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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                                                                                                                                                                                                                                                                                New immunoglobulin molecule comprising a region, where to complementarity determining regions (CDRs) are replaced or a TPO mimetic, useful for treating thrombocytopenia.
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                                                                                                                                                                                The invention
                                                                                                                                                                                                                                       Example 1; SEQ ID NO 45; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowdish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ALEX-) ALEXION PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO mimetic peptide with random flanking residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mmunoglobulin;
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                                                                                                                                                                                  relates to a novel immunoglobulin molecule or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide;
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Pred.
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No.
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RESULT 20
ADQ16629
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Best Local
                                                                                                                                   The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoslobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of Chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide with flanking residues.
                                                                                                                                                                                                                                                                                                         New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-460973/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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immunotherapy; t
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                                                                                                   Sequence
                                                                                                                            The present
residues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO mimetic peptide with random flanking residues SEQ ID NO:49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ16629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin; complementarity determining region; CDR; peptide mimetic;
erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
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TIEGPTLRQWLAAR 15
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                                                                                                                                                                                                                                                                                   SEQ ID NO 49; 107pp; English.
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78.6%;
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                                                             63.9%;
78.6%;
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RESULT 21
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematcological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dependent cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin receptor-binding/activating peptide(s) and pepmimetic(s) - useful in treatment of haematological disorders, thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-051883/05.
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Thrombopoietin receptor; binding peptide;
                                                                                            11-MAR-1998
                                                                                                                                          AAW36644
                                                                                                                                                                                   AAW36644 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 AA;
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LC, Schatz
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transfusion;
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95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
                                              receptor binding peptide
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m CR, Wrighton
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0.0075;
  treatment; agonist;
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RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombotycopaenia resulting from chemotherapy, radiation therapy or thrombotycopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoletin signal transduction and investigate the mechanism of thrombopoletin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                        haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                            Human thrombopoietin receptor (TPO-R) activator peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigate the mechanism of thrombopoietin receptor activation, or to maintain the prol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombopotopaenia resulting from chemotherapy, radiation therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
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              01-MAR-2000; 2000US-00516704
                                          26-JUN-2001.
                                                                                                                                                                                               Peptide mimetic;
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                                                                                                                            expansion; megakaryocyte; Headpiece Dimer
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LC, Schatz
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95US-00485301
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                                                                                                                                                                                                  human; thrombopoietin receptor;
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                               Agonist; immunoglobulin; Ig; variable domain; heavy chain; light chain, complementarity determining region; CDR; antigenic; thrombopoietin; TPK thrombopoietin receptor; MPL; cytotoxic T-lymphocyte; CTL; epitope; T-helper cell; B-helper cell; synthebody; pharmaceutical; vaccine; proliferation; growth; differentiation; haematopoietic cell; antibody; platelet progenitor cell; immune disorder; thrombocytopenia; disseminated intravascular coagulation; stem cell; transplantation; gene therapy; diagnostic; haemostatic; immunomodulator; anticoagulant; coagulatic; immunomodulator; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombocytetin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached hydrophilic polymers. The methods are used to treat thrombocytopenia su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
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                                                                                                                                    domain;
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Key

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC also has added or substituted to it, at least one binding sequence which contrologous to the CDR and is an antigenic, agonistic sequence from a CC thrombopoietin (TPO) receptor binding sequence. The antigenic sequence CC can be a binding sequence heterologous to the CDR, a cytotoxic T-cC lymphocyte (CTL)-epitope sequence, a T-helper cell sequence, a B-helper CC ells sequence or a combination of each. The variant or thrombopoietin CC synthebody, pharmaceutical and vaccine compositions are useful for CC ells, particularly platelet progenitor cells. The variants are also CC useful for treating or preventing haematopoietic or immune disorders cells for treating or preventing haematopoietic or immune disorders cesulting from chemotherapy, radiation therapy, or bone marrow transfusions (e.g. thrombocytopenia or disseminated intravascular CC coagulation). Compositions comprising the synthebodies can be used for CC committed precursor cells for autologous and allogeneic transplantation cas well as for the expansion of stem cells for gene therapy. They are CC also useful as diagnostic or analytical reagents for studying the sequence presented, TPOVHCDR1, is the TPO receptor (MPL) agonist peptide sequence contained within the immunoglobulin CDR consensus variable heavy
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Best Local (
                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention discloses a variant of an immunoglobulin (Ig) variable heavy or light chain domain that comprises at least one complementary determining region (CDR) and framework regions flanking the CDR. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-2001;
                                                                                                                                                                                               AAU26006 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preventing hematopoietic or immune disorders, e.g. thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New thrombopoietin synthebodies, useful for stimulating proliferation, growth, or differentiation of hematopoietic cells, for treating or
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                    bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                  haemostatic; thrombocytopenia;
bone marrow transplantation; h
                                                    Peptide mimetic; human; thrombopoietin receptor;
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                                                                                       thrombopoietin receptor (TPO-R) activator peptide
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78.6%;
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                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                 14
              mbopoietin receptor; TPO-R; TPO; cytokine;
a; chemotherapy; radiation therapy; ELISA;
haematological disorder; platelet disorder;
                                                                                                                                                                                                                                                                                                                                                                          Score 62; I
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situ staining; biological fluid;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (BLISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
07-JUN-1995;
07-JUN-1996;
           Haematology; thrombocytopenia; TPO; TR; proliferation; bone marrow transfusion; chemotherapy; radiation therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached hydrophilic polymers. The methods are used to treat thrombocytopenia su as that due to chemotherapy, radiation therapy or bone-marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 147; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting with peptides and peptide mimetics attached to hydrophilic polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Balasubramanian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                                          Thrombopoietin receptor binding compound peptide.
                                                                                          10-SEP-1997
                                                                                                                         AAW09460;
                                                                                                                                                    AAW09460
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to and activate the human thrombopoietin receptor (TPO-R). Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-564142/63
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                                                                                                                                                                                                                                                             IKGPTLROWLKSRE 15
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                                                                                                                                                                                                                                                                                              Conservative
                                                                                        (first
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95US-00485301.
96WO-US009623.
96US-00699027.
                                                                                                                                                      protein;
                                                                                        entry)
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Wagstrom CR, 1
                                                                                                                                                                                                                                                                                                           59.8%;
                                                                                                                                                       18
                                                                                                                                                                                                                                                                                              Score 58; DB
Pred. No. 0.02
3; Mismatches
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0.023;
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Deprince R
                                                                                                                                                                                                                                                                                                                            Length 14;
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RESULT 27
AAW09498
ID AAW09
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Best Local S
Matches 10
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of 8000 Da, and a binding affinity to TR as expressed by an ICSO of no more than about 100 mum. The compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin receptor-binding/activating peptide(s) and peptimetic(s) - useful in treatment of haematological disorders, thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dower WJ, Barrett RW,
Mattheakis LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996
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    AAW09498 standard; protein; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18
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                                                                                                                                                                                                       SIEGPTLREWLTSR
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
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95US-00478128.
95US-00484090.
95US-00485301.
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95US-00473604.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "Preferably N-terminus is selected from: -NRR1; NRC(O)R; -NRC(O)OR; -NRS(O)ZR; -NHC(O)NIR; succinimide; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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71.4%;
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3; Mismatches
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0.031;
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RESULT 28
AAW36649
ID AAW36
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                      The present sequence is a peptide which binds to thrombopoietin (receptor (TR). The compound can be used for treating patients suffrom haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for determine the properties on living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin receptor-binding/activating peptide(s) and peptimetic(s) - useful in treatment of haematological disorders, thrombocytopenia resulting from chemotherapy, etc.
                      signal
                                                                                                                                                                                                                                                                                                   Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haematology; thrombocytopenia; TPO; TR; proliferation; bone marrow transfusion; chemotherapy; radiation therapy.
Synthetic
                                 haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                          AAW36649;
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 27; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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                                                         Thrombopoietin
                                                                              Thrombopoietin
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                      transduction;
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95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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                                                                             receptor binding peptide.
                                                         receptor; binding peptide; treatment; agonist;
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                                                                                                                                                  peptide;
                                                                                                                                                                                                                                                                  59.8%;
71.4%;
                       receptor activation; cell culture
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                                                                                                                                                                                                                                                                  Score 58; DB 2;
Pred. No. 0.031;
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Wrighton NC;
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RESULT 29
AAW33027
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Best Local
                                                                                                                                                                                 Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present peptide, which binds the thrombopoietin receptor (TR), c used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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07-JUN-1995;
Dower WJ, Barret RW, Cwi
Mattheakis LC, Schatz PJ,
                                                       07-JUN-1995;
07-JUN-1995;
                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                          Thrombopoietin receptor binding peptide
                                                                                                                                                                                                                                                                  11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
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Mattheakis
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                                                                                        07-JUN-1996;
                                                                                                                                      WO9640750-A1
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                                 (GLAX ) GLAXO
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                                                                                                                                                                                                                                                                                                             standard;
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LC, Schatz
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                                 GROUP LID
                                                      95US-00478128.
95US-00485301.
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95US-00485301.
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                                                                                        96WO-US009623
                                                                                                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                              59.8%;
Cwirla SE, Duffin DJ, Gate PJ, Wagstrom CR, Wrighton
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PJ, Wagstrom
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Pred. No. 0.03
3; Mismatches
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om CR, Wrighton N
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             Gates
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 NC;
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RESULT 30
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The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                        Disclosure;
                                                                                Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                          WPI;
                                                                                                                                                                                                                                       07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                               07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin receptor; binding peptide; treatment; ay haematological disorder; thrombocytopaenia; chemotherap radiation therapy; bone marrow transfusion; diagnosis; collature.
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                                                                                                                                                                      Mattheakis
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                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIKGPTLRQWLKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; peptide; 18
                                                                                                                                                                 Barret RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                        Page 27; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                       95US-00478128.
95US-00485301.
                                                                                                                                                                                                                                                                                 96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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71.4%;
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PJ, Wa
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                                                                                                                                                                   la SE, Duffin
Wagstrom CR,
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Pred. No. 0.03
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide; treatment; agonist;
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0.031;
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Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                         chemotherapy;
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G
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CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

CC independently selected from -(L1)C-P1, -(L1)C-P1-(L2)d-P2, -(L1)C-P1-

CC (L2)d-P2-(L3)d-P3, or -(L1)C-P1-(L2)d-P2-(L3)d-P2, -(L1)C-P1-

CC (L2)d-P2-(L3)d-P3, or -(L1)C-P1-(L2)d-P2-(L3)d-P3-(L4)f-P4 where P1, P2,

CC P3, and P4 = are each independently sequences of pharmacologically active

CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,

CC c, d, e, and f = are each independently 0 or 1, provided that at least 1

CC of a and b is 1. The composition can have cytostatic, antiasthmatic,

CC thrombolytic and immunosuppressive activities. DNAs, vectors and host

CC cells from the present invention can be used for producing pharmaceutical

CC compositions. The compositions are useful for treating cancer, asthma,

CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than

CC a Fab domain) can provide a longer half-life or incorporate functions

CC such as Fc receptor binding, protein A binding, complement fixation, and

CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T cell lymphocyte antigen vascular endothelial growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor activation, or to maintain the proliferation and growth thrombopoietin dependent cell lines
                                                                                                                                                                                                                                            The present invention describes composition of matter (I) comprising
                                                                                                                                                                                                                                                                                           Claim 19; Page 222; 608pp;
                                                                                                                                                                                                                                                                                                                          Novel composition of matter active peptides, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease; cytoimmunosuppressive; EPO;
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99US-00428082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic;
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO; CTLA4; mimetic; IL-1; TNF;
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                                                                                                                                                                                                                                                                                           English
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Pred. No. 0.031;
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Best Local S
Matches 10
   transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitras unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological fluids. They may also be used for i situ staining, fluorescence-activated cell sorting, Western blotting and
                                                                                                                                          Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                                                                                Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting with peptides and peptide mimetics attached to hydrophilic polymers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-2001.
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RESULT 33
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Best Local
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07-JUN-1995;
07-JUN-1996;
Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological materials. They may also be used for in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme-linked immunosorbent assay (ELISA). In addition, the peptides be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
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bind to and activate the human thrombopoletin receptor (TPO-R). Methods of activating thrombopoletin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haemacological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoletin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and
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Hendren
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0.031;
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comprises contacting
o hydrophilic polymers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schatz PJ;
Deprince RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-R;
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RESULT 35
ABB72912
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Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in purified or natural biological materials. They may also be used for situ staining, fluorescence-activated cell sorting, Western blotting enzyme-linked immunosorbent assay (BLISA). In addition, the peptides be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EPO mimetic peptide; EPO mimetic peptide; EPO mimetic; antitumour; immunosuppressive; cytostatic; antirheumatory; antitumour; antidiabetic; ophthalmological; antianaemic; antirheumatic; antiinfertility; haemostatic; dermatological;
neuroprotective activities. (I) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (I) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their proteins of interest in a biological sample. Additionally, (I) is useful
                                                                                                        multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective; inflammatory disease; autoimmune disease; tumous cancer; rheumatoid arthritis; diabetic retinopathy; infertility; sleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18
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                                                                                                                                                               The present
                                                                                                                                                                                               Claim 39; Page 44; 176pp; English
                                                                                                                                                                                                                                                                                                      WPI; 2002-130313/17.
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                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-2000; 2000US-00563286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fanconi's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO mimetic
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                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN
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                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                λA;
                                                                                                                                                             invention describes a vehicle-peptide molecule (I) or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide SEQ ID
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71.4%;
                                                                                                                                                                                                                                                                                                                                         JC,
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Pred. No. 0.031;
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 ADJ73064
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Matches 10
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                                                 This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one ligand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that the content of the content invention describes human mimetibodies, including modified immunoglobulins and cleavage products
                                                                                                                                                                                                                                                                   variable region comprising human framework or li-
useful for preparing a composition for treating
cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; anaemia; immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ73064 standard; peptide; 18
that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symmetry compositions.
                                                                                                                                                                                                                                                                                                             New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-2003; 2003WO-US009139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                   Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-804237/75.
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1 SIEGPTLREWLTSR 14
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71.4%;
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0.031;
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                                                                                                                                                                                                                                                                                           e.g., immune,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective;
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RESULT 37
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This invention relates to CHI deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, notropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascula or neurodegenerative disease or disorder, anemia, cancer, or infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-082870/08
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nilarity 71.4%;
Conservative
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Pred. No. 0.03;
3; Mismatches
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This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, gastrointestinal-Gen, gastrointestinal-Gen, gastrointestinal-Gen, gastrointestinal-Gen, gastrointestinal-Gen, muscular-Gen, cytostatic, antiinflammatory, neuroleptic, ophthalmological, nephrotropic or

respiratory-Gen activity

Claim

SEQ ID NO 518; 123pp; English

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                                                                                                                                            New CH1 deleted mimetibody polypeptide and nucleic acid, useful diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                            08-JAN-2004
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used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                          Kutoloski
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19-SEP-2002;
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2002US-0412144P.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive; immunotherapy; thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced
                                                                      The present sequence variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi
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                                                                                                                                                                                                         with a peptide mimetic selected from an erythropoietin (EPO) mimetic a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified immunoglobuiln clone 116
                                                                                                                                      treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia.
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10; Conserv
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                                                                                                          represents immunoglobulin clone 116 heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58; DB 8; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Renshaw M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variable region SEQ ID NO:125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۳.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPO mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Sequence

128 AA;

RESULT 41
AAW36779
ID AAW36
XX
AC AAW36
XX

AAW36779 standard;

peptide;

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AAW36779

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RESULT 40
ADQ16704
ID ADQ16
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                                                Matches
                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                  comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents immunoglobulin clone 116 heavy chain.
                                                                                                                                                                                                                                                                               New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with EPO mimetic or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin;
erythropoietin;
                                                                                              Sequence 225
                                                                                                                                                                                                                                                                                                                                                          Bowdish
                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2003; 2003WO-US036894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified immunoglobuiln clone 116 heavy chain SEQ ID NO:124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ16704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ16704 standard;
                                                                                                                                                                                                                                 The invention relates to a novel immunoglobulin molecule
                                                                                                                                                                                                                                                          Example 8; SEQ ID NO 124; 107pp; English
                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004050017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                  (ALEX-)
                                                          Local
                                                                                                                                                                                                                                                                                                                                   2004-460973/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IKGPTLROWLKSREHT
                     N
                                                10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                  ALEXION
IEGPTLROWLAARANS
                     IKGPTLROWLKSREHT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEGPTLRQWLAARANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                               Conservative
                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                          Frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; EPO; thrombopoietin; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                  PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complementarity determining EPO; thrombopoietin; TPO; in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                          59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225
                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                           Renshaw M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                          No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 29;
                                                            56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ng region; CDR; peptide mimetic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
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                                                                      Length 225;
                                                Indels
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                                                                                                                                                                                                                                    its fragment
                                                Gaps
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RESULT 42
AAW09463
ID AAW09
XX
AC AAW09
DT 10-SE
XX
Throm
XX
Haema
KW Haema
XX
OS Synth
XX
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                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                       The present peptide, which binds the thrombopoietin receptor (TR), coused to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dower WJ,
Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9640750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin receptor binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1998
                                  bone marrow
                                                                    Thrombopoietin receptor binding compound peptide
                                                                                           10-SEP-1997
                                                                                                                                        AAW09463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO
                                           Haematology;
                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and peptide mimetics which bind to and activate the oietin receptor - useful in treatment of haematological
                                                                                                                                        standard;
                                                                                                                                                                                                                      IKGPTLRQWLKSR 14
                                                                                                                                                                                                IEGPTLROWLAAR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barret
                                                                                                                                                                                                                                                                                                                                                                                                                     Page 78; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           eap.
                                                                                                                                                                                                                                                                                         8
                                    transfusion;
                                                                                                                                                                                                                                             Conservative
                                            thrombocytopenia; TPO; TR; proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-00478128.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombocytopenia resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                et RW,
Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                        58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             얁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cwirla SE, Duffin DJ, Gate PJ, Wagstrom CR, Wrighton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erminal carboxy group linked
Lys15 in AAW36780"
                                  chemotherapy; radiation therapy.
                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                        DB 2;
0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                           chemotherapy, etc
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson
                                                                                                                                                                                                                                              <u>.</u>.
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino
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                                                                                                                                                                                                                                                                                                                                                              bone
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RESULT 43
AAW09468
ID AAW0
XX
AC AAW0

AAW09468 standard; protein;

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AAW09468;

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Query Match
Best Local S
Matches 10
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07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an ICSO of no more than about 100 mum. compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bon marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombogoietin receptor-binding/activating peptide(s) and pepmimetic(s) - useful in treatment of haematological disorders, thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                              Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 89; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-051883/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD
                                            N
                                                                                     l Similarity
10; Conserv
                                            IKGPTLROWLKSR
IEGPTLROWLAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barrett RW,
LC, Schatz
                                                                                                                                                                              A,
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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95US-00473604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US008998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     selected from hydroxy, lower alkoxy, and rance, selected from hydroxy, lower and R4 are independently selected from hydrogen and lower alkyl, and where the nirrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the neptide forming a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Preferably N-terminus is selected in NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH2OC(O)NR-; phosphonate; -CH2S(C; -NHC(O)NH; where R is hydrogen lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           benzyloxycarbonyl-NH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Preferably C-terminus is -C(0)R2 where R2 is
selected from hydroxy, lower alkoxy, and -NR3R4, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Preferably linkages are selected from: -
H2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-;
                                                                                                             58
76
                                            14
                                                                                                               .98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cwirla SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wagstrom
                                                                                        .
-
                                                                                                          Score
Pred.
                                                                                        Mismatches
                                                                                                             57; DB 2;
No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duffin DJ, Gates
m CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    benzyloxycarbonyl-NH with 1-3
                                                                                        ۲.
                                                                                                                                 Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ę
                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; -C(O)NR6
and R6 is
                                                                                        Gaps
                                                                                                                                                                                                                                                                                               or bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS
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RESULT 44
AAW33030
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                                                                                                                                                                                                                       Query Match
Best Local S
Matches 10
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07-JUN-1995;
07-JUN-1995;
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07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                         The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It is part of a dimer linked by the omega amino acid to the omega amino acid in the sequence in AAW19534. The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bon marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                    Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                Claim 30; Page 91; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       thrombocytopenia resulting
                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor-binding/activating peptide(s) and pepmimetic(s) - useful in treatment of haematological disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-051883/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1996;
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                                                                     11-MAR-1998
                                                                                                                 AAW33030 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dower WJ
                                             Thrombopoietin receptor binding peptide.
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LC, Schatz PJ,
                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transfusion; chemotherapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Linked to the omega Lys from AAW19534"
                                                                     entry)
                                                                                                                                                                                                                                   58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wagstrom
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0.033;
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ton NC;
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                                                                                                                              Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders,
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Mattheakis
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LC, Schatz
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                                            group of
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                                             /note= "terminal carboxy group linked
group of Lys16 in AAW33035"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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hypothetical prote UTP-glucose-1-phos methylase LlaPI hypothetical prote hypothetical prote tRNA guanine-N1 me ecombinase XFa001 polyprotein

phosphoprotein pho carboxypeptidase A hypothetical prote hypothetical prote hypothetical prote hypothetical prote glucan 1,4-alpha-g conserved hypothet pol polyprotein -C50C3.2 protein -C50C3.2 protein HIV-1 retropepsin HIV-1 retropepsin hypothetical prote probable transposa glyceraldehyde-3-p short-chain alcoho dTDP-glucose 4,6-d probable activator hypothetical prote adhesin AP65-1 pre DNA43 protein - ye HIV-1 retropepsin pol polyprotein - HIV-1 retropepsin Collagen alpha 2(I probable transport probable soluble I probable G2-specif hypothetical proteinam probable nicotinam probable nicotinat uracil DNA glycosy telomerase reverse hypothetical prote probable glutathio dihydropteridine r hypothetical prote ABC transporter, A probable transcrip UTP-glucose-1-phos tryptophan synthas carboxypeptidase A probable papA3 pro site-specific DNAhypothetical prote El protein - human erythrocyte membra phosphoribosylform hypothetical prote nitrate reductase hypothetical prote protein export [im dTDPglucose 4,6-de hypothetical prote HIV-1 retropepsin prote n - ye prote human

microtubule-assoc:

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hypothetical protein jhp0682 - Helicobacter pylori
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999
C;Accession: B71900
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C;Superf
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: A10380
C;Accession: A10380
R;Parkhill, J: Wreen, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. R;Parkhill, J: Wreen, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Pougan, G.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; i., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                   RESULT 3
A90167
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9ZL98;
A;Experimental source: strain J99
C;Genetics:
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awa: Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
                                                             adenylate cyclase, cyaB-type, probable (cyaB) [imported] - Sulfolobus solfa C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004 C;Accession: A90167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; ; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Nature 397, 176-180, 1999
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A; Residues: 1-122 < KUR>
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Pred. No. 1
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Pred. No. 8;
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1.3;
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                            Awayez, M.J.;
goc, H.P.; Redo
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C; Superfamily:
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Matches
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                              Similarity
8; Conserv
                              Conservative
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submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: A90167
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A;Molecule type: DNA
A;Residues: 1-186 <KUR>
                                                                                                                                                                                                                                         R;Hirsch, V.M.; Adger-Johnson, D.; Cambell, B.; Goldstein, J. Virol. 71, 1608-1620, 1997
A;Title: A molecularly cloned, pathogenic, neutralization-A;Reference number: Z17285; MUID:97151152; PMID:8995688
                                                                                                                                                                                                                                                                                                                       A;Variety: strain E543
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11560
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C;Superfamily: Thermophilic adenylate cyclase, CyaB type
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                                                                                                                                         A;Residues: I-1019 <HIR>
A;Cross-references: UNIPROT:P89154; EMBL:U72748; NID:g1695908; PIDN:AAC56559.1; PID:g16
                                                                                                                                                                                                                                                                                                                                                                                 pol polyprotein - simian immunodeficiency virus C;Species: simian immunodeficiency virus SIVsm
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A; Residues: 1-161 <BUC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-fructofuranosidase (EC 3.2.1.26) II - N;Alternate names: cell wall invertase II
                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1019 <
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                                                            ly: pol polyprotein AIDS; immunodeficiency
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Similarity 46.7%;
7; Conservative
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1; Mismatches
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pol polyprotein - human immunodeficiency virus type 2 D205 (fragment) C;Species: human immunodeficiency virus type 2 D205, HIV-2 D205 C;Species: human immunodeficiency virus type 2 D205, HIV-2 D205 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004 C;Accession: S08436 R;Dietrich, U.; Adamski, M.; Kreutz, R.; Seipp, A.; Kuehnel, H.; Ruebsamen-Wature 342, 948-950, 1989 A;Title: A highly divergent HIV-2-related isolate. A;Reference number: S08434; MUID:90081881; PMID:2594088 A;Accession: S08436
                                                                                                                                               RESULT 8
S35151
                 photosystem I chain XI precursor - spinach C;Specles: Spinacia oleracea (spinach) C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 C;Accession: S35151; S14446 R;Flieger, K.; Oelmueller, R.; Herrmann, R.G. Plant Mol. Biol. 22, 703-709, 1993 A;Title: Isolation and characterization of cDNA clo
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Science 273, 813-816, 1996
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A;Cross-references: UNIPROT:P15833;
A;Note: this sequence was submitted
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A; Residues: 1-63 <SEN>
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A; Accession: T30614
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A;Title: Isolation and characterization of cDNA clones encoding A;Reference number: S35151; MUID:93344519; PMID:8343606
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Molluscum contagiosum virus 1; Species: Molluscum contagiosum virus 1; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
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Pred. No.
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Pred.
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5.8;
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                                                                                         #text_change
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                                                                   C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000
C;Accession: A83862
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                 R;Takami, H.; Nakasone, K.; Takaki, Y.
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of t
                                                                                                                                                                   RESULT 10
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 A; Reference number:
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                                                                                                                            initiation of chromosome replication dnaD [imported] -
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A;Cross-references: EMBL:U04018; NID:g466250; PIDN:AAA21512.1; PID:g466251
A;Experimental source: isolate SABD37; sabaeus monkey
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, De
                                                                                                                                                                                                                                                                                                                                                                                                     R;Jin, M.J.; Hui, H.; Robertson, D.L.; Muel
EMBO J. 13, 2935-2947, 1994
A;Title: Mosaic genome structure of simian
A;Reference number: S46335; MUID:94298785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pol polyprotein - simian immunodeficiency virus SIVagm (isolate SABD37) (fr.
C;Species: simian immunodeficiency virus SIVagm
A;Variety: isolate SABD37
C;Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999
C:Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: this protein is a component of photosystem I which catalyzes the light-1 C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid; transmembrane protein F;1-47/Domain: transit peptide (chloroplast) #status predicted <TNP> F;48-216/Product: photosystem I chain XI #status predicted <MAT> F;131-153/Domain: transmembrane #status predicted <TM1> F;187-209/Domain: transmembrane #status predicted <TM2>
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A; Residues: 1-217 <JIN>
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A; Reference number: S14316; MUID: 91192162; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: seed R;Ikeuchi, M.; Inoue, Y. FEBS Lett. 280, 332-334, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-216 < FLI>
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                                                                                                                                                                    ;Superfamily: pol polyprotein;Keywords: polyprotein
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8; Conserv
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GPRLRQWPLSKE
                                      GPTLROWLKSRE 15
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                                                                                                                                                                                                                                                                                                                                                                    acid sequence not shown;
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Pred. No. 22;
1; Mismatches
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PMID:8026477
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PMID:2013332
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Y.; Maeno,

G. ;

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Masui, N.; Fuji, Bacillus halodurans

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#text_change Sasaki,

09-Jul-2004 halodurans

Bacillus

(strain

C-12

the alkaliphilic bacterium 12582; PMID:11058132

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A;Accession: A83862
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <STO>
A;Cross-references: UNIPROT:Q9KC77; GE
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Start codo:
C;Superfamil:
C;Keywords:
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R;Pritchard, A.E.; Seilhamer, J.J.; Mahalingam, R.; Sable, C.L.; Venuti, S.E.;
Nucleic Acids Res. 18, 173-180, 1990
A;Title: Nucleotide sequence of the mitochondrial genome of Paramecium.
A;Reference number: S07725; MUID:90174913; PMID:2308823
                                                                                                                                                                                                                   R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia, A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73999
                                                                                                                                                                                                                                                                                                                                                          C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein yaaC homolog VXpSPT7_orf269 - Mycoplasma pneumoniae (strain N;Alternate names: hypothetical protein VXpSPT7_orf269
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C;Species: mitochondrion Paramecium tetraurelia
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
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A; Residues: 1-269 < HIM>
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Best Local S
Matches 7
                                                                                                                        Cross-references: UNIPROT:P75587; EMBL:AE000062; GB:U00089; NID:g1674373; PIDN:AAB963; Ote: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                     Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004;Accession: S73999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetic code: SGC6
Query Match
Best Local
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Best Local
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  Score 43;
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sister chromatid cohesion molecule Mis4p - fission yeast (Schizosaccharomyce; Species: Schizosaccharomyces pombe C;Species: 14-Jan-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004 C;Accession: T38603; T43392; S59644 R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                              RESULT
S59644
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A;Description: Human infection by genetically diverse SIVSM-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.; submitted to the EMBL Data Library, December 1992
A;Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa
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C;Superfamily: pol polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: human immunodeficiency virus type 2, HIV-2 C;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: human :
A;Molecule type: DNA
A;Residues: 1-1583 <DE2>
                                                        A;Reference number: Z21731
A;Accession: T38603
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A; Residues: 1-656 < GAO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S30484
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                                    A;Status: preliminary; translated from GB/EMBL/DDBc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ol polyprotein - human immunodeficiency virus type 2;Species: human immunodeficiency virus type 2, HIV-2;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 23-Mar-2001
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Matches 8; Conserv
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1; Mismatches
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Pred. No.
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UNIPROT: Q09725; EMBL: Z50113; NID: g914878; PIDN: CAA90463.1; PID: g914

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A;Title: Genome sequence of Yersinia pestis, A;Reference number: AB0001; MUID:21470413; PA;Accession: AC0189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: T43392
A;Status: prelimina
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R;Furuya, K.; Takahashi, K.; Yanagida, M.
submitted to the EMBL Data Library, August 1998
A;Description: Faithful anaphase is ensured by Mis4, a sister chromatid cohesion molecul
                                                                                                                            R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Y
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the
A;Reference number: A71000;.MUID:98344137; PMID:9679194
A;Accession: E71171
A;Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                hypothetical protein PH0569 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: E71171
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A; Residues: 1-275 < KUR>
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                A;Experimental source: A;Note: this accession C;Genetics:
                                                                   A;Molecule type: DNA
A;Residues: 1-114 <KAW>
A;Cross-references: UNIPROT:058304; GB:AP000002; NID:g3236129; PIDN:BAA29658.1;
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Best Local S
Matches 6
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;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004;Date: AC0189
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Best Local
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PH0569
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                                                    strain OT3
                                    replaces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.8%;
                                                                                                                                                                                                                             M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
                                    an interim accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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Pred. No. 34;
1; Mismatches
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Pred. No.
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                                                                                                                                  sequence not shown; translation
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RESULT S71157

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cytochrome C; Species:

c biogenesis protein 454 - evening mitochondrion Oenothera berteriana

primrose (evening

mitochondrion primrose)

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RESULT 19
D72456
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T20567
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A:Reference number: A72450; MUID:99310339; PMID:10382966
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A;Reference number: Z19293
A;Accession: T20567
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                                                                                                                                                                                                                                                                                                                              R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka,
                                                                                                                                                                                                                                                                                                                                                                C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72456
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                                                                                                                               C; Superfamily:
                                                                                                                                                  A;Gene: APE2296
                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-416 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                probable glutamy1-tRNA reductase APE2296 - Aeropyrum pernix (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position:
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                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                              A; Accession: D72456
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Best Local S
Matches 7
                                                               Query Match
Best Local S
Matches 8
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8; Conserv
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8; Conser
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 VLGQVRRAWLKSRE 118
                                IKGPTLROWLKSRE 15
                                                                                                                               glutamyl-tRNA reductase
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63.6%;
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                                                                 Score 42; DB Pred. No. 65; 1; Mismatches
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Pred. No. 16;
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                                                                                                Length 416;
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A;Genome: mi
A;Introns: 2
C;Keywords:
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C;Accession: C86160

C;Ancession: C86160

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D.

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.;

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004 C;Accession: S71157; S55283; $\overline{S}42984$ R;Gruska, I.; Jekabsons, W.; Schuster, W.
Mol. Gen. Genet. 247, 529-536, 1995
A;Title: Oenothera mitcochondrial orf454, a gene involved in cytochrome c bio A;Reference number: S55283; MUID:95327048; PMID:7603431
A;Accession: S71157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: differences are due to RNA editing; premature stop codon is due to RNA editing A;Accession: S55283
A;Molecule type: DNA
A;Residues: 1-16,'PR',19-34,'P',36-39,'SS',42-48,'P',50,'PS',53,'P',55-108,'L',110-130,A;Cross-references: EMBL:X78036; NID:g459536; PIDN:CAA54966.1; PID:g459537
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9SRY9;
C;Genetics:
A;Map position: 1
Plant Cel
A; Title:
                                                                          beta-fructofuranosidase (EC 3.2.1.26), cell wall - fava bean N;Alternate names: cell wall invertase II C;Species: Vicia faba (fava bean) C;Species: Vicia faba (fava bean) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F22D16.3 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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A;Note: differences are due to RNA editing; pre
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A; Residues: 1-438 <GRU>
                   R; Weber, H.; Borisjuk, L.; Heim, U.; Plant Cell 7, 1835-1846, 1995
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                                                                                                                                                                                     RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Molecule type: DNA
;Residues: 1-519 <S'
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Best Local
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                                                             Accession:
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Seed
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6; Conserv
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  coat-associated invertases of
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40.0%;
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Pred. No.
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                                         Buchner,
                                                                                                                                                                                                                                                                                                                                         Mismatches
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    Fava
                                       P.; Wobus,
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  bean control
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  both unloading
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Dewar, K.;
  and
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Marziali,
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    storage
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    A;Cross-references: EMBL:X07805; NID:g61748; PID:g1335593 C;Comment: Specific enzymatic cleavages may yield mature
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A;Start_codon:
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                                             A;Residues: 1-1061 <FUK>
                                                             A; Molecule type:
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Best Local :
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A;Reference number: Z17416; MUID:950951.
A;Accession: T12095
A;Status: preliminary; translated from A;Status: preliminary; translated from A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-581 < WEBP
A;Cross-references: UNIPROT:Q43856; EME
A;Cross-references: UNIPROT:Q43856; EME
                                                                                           ONLUGA
HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green N;Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed C;Species: simian immunodeficiency virus, SIV C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Jun-2002 C;Accession: B30045
T. Hasserawa. A.: Morikawa, S.; Tsujimoto, H.; Miki, K.;
R; Pukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; T
Nature 333, 457-461, 1988
A;Title: Sequence of simian immunodeficiency virus from
A;Reference number: A30045; MUID:88232906; PMID:3374586
A;Accession: B30045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-617 < KAN >
A; Cross-references: UNII
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C;Keywords: cell wall; glycoprotein; glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: C; Genetics:
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R; Kaneko, T.; Sato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proline-tRNA ligase - Synechocystis
N;Alternate names: protein sll1425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: the nucleotide sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 3, 109-136, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Synechocystis
A;Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
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K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIPROT:P73942; EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAA180.
                                                                                                                                                                                                                                                                                                                                                                                                                           43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                   617
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ďs.
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                                                    African green
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                                                        monkey,
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da, M.; Yasud
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proteins

including

protease,

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A;Gene: pks5
C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I nase homology; [acyl-carrier-protein] S-malonyltransferase homology <OAS> F;Seywords: carrier protein synthase I homology <OAS> F;36-434/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <AMT> F;146-826/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT> F;1444-173/Domain: short-chain alcohol dehydrogenase homology <LADH> F;1765-1945/Domain: short-chain alcohol dehydrogenase homology <SADH> F;2029-2094/Domain: acyl carrier protein homology <ACPl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; SKELLUL, S.; C. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Bar A; Title: Deciphering the biology of Mycobacterium tuberculosis from A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Reference preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: pol
A;Gene: pol
C;Superfamily: pol polyprotein
C;Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; pol
E;111-210/Product: retropepsin #status predicted <RTP>
F;134/Active site: Asp (shared with dimeric partner) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-2108 «COL»
A; Cross-references: UNITROT: 053901;
A; Experimental source: strain H37Rv
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable polyketide synthase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70819
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HC
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                      R;Matsuura, T.; Kasper, L.
Mol. Biochem. Parasitol. 90, 403-413, 1997
A;Title: Molecular analysis and characterization of a A;Title: Molecular analysis and characterization of a A;Reference number: Z14838; MUID:98135655; PMID:947678
A;Accession: T03098
                                                                                                                                                                                                                                                                       C; Date: 24-Ma
C; Accession:
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                                             A; Cross-references: UNIPROT: 015644; A; Experimental source: strain RH
                                                                                        A; Molecule type: mRNA
A; Residues: 1-877 < MAT>
                                           A; Experimental
                                                                                                                                 A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                          ;Species: Toxoplasma gondii
;Date: 24-Mar-1999 #sequence_revision
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Best Local
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Description: involved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42;
Pred. No.
                                                                                                                                      from
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                                                                   EMBL: AF005059;
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of intracellular Toxoplasma gondii
                                                                                                                                      GB/EMBL/DDBJ
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                                                                NID:g2581824; PIDN:AAC47857
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C; Superfamily: Escher C; Keywords: cyanelle;
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C;Species: cyanelle Cyanophora paradoxa
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                   A;Map positTon: circular chromosome
C;Superfamily: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine
                                                                                                                                                                                                                                                                                                                                             R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P48129; EMBL:U30821; NID:g1016083; A;Experimental source: strain Pringsheim LB555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-70 <STI>
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A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora par:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession:
R;Stirewalt,
                                                                                                                                                                       A; Gene: AGR_C_2500
                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-153 < KUR>
                                                                                                                                                                                                                                                                                                                                Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein AGR C 2500 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: T06920
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                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q8UFP3; GB:AE007869; PIDN:AAK87146.1; PID:g15156416;
                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: A97524
                                                                                                                                                                                                                                                                                                            A; Title: Genome Sequence of
                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: A97524
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A97524
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                                                                                                                                                                                                                                                           A;Status: preliminary
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Best Local S
Matches 8
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Best Local
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                                                                 Matches
                                                                                                  Query Match
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119
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                                                                 Similarity 6; Conserv
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8; Conserva
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8; Conserv
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VKGKPVRQWLQQADRS
                              IKGPTLROWLKSREHT 17
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                                                                   Conservative
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                                                                                42.3%;
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                                                                                                                                                                                                                                                                                              the Plant Pathogen and Biotechnology MUID:21608551; PMID:11743194
134
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Pred. No. 1.7e+02;
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Pred.
                                                                                     Pred
                                                                                                  Score 41;
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Doughty, D.;
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                                                                                                    Length 153
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                                                                                                                                                                                                                                                                                                                                                                   M.; Qurollo,
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                                                                                                                                                                                                                                                                                                                Agent Agrobacterium
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GSPDE

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A;Cross-references: UNIPROT:Q9PHI6; GB:AE003851; NID:g9112238; PIDN:AAF85588.1; GSPDB:G A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Ccamargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.A., Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Palmieri, D., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D., F.G.; Nunes, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa A;Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.D.; A.D. George T. M. Silva Jr., Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.D. Deference T. M. Silva Jr., Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.D., Deference T. M. Silva Jr., Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.D., Deference T. M. Silva Jr., Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.C.; Palmieri, D. D., Deference T. M. Silva Jr., Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.C.; Palmieri, D. D., Deference T. M. Silva Jr., Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Cher erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: The genome sequence of the plant pathogen Xylella fastidiosa A,Reference number: A825.15; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 bela,Rocession: C82863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;anonymous, The Xylella fastidiosa Consortium of the Organization Nature 406, 151-157, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinase XFa0019 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                         A; Note: plasmid pXF5.1
C; Superfamily: transposase
                                                                                                                                                  ;Genome: plasmid
;Note: plasmid pXF5.1
                                                                                                                                                                                                                                                                                                          ;Reference number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Residues: 1-188 <SIM>
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nilarity 37.5%;
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42.3%;
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                                                                                                TRNA guanine-N1 methyltransferase - Aquifex aeolicu
C;Species: Aquifex aeolicus
C;Date: 08-May.1998 #sequence_revision 08-May-1998
C;Accession: E70429
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         Nature 392, 353-358,
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RESULT
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C; Superfamily: Schizosaccharomyces
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A; Residues: 1-203 < WOO>
                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-238 < KAN>
                                                                                                                                                                                                                                                                                                                                      R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacte:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: SPDB:SPBC31F10.03
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A;Experimental source: strain 972h-;
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                                                                                                                                                                                                                                                                                                           A; Reference number: S74322;
                                                                                                                                                                                                                                                                             Status: preliminary;
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Schizosaccharomyces pombe
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August 1997
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Aquifex aeolicus
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G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox,

#text_change 09-Jul-2004

A.L.; Graham,

D.E.;

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A; Molecule type: DNA
A; Residues: 1-257 < AQF>
A; Cross-references: UNIPROT:067463;
A; Experimental source: strain VF5
C; Genetics:
                                                                                                                                                                Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S. Asture 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; A; Title: Deciphering the biology of Mycobacterium tuberculosis fr A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: D70601
                                                                                                                                                                                                                                                                   C;Accession: D70601
C;Accession: D70601
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H.; Connor, R.; Davies, R.; Davies, R.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: AG2095

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi R;Kaneko, T.; Nakamura, Y.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Suna Res. 8, 205-213, 2001

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana, Fittle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana, Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AG2095
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence revision 14-Dec-2001
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                                                                                                                                                                                                                                                                                                                                                             C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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A;Gene: galU
C;Superfamily:
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                                          A; Experimental C; Genetics:
                                                                                                     A; Molecule type: DNA
A; Residues: 1-306 < COL>
                                                                                                                                                                                                                                                                                                                                                                                                          UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)
                                                                                                                                           Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                 Cross-references: UNIPROT:005576; Experimental source: strain H37Rv
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Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
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57;
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodt.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa, Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:41637, NCBI C;Superfamily: Modification methylase (adenine-specific), N1aIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 173, 4363-4370, 1991
A;Title: In vivo genetic exchange of a functional domain
A;Reference number: A47029; MUID:91294179; PMID:1906061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methylase LlaPI - phage nck202.50 (phi 50) (fragment)
C;Species: phage nck202.50 (phi 50)
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 16-Aug-2004
C;Accession: B47029
                                                                                                      A,Description: catalyzes conversion of indoleglycerol phosphate and A,Pathway: tryptophan biosynthesis A;Nathway: tryptophan biosynthesis A;Note: cofactor pyridoxal phosphate; last step in pathway C;Superfamily: tryptophan synthase beta chain; tryptophan synthase c;Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein; pyrid F;12-93/Domain: tryptophan synthase beta chain homology cTRPB> F;12-93/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tryptophan synthase (EC 4.2.1.20) beta chain - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Ju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: B47029
R; Hill, C.; Miller, L.A.; Klaenhammer,
                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-397 < K
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                                                                                  F;94/Binding site: pyridoxal phosphate
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57.1%;
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Pred. No. 67;
2; Mismatches
    Score 41; DB Pred. No. 89; 2; Mismatches
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C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence revision 19-Jan-1996 #text change 09-Jul-2004
C;Accession: S29127; A34205; S08253; S02810; S71394; S02811
R;Catasus, L.; Villegas, V.; Pascual, R.; Aviles, F.X.; Wicker-Planquart, C.; Puigserve Biochem. J. 287, 299-303, 1992
Biochem. J. 287, 299-303, 1992
A;Title: cDNA cloning and sequence analysis of human pancreatic procarboxypeptidase Al. A;Reference number: S29127; MUID:93038569; PMID:1417781
A;Accession: S29127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 330-396 <STE>
A;Note: the authors translated the codon CTG for residue 391 as R;Moulard, M.; Michon, T.; Kerfelec, B.; Chapus, C.
FEBS Lett. 261, 179-183, 1990
A;Title: Further studies on the human pancreatic binary complexe A;Reference number: S08253; MUID:90169111; PMID:2307232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S02810
A;Molecule type: protein
A;Residues: 17-42 <PAS>
A;Residues: 17-42 <PAS>
A;Residues: 17-42 <PAS>
A;Residues: 17-42 <PAS>
A;Laethem, R.M.; Blumenkopf, T.A.; Cory, M.; Elwell, L.; Moxham, C.P.; Ray, P.H.; Walto Arch. Biochem. Biophys. 332, 8-18, 1196
A;Title: Expression and characterization of human pancreatic preprocarboxypeptidase Al A;Teference number: S71394; MUID:96400327; PMID:8806703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 17-43; XXX',114-135 <MOU>
R;Residues: 17-43; XXX',114-135 <MOU>
R;Pascual, R.; Burgos, F.J.; Salva, M.; Soriano, F.; Mendez, Eur. J. Biochem. 179, 609-616, 1989
A;Title: Purification and properties of five different forms
A;Reference number: S02809; MUID:89153096; PMID:2920728
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A;Cross-references: UNIPROT:P15085; EMBL:X67318; NID:g35329; P
A;Cross-references: UNIPROT:P15085; EMBL:X67318; NID:g35329; P
R;Stewart, E.A.; Craik, C.S.; Hake, L.; Bowcock, A.M.
Am. J. Hum. Genet. 46, 795-800, 1990
Am. J. Hum. Genet. 46, 795-800, 1990
A;Title: Human carboxypeptidase A identifies a BglII RFLP and A;Reference number: A34205; MUID:90196012; PMID:1969228
A;Accession: A34205
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A; Residues: 1-419 < LAE >
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Best Local
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53.8%;
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Pred. No. 94;
2; Mismatches
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probable papA3 protein - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: F70876
C;Accession: F70876
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, (
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Title: Deciphering the biology of Mycobacterium tuberculosis from not shown
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A; Residues: 1-622 <HIL>
A; Residues: 1-622 <HIL>
A; Cross-references: UNIPROT: P35516; EMBL: M77136
A; Experimental source: bacteriophage resistance plasmid pTR2030
A; Experimental source: bacteriophage resistance plasmid pTR2030
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R;Hill, C.; Miller, L.A.; Klaenhammer, T.R.
J. Bacteriol. 173, 4363-4370, 1991
A;Title: In vivo genetic exchange of a functional domain A;Reference number: A47029; MUID:91294179; PMID:1906061
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F70876
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submitted to the EMBL Data Library, November 1994
A;Reference number: $77702
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A;Experimental source: strain H37Rv
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A; Residues: 1-472 < COL>
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A; Residues: 1-248
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;Gene: LlaI
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81
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Pred. No.
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1.1e+02;
7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is interchanged in the authors' translation (NCBIN:41635, NCBIP:41636)
                                                                                                                                                                                                                                                               Length 622;
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                                                                                                                                                                                                                                                                                                                                                               system;
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bet

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RESULT 43
$73786
$73786
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997
C;Accession: $73786
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Intror
A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          telomerase reverse transcriptase - Arabidopsis th N;Alternate names: protein F5E19_190 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 18-Aug-2000 #sequence_revision 18-Aug-200 C;Accession: T51517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-1039 <JIN>
A;Cross-references: EMBL:U04005; NID:g466229; PIDN:AAA21505.1; PID:g466231
A;Cross-references: EMBL:U04005; NID:g466229; PIDN:AAA21505.1; PID:g466231
A;Experimental source: isolate SAB-1; sabaeus monkey
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Dev
A;Note: this reading frame extends between two stop codons and does not be;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999 (;Accession: S46347 R;Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; H EMBO J. 13, 2935-2947, 1994 R;Title: Mosaic genome structure of simian immunodeficiency virus from West A;Reference number: S46335; MUID:94298785; PMID:8026477 A;Accession: S46347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pol polyprotein - simian immunodeficiency virus SIVagm (isolate SAB-1) C;Species: simian immunodeficiency virus SIVagm A;Variety: isolate SAB-1 A;Variety: isolate SAB-1 C;Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text change 26-Aug
                 R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of A;Reference number: 873327; MUID:97105885; PMID:894A;Accession: S73786
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A;Residues: 1-1123 <SAT>
A;Residues: 1-1123 <SAT>
A;Cross-references: UNIPROT:Q9SPU7; EMBL:AL391147
A;Experimental source: cultivar Columbia; BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: Z25394
A; Accession: T51517
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A;Status: preliminary; nucleic
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Best Local S
Matches 7
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Best Local
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58.3%;
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acid
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Pred. No.
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Database,
sequence not
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                                  genome of the PMID:8948633
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August 2000
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                                                                                                                                                                                      pneumoniae
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shown; translation
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                                                                                           E.; Li, B.C.; Herrmann,
                                                                                                                                                                                                                                                                                                                                                                                          Length 1123
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                                                      Mycoplasma
 not shown
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3345 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 30B8.4 fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change (C;Accession: T13423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Saigi, F.; Climent, N.; Pique, N.; Sanchez, C.; Merino, S.
J. Bacteriol. 181, 1883-1891, 1999
A;Title: Genetic analysis of the Serratia marcescens N28b O4
A;Reference number: Z20974; MUID:99173913; PMID:10074083
A;Accession: T31091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein wbbK [imported] - Serratia marcescens
C;Species: Serratia marcescens
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1140 <HIM>
A;Residues: 1-1140 <HIM>
A;Cross-references: UNIPROT:P75405; EMBL:AE000045; GB:U00089; NID:g1674145; PIDN:AAB961
A;Cross-references: UNIPROT:P75405; EMBL:AE000045; GB:U00089; NID:g1674145; PIDN:AAB961
A;Cross-references: UNIPROT:P75405; EMBL:AE000045; GB:U00089; NID:g1674145; PIDN:AAB961
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T13423
                                                                                                                                                                                                                                                                                                                                      A; Description: Sequencing the A; Reference number: Z17668
                                                                                                                                                                                                                                                                                                                                                       R;Murphy, L.; Harris, D.; Barrell, B. submitted to the EMBL Data Library, A A;Description: Sequencing the distal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-1191 A; Cross-references:
                                                                                                                                                  A;Note:
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                                                                                                                                                                                   A; Map position: X
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                                                                                                                                                                                                                                            ;Cross-references:
                                                                                         Query Match
Best Local :
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Best Local
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                                                                                                                                                ns: 51/3; 159/1; 476/1; 526/1; 1465/1; 1826/3; EG:30B8.4
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7; Conserv
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Similarity 50.0%;
7; Conservation
                                                                      Similarity 7; Conserv
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                                 IKGPTLROWLKS 13
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58.3%;
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Pred. No. 2.8e
2; Mismatches
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Pred. No. 2.9e+02;
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                                                                        Score 41; DB 2;
Pred. No. 9e+02;
1; Mismatches
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l X chromosome
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2.8e+02;
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Search completed: September 1, 2005, 16:22:54
Job time: 16.7266 secs

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Maximum Match 100%
Listing first 100
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Maximum DB
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                          STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/J5097083;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/J5097083;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.",
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q66DR4;
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
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SEQUENCE FROM N.A.

STRALIN=KIM5 / Biovar Mediaevalis;

STRALIN=KIM5 / Biovar Mediaevalis;

MEDLINE=22137863; PubMed=12142430;

DOI=10.1128/JB.184.16.4601-4611.2002;

Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F.,

Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15358858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=IP 32953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yersinia pseudotuberculosis IP 32953.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORFNames=YPTB0979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q66DR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=632;
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKGPTLRQWLKSREH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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28,
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Pred. No. 4.5;
3; Mismatches
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RESULT 4
Y745_HELF
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Y745 HELPJ Q9ZL98;

STANDARD;

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                                                                                                                                                                                    Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.

REMBL; Y08963; CAA70157.1; -.

RGO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0003755; P:regulation of transcription, DNA-dependent; IEA.

RINTETPO; IPR000847; HTH LysR.

RINTETPO; IPR000847; HTH LysR.

RINTETPO; IPR005119; LysR.

SR InterPro; IPR00958; Wing_hlx_DNA_bnd.

RINTETPO; IPR00958; Wing_hlx_DNA_bnd.

RP60016; HTH 1, 1.

RP60016; HTH 1, 1.

RP60016; HTH LYSR.

RPRONTTE; PS50931; HTH_LYSR; 1.

RPROSTTE; PS50931; HTH_LYSR; 1.

RPROSTTE; PS50931; HTH_LYSR; 1.

RPROSTTE; PS50931; HTH_LYSR; 1.

RPROSTTE; PS50931; HTH_LYSR; 1.
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Best Local
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P95613;
01-MAY-1997
01-MAY-1997
01-MAR-2004
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EMBL; AE013708; AAM84628.1; -.
EMBL; AE017129; AAS61059.1; -.
PIR; AI0380; AI0380
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J. Bacteriol. 184:4601-4611(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium galegae.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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Han Y., Pang X., Zhai J., Chen F.,
Ye C., Du Z., Lin W., Wang J., Yu
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  204
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8; Conserv
KGPSLEQWLSSQ
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                                                 KGPTLRQWLKSR 14
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                                                                                           Conservative
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184:4601-4611(2002).
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66.7%;
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                                                                                                <u>ب</u>
                                                                                                Score 48; DB Pred. No. 20; 2; Mismatches
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, Qin H., Wang J.,
J., Yang H., Wang
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                                                                                                                                             Length 326;
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical pseudouridine synthase JHP0682 (E
(Pseudouridylate synthase) (Uracil hydrolyase)
OrderedLocusNames-JHP0682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doi

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,

Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives

Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete
DOMAIN
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori J99 (Campylobacter pylori J99 Bacteria; Proteobacteria; Epsilonproteobacteria; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD001819; PseudoU_synth; :
SMART; SM00363; S4; 1
TIGREAMS; TIGR00005; rluD_subfam;
PROSITE; PS01129; PSI_RLU; 1
PROSITE; PS50889; S4; 1.
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Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Eremothec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006225; Pseud synth_RluD.
InterPro; IPR006145; PseudoU_synth.
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SIMILARITY: Belongs to the pseudouridine synthase
SIMILARITY: Contains 1 S4 RNA-binding domain.
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pF01479; S4; 1.
pD001819; PseudoU_synth; 1
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Similarity 50.0%;
8; Conservative
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12 79 S4
136 136 By
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37722 MW;
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4 RNA-binding.

/ similarity.

7EDC7F6840D818BD CRC64;
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annotation updat
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Submitted
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P61744;
05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Glycerol-3-phosphate dehydrogenase 2 [NAD(P)+] (dependent glycerol-3-phosphate dehydrogenase 2).
Name=gpsA2; OrderedLocusNames=MAP4061c;
                                                                                               EMBL; AE017241; AAS06611.1; -.

HAMAP; MF 00394; -; 1.

ProDom; PD001278; NAD G193P_C; 1.

PROSITE; PS00957; NAD G35DH; FALSE NEG.

Complete proteome; NAD; Oxidoreductase; Phospholipid b
SEQUENCE 332 AA; 35220 MW; B149EF540B313DB3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lerch A., Brac
Dietrich F.S.;
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=33169;
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CATALYTIC ACTIVITY: Sn-glycerol 3-phosphate + NAD(P) (+ glycerone phosphate + NAD(P)H.
gATHWAY: De novo phospholipid biosynthesis; glycerol-3
                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: SIMILARITY: Belongs to dehydrogenase family.
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1; Mismatches
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pendent glycerol-3-phosphate
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A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
B Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Seniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
B Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.,
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Q6YUC3;
05-JUL-2004
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein B1116H04.2 (Hypothetical protein
B1111C03.14).
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25-OCT-2004 (TrEMBLrel. 28, C

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25-OCT-2004 (TrEMBLrel. 28, L

Similar to tr | 099968 Candida
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Saccharomycetales; Dipodascaceae;
NCBI_TaxID=284591;
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Submitted (JUN-2002) to the EM
EMBL; AP005871; BAD10677.1; --
EMBL; AP005405; BAD10301.1; --
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Submitted (NOV-2002)
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                                                  STRAIN=CLIB99;
                                                                                                                              "Genome evolution in yeasts.";
Nature 430:35-44(2004).
                                                                              SEQUENCE
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C: EMBL; CR382132; CAG78287.1; -.

R: GO; GO:0016616; F:oxidoxeductase activity, acting on the CH-O. . . .

R: GO; GO:0016616; F:oxidoxeductase activity, acting on the CH-O. . . .

R: GO; GO:0006564; F:L-serine biosynthesis; IEA.

R: InterPro; IPR006139; 2-Hacid_DH.

R: InterPro; IPR006139; 2-Hacid_DH.

R: InterPro; IPR006140; 2-Hacid_DH.

R: Pfam; PF00389; 2-Hacid_DH. C: 1.

R: Pfam; PF00389; 2-Hacid_DH. C; 1.

R: Pfam; PF02826; 2-Hacid_DH. C; 1.

R: Pfam; PF02826; 2-Hacid_DH. C; 1.

R: Pfam; PF02826; 2-Hacid_DH. C; 1.

R: PROSITE; PS00670; D-2_HYDROXYACID_DH-2; 1.

R: PROSITE; PS00671; D-2_HYDROXYACID_DH-3; 1.
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                                                                                                                                                                                                        InterPro; IPR002559; Transposase 11.
Pfam; PF01609; Transposase 11; 1.
Complete proteome.
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004803; F:transposase activity;
GO; GO:0006313; P:DNA transposition; IE
                                                                                                                                                                                                                                                                                                                                                                                                 Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
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Sakaki Y., Hattori M.,
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Bacteria, Actinobacteria;
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OrderedLocusNames=SAV256;
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72.78;
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Last annotation updat
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Pred. No.
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GO; GO:0004016; F:adenylate cyclase activit
GO; GO:00016829; F:lyase activity; IEA.
GO; GO:0006171; P:cAMP biosynthesis; IEA.
InterPro; IPR008172; Adenylate_cyc.
InterPro; IPR008173; CyaB.
Pfam; PF01928; CYTH; 1.
ProDom; PD009560; CyaB; 1.
TIGRPAMS; TIGR00318; cyaB; 1.
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STRAINATCC 35092 / DSM 1617 / P2;

MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;

MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

She Q., Singh R.K., Confalonieri F., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchason Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q980N7;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome analysis of the kidney necrosis iridovirus."; Virology 291:126-139(2001).
EMBL; AF371960; AAL98838.1;
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He J.G., Deng M.,
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Infectious spleen and kidney ne
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    proteome;
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OrderedLocusNames=SSO0253;
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 Lyase.
21820 MW;
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Q8XR40;
01-MAR-2002
01-MAR-2002
                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V. Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Ru
                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21681879; PubMed=11823852; DOI=10.1038/415497a; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot Salanoubat Billault A., Brottier P., Camus J.C., Cattolico L., Arlat M., Billault A., Brottier P., Camus J.C., Cunnac S., Demang Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demang Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex
 Submitted (MAR-2002) to the EMBL/Gei
EMBL; AY08935; AAL90073.1; -.
FlyBase; FB9R0063731; bcDNA:AT14183
SEQUENCE 286 AA; 30787 MW; 9937
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL646082; CAD18179.1; -. Complete proteome; Hypothetical SEQUENCE 243 AA; 27220 MW;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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Name=RS02365; OrderedLocusNames=RSp1028;
                                                 Celniker S.;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ datab
R EMBL; AE017230; AAS03241.1; -.
R GO; GO:0016779; F:nucleotidyltransferase activity;
R GO; GO:0019058; P:biosynthesis; IEA.
InterPro; IPR005835; NTP transferase.
Pfam; PF00483; NTP transferase; 1.
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SEQUENCE 302 AA; 32149 MW; 4E5D2B1AB572BAE7 CRC
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Ribosomal pseudouridine synthase.
OrderedLocusNames=HH0783;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                  Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P., Beell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A., Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.; "The complete genome sequence of the carcinogenic bacterium "The complete genome sequence of the carcinogenic bacterium Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 51449 / 3B1;
STRAIN-ATCC 51449 / 3B1;
STRAIN-E22709201; PubMed=12810954; DOI=10.1073/pnae.1332093100;
STRAIN-ATCC STRAIN-C ST
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Helicobacteraceae; Helicobacter.
NCBI_TaxID=32025;
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GO:0009982; F:pseudouridine synthase activity; IEA.
GO:0004730; F:pseudouridylate synthase activity; IEA.
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C STRAIN=CGA009 / ATCC BAA-98;
C STRAIN=CGA009 / ATCC BAA-98;
X PubMed=14704707; DOI=10.1038/nbt923;
X PubMed=14704707; DOI=10.1038/nbt923;
A Larimer F. W., Chain P., Hauser L., Lamerdin J.E., Malfatti S. Larimer F. W., Chain P., Hauser L., Lamerdin J.E., Tabita F. A Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F. A Harrison F.H., Gibson J., Harwood C.S.;
A Harrison F.H., Gibson J., Harwood C.S.;
T "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";
DNat. Biotechnol. 22:55-61(2004).

R Nat. Biotechnol. 22:55-61(2004).
R PROSITE; PS50156; SSD; 1.

R PROSITE; PS50156; SSD; 1.

R Complete proteome.

O SEQUENCE 789 AA; 85214 MW; 31C1C9E9CAC530CC CRC64;
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Q6N3E8;
05-JUL-2004
                                                                             Q7PS78 PRELIMINARY; PRT; 1715 AA.
Q7PS78;
Q7PS78;
Q1-MAR-2004 (TrEMBLrel. 26, Created)
Q1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO000005643 (Fragment).
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Bacteria; Proteobacteria; I
Bradyrhizobiaceae; Rhodopse
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Possible RND Superfamily transporter.
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SMART; SM00363; S4; 1.
TIGRFAMs; TIGR00005; rluD_subfam; 1
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PROSITE; PS50889; S4; 1.
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Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                            Name=ENSANGG00000004323;
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Pred. No. 1.6e+0;
3; Mismatches
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T; IEA.
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J.T., Lang A.S., Tabita F.R.,
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Torres J.L.,
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RESULT 19
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GO; GO:0005975; P:carbohydrate metabolism;
InterPro; IPR001362; Glyco hydro_32.
InterPro; IPR011040; Sialidase.
Pfam; PF00251; Glyco_hydro_32; 1.
SMART; SM00640; Glyco_32; I.
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01-MAY-1997 (TrEMBLrel. 03, Last s
01-JUN-2003 (TrEMBLrel. 24, Last a
Cell wall invertase II (Fragment).
Pisum sativum (Garden pea).
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Submitted (APR-2003) to the
-!- CAUTION: The sequence sh
EMBL/GenBank/DDBJ whole
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; AAAB01008844; EAA06040.2;
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9; Conserv
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161 AA;
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he EMBL/GenBank/DDBJ databases
shown here is derived from an
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GO; GO:0004190; F:
GO; GO:0008233; F:
GO; GO:0003723; F:
GO; GO:00016740; F:
GO; GO:0006508; F:
GO; GO:0006278; P:
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01-MAR-2004
Truncated rev
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-NCC 2705;
MEDLINE=22294977; PubMed=12381787;
MEDLINE=22294977; PubMed=12381787;
                    -!- SIMILARITY: Belongs to the sugar EMBL; AE014641; AAN24075.1; -. HSSP; P95780; 1KEP.
                                                                              "The genome sequence of Bifidobacterium longum reflects to the human gastrointestinal tract."; Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
                                                                                                                                                                                                                                                                                                                                                                         Bifidobacterium
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Pfam; PF00078; RVT 1; 1.
PROSITE; PS00141; ASP PROTEASE; 1.
PROSITE; PS50175; ASP PROT RETROV; 1.
Aspartyl protease; Hydrolase; Proteas
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InterPro; IPR009007; Pept_Aspartic.
InterPro; IPR001969; Pept_Asp_AS.
InterPro; IPR0004477; RVTse.
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ
-|- SIMILARITY: Belongs to peptidase family A2
EMBL; UB3413; AAB41428.1; -.
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                                                                                                                                                   Pessi G., Zwahlen M.-C., D
Pridmore R.D., Arigoni F.;
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GO:0004190; F:aspartic-type endopeptidase activit
GO:0008233; F:peptidase activity; IEA.
GO:0003723; F:RNA binding; IEA.
GO:0003764; F:RNA-directed DNA polymerase activit
GO:0016740; F:transferase activity; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
GO:0003824; F:catalytic activity;
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e enzyme involved in rha
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B., Vilanova D.,
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25-OCT-2004 (TrEMBLrel. 28, Cre-
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25-OCT-2004 (TrEMBLrel. 28, Las
Related to penicillin-binding p
OrderedLocusNames=DP2423;
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01-JUN-2003
01-JUN-2003
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GO; GO:000925; F:nuclectide-sugar metabolism; IEA.
InterPro; IPR00588; dTDP-gluc_dehyt.
InterPro; IPR001509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
TIGRFAMs; TIGR01181; dTDP_gluc_dehyt; 1.
Complete proteome; NAD.
Complete proteome; NAD,
SEQUENCE 347 AA; 39388 MW; 34852801FD1334FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microorganism Streptomyces avermitilis. Nat. Biotechnol. 21:526-531(2003). EMBL; AP005023; BAC68457.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22608306; PubMed=12692562; Ikeda H., Ishikawa J., Hanamoto A. Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MA-4680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MA-4680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=SAV747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein
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                                                                                                                                            Q6AKH3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence and comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome; Hypothetical 377 AA; 41307 MW; (
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                                                                                                                                                                                                                                                            MEGPDLRAWLPNRRY 182
                                                                                                                                                                                                                                                                                                     IKGPTLRQWLKSREH 16
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(TrEMBLrel. 24,
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Last
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Last annotation updat
ng protein (PbpA).
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Pred. No.
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Pred. No. 1e+02;
1; Mismatches
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annotation update)
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Best Local S
Matches 9
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GO; GO:0008658; F:penicillin binding; IEA. GO; GO:0009273; P:cell wall biosynthesis (se InterPro; IPR001460; Pencl bind_tpept. Pfam; PF03717; PBP_dimer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Q9P888;
Q9P888;
01-OCT-2000 (
01-OCT-2000 (
01-MAR-2004 (
Putative MFS)
                                                  Curr. Genet. 39:377-383(2001).

-!- SUBCELULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the sugar transporter family.

EMBL; A277424; CAB75950.1; -.

GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:000531; F:sugar porter activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0005215; P:transporter activity; IEA.
InterPro; IPR005215; Sugar_transporter.

InterPro; IPR005288; Sub transporter.

InterPro; IPR005889; Sugar_transporter.

InterPro; IPR005889; Sugar_transporter.

Pfam; PF00083; Sugar_tr; 1.
                                                                                                                                                                                                                                                                                                               Hypocreomycetidae; Hypocreales; Gibberella fujikuroi complex. GIDI TaxID=5127;
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NCBI_TaxID=84980;
[1]
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Bacteria; Proteobacteria; Delta
Desulfobulbaceae; Desulfotalea.
                                                                                                                                                                                                                         Voss T., Schulte J., Tudzynski B.,
"A new MPS transporter gene next t
cluster of Gibberella fujikuroi is
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Klenk H.-P.;
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Bauer M.,
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                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota;
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                                      Pfam; PF00083; Sugar tr; 1.
PRINTS; PR00171; SUGRTRNSPORT
                                                                                                                                                                                                             secretion.";
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            PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                 MEDLINE=21416226; PubMed=11525413;
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., Zibat A., Lombardot T., Becker I.,
H., Leuschner W.D., Gloeckner F.-O.,
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llarity 47.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               transporter (Fragment).
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Last annotation update)
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Mismatches
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I., Amann J
O., Lupas A
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n J., Gellner K.,
s A.N., Amann R.,
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RESULT 24
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                                                                                                                     InterPro; IPR010661; RVT_t
Pfam; PF00075; RnaseH; 1.
Pfam; PF00075; Rve; 1.
Pfam; PF000765; rve; 1.
Pfam; PF00077; RVT; 1.
Pfam; PF00078; RVT_t)
Pfam; PF06815; RVT_connect
Pfam; PF06817; RVT_thumb;
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InterPro;
InterPro;
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InterPro;
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MEDLINB=22972551; PubMed=14610175;

DOI=10.1128/JVI.77.23.12523-12534.2003;

Courgnaud V., Abela B., Pourrut X., Mpoudi-Ngole
Delaporte E., Peeters M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV). Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11723;
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                                                                               PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0008907; F:integrase activity; IEA.
GO; GO:0008923; F:peptidase activity; IEA.
GO; GO:0008233; F:ribonuclease H activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003944; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:000370; F:zinc ion binding; IEA.
GO; GO:0006270; F:zinc ion binding; IEA.
GO; GO:0006310; P:DNA recombination; IEA.
GO; GO:0006310; P:DNA recombination; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0006508; P:RNA-dependent DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pol protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6VG40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6VG40
                   Transferase.
NON_TER
                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                              Aspartyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
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                                                                                                                                                                                                                                               j IPR001037; Integrase C.

j IPR003308; Integrase Zn N.

j IPR003995; Peptidase A2.

j IPR003907; Pept_Aspartic.

j IPR001969; Pept_Asp AS.

j IPR00156; RMaseH.

j IPR001584; Rve.

j IPR001689; RVT connect.

j IPR010659; RVT thumb.

j IPR010661; RVT thumb.

j IPR010661; RVT thumb.
                                                                               PS00141; ASP_PROTEASE; 1.
PS50175; ASP_PROT_RETROV; 1.
                                                                protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QWLKSQKHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QWLKSREHT
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                                                                Hydrolase; Protease;
                                                                                                                                             connect; 1.
                                                                                                                            thumb;
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Last annotation updat
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Pred. No. 1.9e+02;
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  A1CFE26C001E6E35 CRC64
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                                                                RNA-directed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEA.
                                                                polymerase;
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Pfam; Pfam; Pfam; Pfam; InterPro; InterPro; InterPro;

RnaseH; rve; 1. RVP; 1.

PF00552; PF02022; PF00075; I

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Best Local
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_SIVS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Pol polyprotein [Contains: Protease (Retropepsin)
Reverse transcriptase/ribonuclease H (EC 2.7.7.49)
                                                                                                                                              InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                            EMBL; X14307; -; NOT_ANNOTATED_CDS HSSP; P04584; LMU2.
                                                                                                                                                                                                                                                entities re
or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 339:389-392(1989).
-!- FUNCTION: During replicative cycle of retroviruses, transcribed viral DNA is integrated into the host c
                                                                                                                                                                                   MEROPS; A02.00
HIV; X14307; P
                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                            between
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Hirsch V.M., Olmst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "An African primate lentivirus (SIVsm) closely related to HIV-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrase (IN)].
                                                                                                [nterPro;
                                                                                                            [nterPro;
                                                                                                                        InterPro;
                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 integrase-type zinc finger.
SIMILARITY: Contains 1 peptidase A2 domain.
SIMILARITY: Contains 1 reverse transcriptase domain.
SIMILARITY: Contains 1 RNase H domain.
                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation burpean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphomonoester
CATALYTIC ACTIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the viral integrase enzyme. RNase H
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                                                           | IPRO01037; | IPRO03308; | IPRO01995; | IPRO019967; | IPRO01969; | IPRO01584; | IPRO006477; | IPRO106679; | IPRO106679; | IPRO106679; | IPRO10661;
                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage sites that yield the mature proteins
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                                                                                                                                                                                                                                                           requires
                                                                                                                                                                                                                                                equires a license agreement (email to license@isb-sib.ch)
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                                                                                                                                                                                      POL$SMMH4
                                 001584; Rve.
000477; RVTse.
010659; RVT connect.
010661; RVT thumb.
; Integrase; 1.
; Integrase_Zn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVITY: N deoxynucleoside triphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=2786147; DOI=10.1038/339389a0; tead R.A., Murphey-Corb M., Purcell R.
                                                                                                                    ; Integrase_C.
; Integrase_Zn_N
; Peptidase_A2.
; Pept_Aspartic.
; Pept_Asp_AS.
pwageu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endonucleolytic cleavage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        irus (F236/smH4 isolate) (sooty mangabey).
Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; I
Pred. No. 3
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                                                                                                                                                                                                                                                              (See
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3.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity is as
                                                                                                                                                                                                                                                              . Usage by and for http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1017;
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t chromosome by
associated with
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C 3.1.26.4)
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RESULT
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Matches
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Pfam; PF06815; RVT_connect; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06815; RVT_thumb; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS50175; ASP_PROTEST; 1.
PROSITE; PS50878; RT_POT; 1.
PROSITE; PS50878; RT_POT; 1.
PROSITE; PS50876; ZF_INTEGRASE; 1.
PROSITE; PS50876; ZF_INTEGRASE; 1.
AIDS; Aspartyl protease; DNA integration; DNA recombination; PROGUCLEASE; Hydrolase; Metal-binding; Multifunctional enzyme; Endomuclease; Hydrolase; Metal-binding; Multifunctional enzyme; Transferase
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ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Virol. [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE .... SEQUENCE .... STRAIN=SUSSME543;
MEDLINE=97151152; PubMed=8995688;
Hirsch V., Adger-Johnson D.C., Camp
Hirsch V., Adger-Johnson D.C., Camp
               MEROPS, 60:00 GG,          MEROPS; A02.002; -...

GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0008207; F:integrase activity; IEA.

GO; GO:0004523; F:ribonuclease H activity; IEA.

GO; GO:0004523; F:RNA-binding; IEA.

GO; GO:0004523; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:00016740; F:transferase activity; IEA.

GO; GO:0016740; F:zinc ion binding; IEA.

GO; GO:0005310; P:DNA recombination; IEA.

GO; GO:0006310; P:DNA recombination; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

GO; GO:0006578; P:RNA-dependent DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elkins W.R., Montefior1 D.C.; molecularly cloned, pathogenic, neutralization-resistant simian manunodeficiency virus, SIVsmE543-3.";
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                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to p
EMBL; U72748; AAC56559.1; -.
PIR; T11560; T11560.
HSSP; P04584; 1MU2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P89154;
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                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SIVsmE543;
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                 (SEP-1996) to the EMBL/GenBank/DDBJ databases. ARITY: Belongs to peptidase family A2.
  IPR001037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71:1608-1620(1997).
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401
723
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115465 h
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Integrase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196
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Reverse transcri
RNase H.
Integrase-type.
By similarity.
S MW; 8D3DE0B85FC5
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Last sequence Last annoted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campbell
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3;
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Best Local S
Matches 8
                   Q7ZBR5;
Q7ZBR5;
01-JUN-2003
01-JUN-2003
01-MAR-2004
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Pfam;
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Pfam;
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                     Dehghani H., Puffer B.A., Doms R.W., Hirsch V.M.; "Unique pattern of convergent envelope evolution in simian immunodeficiency virus-infected rapid progressor macaques: association with CD4-independent usage of CCR5."; J. Virol. 77:6405-6418(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS00175; ASP_PROTEEPOV; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN
PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN
Aspartyl protease; Hydrolase; Polyprotein; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=22628501; PubMed=12741298;

DOI=10.1128/JVI.77.11.6405-6418.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV) Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-directed DNA polymerase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                   EMBL; AY221515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11723;
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                                    30; GO:0004190; F:aspartic-type endopeptidase activ

30; GO:0003677; F:DNA binding; IEA.

30; GO:0008907; F:integrase activity; IEA.

30; GO:0008233; F:peptidase activity; IEA.

30; GO:0004523; F:ribonuclease H activity; IEA.

30; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

30; GO:000374; F:RNA-directed DNA polymerase activity; IEA.

30; GO:0006740; F:riansferase activity; IEA.

30; GO:000670; F:zinc ion binding; IEA.

30; GO:000670; F:DNA recombination; IEA.

30; GO:0006310; P:DNA recombination; IEA.

30; GO:0006508; P:proteolysis and peptidolysis; IEA.

30; GO:000678; P:RNA-dependent DNA replication; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
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i; PF00077; RVP; 1.
i; PF00077; RVT; 1; 1.
i; PF06815; RVT_connect; 1
i; PF06817; RVT_thumb; 1.
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                                                                                                                                                                                                                                                                                                           P04584;
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8; Conserv
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IPR001037; Integrase_C.
IPR003308; Integrase_Zn_N.
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IPR005829;
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: RnaseH; 1.
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RVT_connect.
RVT_thumb.
Sug_transport
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Peptidase_A2.
Pept_Aspartic.
Pept_Asp_AS.
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                    peptidase
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Last annotation updat
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                                                                                                                                                                                                                                                                                            activity; IEA.
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                                              IEA
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OR FTT
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Best Local
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PROSITE;
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Pfam;
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DOI=10.1128/JVI.77.11.6405-6418.2003;
Dehghani H., Puffer B.A., Doms R.W., Hirsch V.M.;
"Unique pattern of convergent envelope evolution immunodeficiency virus-infected rapid progressor
                                                                                                                                                                                                                                                                                                                                                Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
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01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7ZBR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7ZBR7;
01-JUN-2003
                                                                                                                                                                                                                                      with CD4-independent usage of CCR5. J. Virol. 77:6405-6418(2003).
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
           InterPro;
                               GO; GO:0004190; F:aspartic-type endopeptidase activ:
GO; GO:0003677; F:INA binding; IEA.
GO; GO:0008907; F:integrase activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008233; F:RIBONUCLEASE H activity; IEA.
GO; GO:0004523; F:RNA-directed DNA polymerase activ.
GO; GO:0003723; F:RNA-directed DNA polymerase activ.
GO; GO:000374; F:RNA-directed DNA polymerase activ.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0015074; P:DNA integration; IEA.
GO; GO:0015074; P:DNA recombination; IEA.
GO; GO:0015074; P:DNA recombination; IEA.
GO; GO:0006510; P:DNA recombination; IEA.
GO; GO:0006518; P:proteoly8is and peptidoly8is; IEA.
GO; GO:0006598; P:proteoly8is and peptidoly8is; IEA.
GO; GO:0006598; P:RNA-dependent DNA replication; IEB
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PF06815; RVT_connect;
PF06817; RVT_thumb; 1.
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PF00075; RnaseH; 1.
PF00665; rve; 1.
PF00077; RVP; 1.
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IPR001037; Integrase_C.
IPR003308; Integrase_Zn_N
IPR001995; Peptidase_A2.
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ASP_PROT_RETROV; 1.
SUGAR_TRANSPORT_2; UNKNOWN_
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RVT_connect.
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Sug_transporter.
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Pept_Asp_AS.
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                sequence update) annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1019
                                                                                                                                                                                                                            family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB
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                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                              activity;
                                                                                                                                                                                       activity;
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                                 IEA.
                                                                                                                                                                                                                                                               macaques: association
                                                                                                                                                                                                                                                                            in simian
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                     JULT 29
L HV2D2
POL HV2D2
P15833;
01-APR-1990
                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Pol polyprotein (Contains: Protease (Retropepsin)
Reverse transcriptase/ribonuclease H (EC 2.7.7.49)
Integrase (IN)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
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           This
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                                                                                                                                                                                                               "A highly divergent HIV-2-related isolate."; Nature 342:948-950(1989).
                                                                                                                                                                                                                                    MEDLINE=90081881; PubMed=
Dietrich U., Adamski M.,
Ruebsamen-Waigmann H.;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Viruses; Retroid
NCBI_TaxID=11716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                               Human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                             - SIMILARITY: Belongs to t
SIMILARITY: Contains 1 ip
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                                                                                           preferably hydrophobi
PTM: Cleavage sites t
                                                                                                                                      phosphomonoester.
CATALYTIC ACTIVIT
                                                                                                                                                           the reverse transcriptase. CATALYTIC ACTIVITY: Endonucleolytic cleavage to
                                                                                                                                                                                FUNCTION: During replicative cycle of retroviruses, the reverse-transcribed viral DNA is integrated into the host chromosome by the viral integrase enzyme. RNAse H activity is associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n; PF00665; rve; 1.
n; PF00077; RVP; 1.
n; PF000078; RVT_; 1.
n; PF06815; RVT_connect; 1
n; PF06817; RVT_thumb; 1.
                                                                                                                                                                               the viral integrase enzyme.
           SWISS-PROT entry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00075; RnaseH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF02022;
                                                                                                                              DNA
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8; Conserv
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PS00175; ASP PROT RETROV; 1.
PS00217; SUGAR TRANSPORT 2; UNKNOWN 1.
PROTEASE; Hydrolase; Protease; RNA-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGPKLROWPLSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGPTLROWLKSRE
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1019 AA;
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                                                                                                                   ACTIVITY:
                                                                                                                                        ACTIVITY: N
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                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                              PubMed=2594088; DO
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115340
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RVT_connect.
RVT_thumb.
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61.5%;
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Pept_Asp_AS.
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es; Retroviridae; Lenti
                                                                                                                  Endopeptidase
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           copyright.
                              o the retroviruses I
1 integrase-type zir
1 peptidase A2 domai
1 reverse transcript
1 RNase H domain.
                                                                                                                                       deoxynucleoside
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Pred. No. 3.2e+02
2; Mismatches
ght. It is produced through a collaboration
Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                               DOI=10.1038/342948a0; ., Seipp A., Kuehnel H
                                transcriptase domain.
                                                                                              the mature proteins
                                                                                                                   for which
                                                     domain
                                                               zinc
                                                                                                                                       triphosphate
                                                                          Po1
                                                                                                                                                                                                                                                                                                               D205,7)
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                                                              l polyprotein
finger.
                                                                                                                   the
                                           domain
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RESULT 30
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Matches
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InterPro; IPR001584; Rve.
InterPro; IPR010659; RVT_con
InterPro; IPR010661; RVT_thun
InterPro; IPR000477; RVTse.
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ZN FING
ACT SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF06817; RVT_thumb; 1.

PROSITE; PS00175; ASP_PROT_EATROV; 1.

PROSITE; PS00141; ASP_PROTEASE; 1.

PROSITE; PS50879; RNASE H; 1.

PROSITE; PS50878; RT_POL; 1.

PROSITE; PS50876; ZT_INTEGRASE; 1.

PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
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                       STRAIN=CMCP6;
Rhee J.H., Kim S.Y.,
Choy H.E.;
                                                                                                                                                                                                                                                                                                              01.MAR-2003 (TrEMBLrel. 23, Created)
01.MAR-2003 (TrEMBLrel. 23, Last sequence up
01.MAR-2004 (TrEMBLrel. 26, Last annotation
ATP-dependent exoDNAse, alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8D674
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Pfam;
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                                                                                                                                                                                                                                                         Vibrio vulnificus
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InterPro; IPR009007;
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                Vibrionaceae; V
NCBI_TaxID=672;
                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                         OrderedLocusNames=VV20663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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"Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  m; PF00552; Integrase; 1.
m; PF02022; Integrase Zn; 1.
m; PF00075; RnaseH; 1.
m; PF00065; rve; 1.
m; PF00077; RVP; 1.
m; PF00078; RVT; 1.
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A02.002; -.
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IPRO01037; Integrase_C.
Integrase_Zn_N.
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248
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1058
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                                                                                                                                                                                                   Vibrio.
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437
759
806
130
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RVT connect.
+humb.
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; Pept_Asp_AS.
; Pept_Aspartic.
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66.7%;
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                                                                                                                                                                                                                              Gammaproteobacteria; Vibrionales;
of Vibrio vulnificus
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RNase H.
Integrase-type.
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                                                     J.J.,
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                                                     Ү.Н.,
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RESULT
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Matches 8
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Q88L07;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horn M., Collingro A., Schmitz-Esser S., Beier Fartmann B., Brandt P., Nyakatura G.J., Droege Rattei T., Newes H.-W., Wagner M., "Genome sequence of an amoeba symbiont and its the evolutionary history of chlamydiae."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ EMBL; BX908798; CAF23333.1; -. InterPro; IPR008938; ARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6MDL6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypoturetitus F---
OrderedLocusNames.pc0609;
Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
Parachlamydia sp. (chlamydiales; Parachlamydiaceae; Parachlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004
05-JUL-2004
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                                                                                                                                       Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T.,
Martins dos Santos V.A.P., Fouts D.E.,
                                                          SEQUENCE FROM N.A.
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                                                                                             NCBI_TaxID=160488;
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                                                                                                                      eudomonadaceae; Pseudomonas.
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8; Conserv
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Pred. No. 2e+02;
3; Mismatches
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l; Mismatches
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                                MEDINE=97352177; PubMed=9208457; DOI=10.1023/A:1007991508159; Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J., Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.; "A random DNA sequencing, computer-based approach for the gene "A random DNA sequencing, computer-based approach for the gene of a gene map of molluscum contagiosum virus."; Virus Genes 14:73-80(1997).

EMBL; U60315; AAC55140.1; -.

EMBL; U60894; AAB57932.1; -.
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Q98183; O12598; O12879;
01-FEB-1997 (TrEMBLrel 02, Created)
01-FEB-1997 (TREMBLrel 02, Last sequence update)
05-JUL-2004 (TrEMBLrel 27, Last annotation updat
MC012L (Hypothetical protein B-M,N,L.2).
Name=MC012L; Synonyms=B-M,N,L.2;
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Science 2
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                                                                                                                                                                                  "Sequence analysis of a includes the gene encodiunique organization.";
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Martin-Gallardo A.,
Varas A.J., Collado
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TIGR; PP2130; -.
 Hypothetical
SEQUENCE 6:
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MEDLINE=96325459;
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                        PIR; T30614;
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InterPro; IPR008258; SLT.
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ilarity 56.2%;
Conservative
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A., Moratilla M.,
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ugert J.J., Sisler
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Pred. No. 2.
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Lopez-Estebaranz J.
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Coretjens P.I.;
Coretjens P.I.;
Thesis (1993), BioChemistry, Leiden University.
EMBL; 725772; CAA81034.1; -..
GO; G0:0005215; Fitransporter activity; IEA.
GO; G0:0006810; P:transport; IEA.
InterPro; IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
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Q8VLU9;
01-MAR-2002
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Bacteria; Proteobacteria;
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HSSP; P09152; 1Q16
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_TaxID=77133;
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STRAIN=cv. Monatol;
MEDLINE=93344519; PubMed=8343606;
Flieger K., Oelmueller R., Herrmann R.G.;
                                                              Spinacia oleracea (Spinach).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledona; core eudicota; Caryophyllales; Amaranthaceae; Spinacia.
                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
Photosystem I reaction center subunit XI, c
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Q41385;
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Bauer M., Zibat A., Lombardot T., Becl
Teeling H., Leuschner W.D., Gloeckner
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PubMed=15305914;
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NCBI_TaxID=84980;
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Bacteria, Proteobacteria, Deltaproteobacteria, Desulfobacterales,
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30; GO:0016021; C:integral to membra
InterPro; IPR0C4254; HJYIII_related
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Best Local S
Matches 9
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Q87115;
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01-NOV-1996
01-MAR-2004
                EMBL; U04018; AAA21512.1; -. GO:0004190; F:aspartic-type endopeptidase activity; GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA-directed DNA polymerase activity; GO; GO:00016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006278; P:protecolysis and peptidolysis; IEA.
GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
InterPro; IPR001995; Peptidase_A2.
InterPro; IPR001995; Peptidase_A2.
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TRANSIT
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
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-i- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast thylakoid membrane (Probable).
-i- SIMILARITY: Belongs to the psaL family.
                                                                                                                                                                                                                           STRAINSIVEGRSABD37;
MEDLINE9428785; PubMed=8026477;
MEDLINE9428785; PubMed=8026477;
Jin M.J., Hui H., Robertson D.L., Muller M.C., Barre-Sinoussi F.,
Hirsch V.M., Allan J.S., Shaw G.M., Sharp P.M., Hahn B.H.;
"Mosaic genome structure of simian immunodeficiency virus from wer
African green monkeys";
African green monkeys ";
EMBO J. 13:2935-2947(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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fam; PF02605; PsaL;
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1 47 Chloroplast
48 216 Photosystem
48 134 Stromal (Pot
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9; Conserv
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; Peptidase_A2.
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PYRF_GLOVI
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Best Local S
Matches 8
                                                                                                                           PYRF GLOVI STANDARD; PRT; 237 AA.

Q7NKZ2;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Orotidine 5' phosphate decarboxylase (EC 4.1.1.23)
(OMPDCase) (OMPdecase).
Name=pyrF; OrderedLoccusNames=gl11658;
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Pfam; PF00078; RVT_1; 1.

PROSITE; PS50175; ĀSP PROT RETROV; 1.

RNA-directed DNA polymerase; Transfer.

NON_TER 1 1 1

NON_TER 217 217

SEQUENCE 217 AA; 24503 MW; C1162E
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Initiation of chromosome replication.
Name-dnaD; OrderedLocusNames=BH1697;
BB261111.
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InterPro; IPR009058; Wing_hlx_DNA_bnd.
Pfam; PF04271; DnaD; 1.
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Bacteria; Firmicute
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STRAIN-PCC
                     SEQUENCE FROM N.A.
                                                                                         Bacteria; Cyanobacteria;
                                                                                                               Gloeobacter violaceus
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                                                              NCBI_TaxID=33072;
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8; Conserv
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233 AA;
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Pred. No. 89;
3; Mismatches
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                                                                                                                                   MEDLINE-21681679; PubMed=11823852; DOI=10.1038/415497a; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Rature 415:497-502(2002).

EMBL; AL646078; CAD17614.1; -.

EMBL; AL646078; CAD17614.1; -.

Complete proteome; Hypothetical protein; Plasmid.

Complete proteome; Hypothetical protein; Plasmid.
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Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa (
Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of Gloebacter violaceus PCC 7421,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Last annotat Hypothetical protein RSp0463. Name=RS00951; OrderedLocusNames=RSp0463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
Burkholderiaceae; Ralston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid megaplasmid
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PIR; S07740; S07740.

InterPro; IPR010979; Ribosomal_H2TH.

InterPro; IPR010979; Ribosomal_S13.

Pfam; PF00416; Ribosomal_S13; I.

PROSITE; PS00646; RIBOSOMAL_S13_1; FALSE_NEG.

PROSITE; PS0159; RIBOSOMAL_S13_2; 1.

PROSITE; PS50159; RIBOSOMAL_S13_2; 1.

Hypothetical protein; Mitochondrion.

SEQUENCE 241 AA; 28648 MW; 7410BAA96B37FA8F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. )
01-APR-1990 (Rel. )
25-OCT-2004 (Rel. 4
Hypothetical 28.6 k
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                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UIL-2004 (Rel. 44, Last annotation update)
Putative riboflavin biosynthesis protein ribr [Includes: Rilkinase (EC 2.7.1.26) (Flavokinase); FM ademylyltransferase (EC 2.7.7.2) (FAD pyrophosphorylase) (FAD synthetase)].
Name=ribr; OrderedLocusNames=MPN158; ORFNames=MP673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http:\bar{//www}.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=90174913; PubMed=2308823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129
                                                                                                         Mycoplasma pneumoniae Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                    RIBF_MYCPN
P75587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venuti S.E., Cummings D.J.;
"Nucleotide sequence of the mitochondrial
Nucleic Acids Res. 18:173-180(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paramecium
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                                                                         NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the ribosomal protein S13P family.
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14, Last sequence update)
45, Last annotation update)
kDa protein (ORF8).
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41.2%;
                                                                                                         Mollicutes; Mycoplasmataceae; Mycoplasma
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Pred. No. 93;
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01-MAR-2002
01-MAR-2002
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NON TER
SEQUENCE
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TIGRPAMS; TIGR00083; TibF; 1.
Complete proteome; FAD; FMN; Multifunctional enzyme;
Nucleotidyltransferase; Transferase.
SEQUENCE 269 AA; 30435 MW; 2E63D7BC7A8FA12D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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Nucleic Acids Res. 24:4420-4449(1996).
-I- CATALYTIC ACTIVITY: ATP + riboflavin = ADP + FMN
-I- CATALYTIC ACTIVITY: ATP + FMN = diphosphate + FAI
                                                                                                                                                                                                                                              GO; GO:0003723; F:RNA binding; IEA.
GO; GO:000364; F:RNA-directed DNA polymerase act
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; P:RNA-dependent DNA replication;
Pfam; PF06815; RVT_1; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Diamond T.L., Lee K.Y., Kimata J.T., Kim B.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ
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InterPro; IPR0026O6; FAD_Synth.
Pfam; PP0.687; FAD_Synth; 1.
Pfam; PP0.6574; Flavokinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                       RNA-directed DNA polymerase; Transferase
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P04584; 1MU2.
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                                              Similarity
8; Conserv
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340 AA;
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39547 MW;
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66.7%;
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(See http://www.isb-sib.ch/announce/
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1e+02;
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SEQUENCE FROM N.A.

Diamond T.L., Lee K.Y., Kimata J.T., Kim B.;

A Diamond T.L., Lee K.Y., Kimata J.T., Kim B.;

Bubmitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF458219; AAL59619:1; -.

REMBL, AF458219; AAL59619:1; -.

REMBL, AF458219; AAL59619:1; -.

REGO; GO:0003733; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000364; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000364; F:RNA-dependent DNA replication; IEA.

REGO; GO:0006278; F:RNA-dependent DNA replication; IEA.

REGO; GO:0006278; RVT_1; 1.

REGO; GO:0006278; RVT_Connect; 1.

REGO; GO:006278; RVT_thumb; 1.

REGO; GO:006278;
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C QBUN04;
C O1-MAR-2002 (TrEMBLrel. 20, Created)
C O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
C O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Reverse transcriptase (Fragment).
Reverse transcriptase (Fragment).
Vanmespol;
Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
(NCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                      Query Match 44.3%; Score 43; DB 2; Length 34(Best Local Similarity 66.7%; Pred. No. 1.4e+02; Matches 8; Conservative 1; Mismatches 3; Indels
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                                                                                            Thrombopoietin receptor-binding/activating peptide(s) and pep mimetic(s) - useful in treatment of haematological disorders, thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW09460 standard;
The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mum. compound (especially if modified, see features table) can be used for
                                                                                                                                                                                        Dower WJ,
                                                                                                                                                                                                                                                                                                                                      05-JUN-1996;
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LC, Schatz
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95US-00485301.
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Schatz PJ, Wagstr
                                                                                                                                                                                                                                                                                                                                                                                                                 selected from hydroxy, lower alkoxy, and -NR3R4, where and R4 are independently selected from hydrogen and log alkyl, and where the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide forming a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRC(0)R; -NRC(0)OR; -NRS(0)2R; -NHC(0)NHR; succinimide; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Preferably linkages are selected from: -
CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6
; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Preferably C-terminus is -C(0)R2 where R2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Preferably N-terminus is selected from:
NRC(0)R; -NRC(0)OR; -NRS(0)2R; -NHC(0)NHR; succ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lower alkyl"
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m CR, Wrighton
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iton NC;
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Adm72479 TPO mimet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                            The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                             Sequence 18
                                                                                                                                                                                                Thrombopoietin receptor-binding/activating peptide(s) and pep mimetic(s) - useful in treatment of haematological disorders,
                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
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bone marrow t
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                                                                                                                                                             Disclosure; Page 27; 106pp; English.
                                                                                                                                                                                     thrombocytopenia resulting
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LC, Schatz
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PJ, Wagstr
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                                                                                                                                                                                                                                                                                 thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                  The present peptide, which binds the thrombopoietin receptor (TR), can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, et
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                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                        thrombopoietin agonist, preferabl thrombocytopaenia resulting from
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             Thrombopoietin receptor binding peptide.
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                                                                                       AAW33027 standard; peptide; 18
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95US-00485301.
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Schatz PJ, Wagstrom CR, Wrighton NC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signal transduction; receptor activation; cell culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  or to maintain cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
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07-JUN-1996;
                         19-DEC-1996.
                                                                                                                                                                     Thrombopoietin receptor binding peptide.
                                                                                                                                                                                               11-MAR-1998
                                                                                                                                                                                                                                                   AAW36652 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mattheakis
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                                                  WO9640750-A1
                                                                            Synthetic
                                                                                                   signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 89; 106pp; English.
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LC, Schat:
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                                                                                                                                                                                                                                                                                                                                                                    100.0%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                (first entry)
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95US-00485301.
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 96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombocytopenia resulting from chemotherapy, etc
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Schatz PJ, Wagstrom CR,
                                                                                                                                                                                                                                                 peptide; 18
                                                                                                      receptor
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                                                                                                   activation; cell
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rom CR, Wrighton NC;
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ches 0;
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Best Local S
Matches 18
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07-JUN-1995;
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Mattheakis LC, Schatz PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; autoimmune disease; cytostatic; anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17026 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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                                                                                                                                                                                                   23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
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endothelial growth factor; matrix metalloproteinase; asthma;
is; pharmaceutical.
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99US-00428082.
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Wrighton NC;
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Activating thrombopoietin receptors in cells, used to treat

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fc domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P3, and P4 = are each independently segmences of charmacologically part of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the pro
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07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human thrombopoietin receptor (TPO-R) activator peptide #54.
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                                                                         WPI; 2001-564142/63
                                                                                                                                                                                               Balasubramanian
                                                                                                                                                                                                                                    Dower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in vitro expansion; megakaryocyte;
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                                                                                                                                                                                                                                                                                                                  (GLAX ) GLAXO
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thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.

128pp; English

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RESULT 8
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Best Local (
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haemostatic; thrombocytopenia; chemotherapy; radiation therapy; RLISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 AA;
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                                 WPI; 2001-564142/63
                                                                                                                     Balasubramanian
                                                                                                                                                    Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2000; 2000US-00516704.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human thrombopoietin receptor (TPO-R) activator peptide #10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vitro
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              megakaryocyte;
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receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                  transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO
                                                                                                                                                                                                                                                                                                                                                                                                                                of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences
bind to an
                                                                                                                                                                                                                                                                                                                                                                         hydrophilic polymers. The methods are used to treat thrombocytopenia as that due to chemotherapy, radiation therapy or bone-marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 67-68; 128pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptides and peptide mimetics attached to hydrophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU25815-AAU26049 represent peptides and peptide mimetics that id activate the human thrombopoietin receptor (TPO-R). Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contacting cells
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such
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Query Match
Best Local
                                    Matches
             1 SIEGPTLREWLTSRTPHS 18
                                             Similarity
SIEGPTLREWLTSRTPHS 18
                                     Conservative
                                             100.0%;
                                    0;
                                             Score 98;
Pred. No.
                                      Mismatches
                                     1.1e-08;
hes 0;
                                                        DB 4;
                                                      Length 18
                                      Indels
                                      0,
                                      Gaps
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0

Sequence 18

AA;

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RESULT 9
AAU25871
ID AAU2
Human thrombopoietin receptor
                            17-DEC-2001
                                                     AAU25871;
                                                                               AAU25871 standard;
                          (first entry)
                                                                             peptide;
                                                                               18
  (TPO-R)
 activator peptide #57.
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Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; tissue homogenate; fluorescence-activated cell enzyme-linked immunosorbent assay; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene in situ staining; biological fluid; tivated cell sorting; Western blotting;

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Homo sapiens
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26-JUN-2001.
                         US6251864-B1
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07-JUN-1995;
                                01-MAR-2000; 2000US-00516704
 95US-00478128
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15-AUG-1996;	07-JUN-1996;	1966T-NON-10
96US-00699027.	96WO-US009623.	95US-00485301.

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(GLAX )
 GLAXO GROUP LTD
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Balasubramanian
Yin Q;
WPI; 2001-564142/63
                            Dower
                            ξ
                    Barrett
anian P,
                            RW,
                     Wagstrom
                     Cwirla SE
Jstrom CR,
                            SE,
                      , Gates
Hendren
                     RY,
                     Schatz PJ
Deprince
                 2 PJ;
'9 RB,
                      Podduturi
                      S
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hydrophilic polymers. The methods are used to treat thrombocytopenia as that due to chemotherapy, radiation therapy or bone-marrow

such

sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoieth receptor (TPO-R). Methods of activating thrombopoiethin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to

Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting c with peptides and peptide mimetics attached to hydrophilic polymers.

contacting cells

20;

128pp; English.

transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines

Query Match Best Local

Similarity

100.0%;

Length 18

Sequence 18

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                                                                                                                                                                                                                                     Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TNF-alpha inhibitor; interleukin 1 peptide; EMP; VEGF antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; sleep disorder; neurological degenerative disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB72912 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                          TPO mimetic peptide SEQ ID NO:82.
                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2002
                                          03-MAY-2000; 2000US-00563286
                                                                                                                                   WO200183525-A2
                                                                        02-MAY-2001; 2001WO-US014310
                                                                                                      08-NOV-2001
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                          thrombocytopaenia; metastatic
               (AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
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Pred. No. 1.1e-08;
                                                                                                                                                                                                                          tumour; systemic
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                                                                                                                                                                                                                           lupus erythematosus
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Heavner GA,

Knight DM,

Scallon BJ,

Ghrayeb J;

(CENZ) CENTOCOR INC.

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RESULT 11
ADJ73064
ID ADJ73
XX
AC ADJ73
XX
DT 06-MA
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DT 06-MA
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mimet
KW mimet
KW cardi
KW inmuni
KW inmuni
KW inmuni
KW inmuni
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OS Synth
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OS Synth
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PD 16-OC
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PF 24-MI
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PF 24-MI
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PF 24-MI
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PR 29-MI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a vehicle-peptide molecule (I) or its cultimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antitheumatic, antiarthritic, antidiabetic, ophthalmological, can improve activities. (I) can be used as therapeutic or cytostatic agent as well as for screening purposes. (I) is useful for city protein of interest, for identifying normal or abnormal proteins of interest in a biological sample. Additionally, (I) is useful cy proteins of interest in a biological sample. Additionally, (I) is useful cor interest in a biological sample. Additionally, (I) is useful cor rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, cinfertility, and neurological degenerative diseases, tumour growth, cancer, commettic compounds are useful for treating disorders characterised by low compounds are useful for treating conditions that involve an existing megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected meg
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 39; Page 44; 176pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ73064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ73064 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of
                                                                                                                                                                       24-MAR-2003; 2003WO-US009139.
                                                                                                                                                                                                                                                                        WO2003084477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPO mimetic peptide sequence SeqID 518.
                                                                                                                                                                                                                          16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                             mmunomodulator; cardiant; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
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                                                                                                                          2002US-0368791P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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WPI; 2003-804237/75

New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.

Disclosure;

SEQ ID NO

518;

97pp; English

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RESULT 12
ADJ52699
ID ADJ52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody CC fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which CC testif comprises at least one human framework region and at least one CC tiself comprises at least one human framework region and at least one CC ligand binding region (LBR). The present invention describes human CC mimetibodies, including modified immunoglobulins and cleavage products CC that can be useful in gene therapy and the generation of transgenic CC plants and animals. Furthermore, the CDR mimetibody is useful for CC preparing compositions for modulating, treating or reducing the symptoms CC of immune, cardiovascular, infectious, malignant and/or neurologic CC diseases, as well as ansemia. Accordingly, they exhibit immunomodulator, CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This CC peptide sequence is a TPO mimetic peptide sequence used to make a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                              CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant; hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mimetibody of the
                                                                                                                                                                                                                                                                                                                                                  arrhythmia; hypertension; heart failure; neurodegenerative;
multiple sclerosis; dementia; Alzheimer's disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CH1 deleted mimetibody-related peptide SeqID518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ52699 standard; peptide; 18
                 WPI; 2004-082870/08
                                                Heavner GA,
Kutoloski KA;
                                                                                                                                  28-JUN-2002; 2002US-0392431P
                                                                                                                                                               27-JUN-2003; 2003WO-US020347
                                                                                                                                                                                                  08-JAN-2004
                                                                                                                                                                                                                                 WO2004002417-A2
                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                  cancerous condition; infectious disease; bacterial
                                                                                                 (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIEGPTLREWLTSRTPHS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIEGPTLREWLTSRTPHS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                Knight DM,
                                                                                                                                                                                                                                                                                                                  fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                Ghrayeb J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                   Scallon BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                 Nesspor TC;
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which encode them), compositions, methods and uses. The invention way weight for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclose sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, demential conditions, or infectious diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may leading the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                 invention relates to CH1 deleted mimetibodies (and the DNA sequences nencode them), compositions, methods and uses. The invention may be
                                                 during the creation of a mimetibody of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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     AΑ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          518; 129pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                              the disclosed
                                                                                   which may be
                                                                                                                                                            dementia
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Best Loc Matches Query Match Local 18; Similarity SIEGPTLREWLTSRTPHS 18 SIEGPTLREWLTSRTPHS 100.0%; ilarity 100.0%; Conservative 0 18 0, Score 98; DB 8; Pred. No. 1.1e-08; Mismatches Length 18 Indels 0; Gaps

0,

0;

Gaps

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밁 5

RESULT 13
ADJ51660
ID ADJ51
XX
ADJ51
AC ADJ51
XX
ADJ7
DT 06-MA
XX
CH1 d
XX
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XX CH1 deleted mimetibody; osteopathic; cardiovascular-Gen; dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gymaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TWF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gymaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; oncological disorder; neurological disorder; nutritional disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder; ADJ51660 standard; peptide; disorder; mimetibody-related peptide SeqID518 (first entry) pulmonary disorder.

Unidentified

Synthetic

08-JAN-2004.

30-JUN-2003; 2003WO-US020495

28-JUN-2002; 19-SEP-2002; 2002US-0392431P 2002US-0412144P

(CENZ) CENTOCOR INC

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RESULT 14
ABP5163
ID ABP51
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cc cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
cc gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
cc immunomodulator, antiallergic, muscular-Gen, cytostatic,
cc immunomodulator, neuroleptic, ophthalmological, nephrotropic or
cc respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
cc modulator or cytokine-agonist. The methods and compositions of the
creatment of diseases or conditions associated with aberrant expression
cc ractivity of the CH1 deleted mimetibody, such as abone or joint,
cc cardiovascular, dental or oral, dermatological, ear, nose or throat,
cc obstetric, haematologic, immunological, allergic, infectious,
cc musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
cc gediatric, psychiatric, renal or pulmonary disorders. The present
cc mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; SEQ ID NO 518; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-082872/08.
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                                                                                                                   05-DEC-2000; 2000US-0251448P
04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP51693 standard; peptide; 18 AA
                                                                                                                                                                                                                                    05-DEC-2001; 2001WO-US047656
                                                                                                                                                                                                                                                                                                                                                        WO200246238-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPO mimetic
                                                                 (ALEX-) ALEXION PHARM INC
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Pred. No. 1.1e-08
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Cleast a portion of the complementary determining region (CDR) are commetted such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has carbinated to fine proliferation, differentiation and maturation of chaematopoietic cells, and a stimulator of proliferation, differentiation and maturation of commegakaryocytes or megakaryocytes, which results in increased platelet corpoduction. (I) with a region where (I) is contacted with corpoduction. (I) with a region where (I) is contacted with corpoduction. (I) with a region where (I) is contacted with corpoduction of CDR is replaced with an EPO mimetic, or which has one or more of its CDRs fused to an EPO mimetic, is useful for increasing the corpoduction of red blood cells, where (I) is contacted with haematopoietic stem cells or their progenitors. (I) is useful for diagnostics or therapeutics, in cell jsolation strategies, and for treating pattents confered with increasing the confered with a cell isolation strategies, and for treating pattents affering from deficiency in cell populations caused by disease, confered with an EPO mimetic, is useful for diagnostics or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Fig 5; 113pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes an immunoglobin molecule or its fragment comprising a region where amino acid residues corresponding to at
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N
TIEGPTLRQWLAARAP
               SIEGPTLREWLTSRTP
                               Conservative
                                     68.48;
               16
                               ω
                                      Score 67; DB 5;
Pred. No. 0.0011;
                               Mismatches
                                2
                                              Length 18;
                                Indels
                                0;
                                Gaps
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05-DEC-2000; 2000US-0251448P.
04-MAY-2001; 2001US-0288889P.
29-MAY-2001; 2001US-0294068P.
                                                                                                                                  Homo sapiens.
Synthetic.
                                                                                                                                                                  TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
                                                                                                                                                                                                                                      01-OCT-2002
                                                                                                                                                                                                                                                                                ABP51691 standard; peptide; 18
                                                                                                                                                                                                               TPO mimetic peptide SEQ ID NO:45.
                                                                                                                                                                                                                                                           ABP51691;
                                                                 05-DEC-2001; 2001WO-US047656.
                                                                                        13-JUN-2002
                                                                                                             WO200246238-A2
(ALEX-) ALEXION PHARM INC
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Bowdish KS,

Barbas-Frederickson

Renshaw

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RESULT 16
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Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or more of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with haematopoietic stem cells or their progenitors. (I) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, and disorders or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoletin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPC) or thrombopoietin (TPC) mimetic, that is flanked with proline at its carboxy terminus. (1) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haemotopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determining region are thrombopoetin mimetic.
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                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin;
erythropoietin;
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                                                                                  02-DEC-2002; 2002US-00307724
                                                                                                                                      17-NOV-2003; 2003WO-US036894.
                                                                                                                                                                                              17-JUN-2004
                                                                                                                                                                                                                                                      WO2004050017-A2
                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPO mimetic peptide with random
                                                                                                                                                                                                                                                                                                                                                               immunotherapy;
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                          ALEXION
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                                                                                                                                                                                                                                                                                                                                                                  thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                          complementarity determining region; CDR; peptide mimetic; BPO; thrombopoietin; TPO; immunosuppressive;
                          PHARM
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Pred. No. 0.0011;
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Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO mimetic peptide with random flanking residues SEQ ID NO:49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ16629 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 45; 107pp; English.
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                                                                                                                                                                                                                                                                      WPI; 2004-460973/43
                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-2002; 2002US-00307724
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New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.

are replaced with

EPO mimetic

ADQ16630.

The invention relates to a novel immunoglobulin molecule or comprising a region where amino acid residues corresponding

its fragment to at least (

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Matches 11
                   The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that binds to the c-mpl (mpl) receptor, and which stimulates the production of platelets and/or the production of platelet precursors, is new Further disclosed is a composition of platelet precursors, is new Further and a pharmaceutical composition comprising (II) and a carrier. The pharmaceutical composition of the invention is useful for treating thrombocytopaenia in an animal, and for increasing megakaryocytes or platelets in a patient. The TMP of the invention is useful for treating conditions involving a megakaryocyte and/or platelet deficiency, e.g. disease conditions involving thrombocytopaenia such as aplastic anaemia, autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production platelet precursors, useful for treating thrombocytopenia.
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10-OCT-2002; 2002US-00269806.
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                                                                                                                                                                                                                                                                                                                                                                                                                  6; Page 83; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sitney KC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.4%;
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Pred. No.
   Hughe's syndrome and
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Matches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                       platelet
                                                                                                                                                   Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production
                                                                                                                                                                                                            WPI; 2003-403101/38
                                                                                                                                                                                                                                        Min H,
                                                                                                                                                                                                                                                                                              11-OCT-2001;
10-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemostatic; antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin mimetic peptide TMP12, seq id
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                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ransmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   upoid thrombocytopaenia.
                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c-mpl receptor; platelet precursor; megakaryocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEGPTLREWLTSR-TPHS
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                                                                                                                                       precursors,
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2002US-00269806
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72.2%;
                                                                                                                                       useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive; platelet;
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Pred. No. 0.0017;
1; Mismatches
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                                                                                                                                       thrombocytopenia.
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The invention relates to a thrombopoietin minetic peptide (TMP) (I) binds to the c-mpl (mpl) receptor, and which stimulates the product platelets and/or the production of platelet precursors, is new. Ful disclosed is a composition of matter (II) that binds to an mpl rece and a pharmaceutical composition comprising (II) and a carrier. The pharmaceutical composition is useful for treating pharmaceutical composition of the invention is useful for treating

Disclosure; SEQ ID

NO 57;

126pp; English

peptide

production

Of.

Further (I) that

receptor,

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RESULT 20
ABP51670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conditions involving a megakaryocyte and/or platelet deficiency, e.g. disease conditions involving thrombocytopaenia such as aplastic anaemia, autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, autoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for megakaryocytes and its derived cells. The compounds demonstrate an ingroved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thrombopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vitro, the production of platelets and/or and in vitro, the production of platelets and/or and in vitro, the production of platelets and/or and in vitro, the production of platelets and/or and in vitro, the production of platelet precursors. Further, certain of the compounds also exhibit superior therapeutic properties, such as improved plasma half-life, biological activity and in vivo circulation time. The current sequence
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Best Local S
Matches 13
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04-MAY-2001;
29-MAY-2001;
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                                                                                                                         A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoletin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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; 2001US-0288889P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nephrotropic; haematopoietic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
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72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region;
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Claim 19;

Page

6; 113pp;

English.

The present least a

comprising a region where it a portion of the complem

invention describes an immunoglobin molecule or its ing a region where amino acid residues corresponding tion of the complementary determining region (CDR) are fused with biologically active peptides e.g. a pepti

e.g. a peptide

fragment to at

with a peptide mimetic selected from an erythropoletin (BPO) mimetic attrombopoletin (TPO) mimetic. An immunoslobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoslobulin molecule is useful for diagnosing

The invention relates to a novel immunoglobulin molecule or comprising a region where amino acid residues corresponding portion of a two complementarity determining regions (CDRs)

to at least a are replaced

mimetic

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Disclosure; SEQ ID

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107pp; English

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thrombopoetin mimetic.

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RESULT 21
ADQ16585
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XX ADQ16
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                                                                                                                                                                                                                                                                                      New immunoglobulin molecule comprising a region, where complementarity determining regions (CDRs) are replaced or a TPO mimetic, useful for treating thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHARM
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The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has attimulator of proliferation, differentiation and maturation of a stimulator of proliferation, differentiation and maturation of the stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with production. (I) with a region where amino acid residues corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or more of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with has one or the contacted blood cells, where (I) is useful for diagnostics or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel immunogen molecule comprising a region in which amino acic residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin ot thrombopoetin mimetic.
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
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The present invention describes an immunoglobin molecule or its fragment (C (I) comprising a region where amino acid residues corresponding to at CC least a portion of the complementary determining region (CDR) are CC replaced or fused with biologically active peptides e.g. a peptide CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, C that is flanked with proline at its carboxy terminus. (I) has can be used as a stimulator of proliferation, differentiation and maturation of C a stimulator cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic colls, and a stimulator of haematopoietic colls, and stimulator of haematopoietic cells, and stimulator of haematopoietic colls, colls a stimulator of haematopoietic cells, and stimulator of haematopoietic colls colls colls a stimulator of haematopoietic colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls colls c
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Matches 11
The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoietis (I) is useful for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
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Matches 11
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The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with
                                                                                                                                                                                                                                      A novel immunogen molecule comprising a region in which amino active residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin otherombopoetin mimetic.
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
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                                                                                                                                                                                                        Claim
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antianaemic;
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The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a stimulator of haematopoietic cells, and a
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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04-MAY-2001; 2001US-0288889P.
29-MAY-2001; 2001US-0294068P.
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RESULT 27
ABP51690
ID ABP51
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                                                                                                                                       A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO mimetic peptide SEQ ID NO:43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP51690;
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                                                                                                     Claim
                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                    Bowdish
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                                                                                                                               thrombopoetin
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                                                                                                                                                                                                                                                              (ALEX-)
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setatic; nephrotropic; haematopoietic cell; h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPO; thrombopoietin; erythropoietin; antibody; CDR region;
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nilarity 73.3%;
Conservative
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                                                                                                   5; 113pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell; haematopoiesis
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replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mir that is flanked with proline at its carboxy terminus. (I) has The present invention describes an immunoglobin molecule or its () comprising a region where amino acid residues corresponding least a portion of the complementary determining region (CDR) ar replaced or fused with biologically active peptides e.g. a peptireplaced or fused with biologically active peptides e.g. a pepti

nephrotropic activities,

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RESULT 28
ABP51675
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                   A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoletin (EPO) or thrombopoletin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has
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                                                                                                                                                                                                         Example 4; Page 55; 113pp; English.
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73.3%;
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RESULT 29
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Best Local
The invention relates to a novel immunoglobulin molecule or its frag comprising a region where amino acid residues corresponding to at le portion of a two complementarity determining regions (CDRs) are repl with a peptide mimetic selected from an erythropoietin (EPO) mimetic a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a portion of CDR is replaced with an EPO mimetic, or which has one or more of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with haematopoietic stem cells or their progenitors. (I) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, disorders or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoiesic cells, and a stimulator of haematopoiesis. (I) is useful for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet promegakaryocytes, which results in increased platelet promegakaryocytes.
                                                                                                                                                                                        New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with or a TPO mimetic, useful for treating thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                    Bowdish
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                                                                                                                                                         Example 1; SEQ ID NO 31; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO mimetic peptide with random flanking residues SEQ ID NO:31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunotherapy; thrombocytopenia.
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                                                                                                                                                                                                                                                                                2004-460973/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18
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                                                                                                                                                                                                                                                                                                                 New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with EPO mimetic or a TPO mimetic, useful for treating thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO mimetic peptide with random flanking residues SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALEX-) ALEXION PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunotherapy;
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IEGPTLROWLAARAP 17
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                                                   TPO mimetic peptide SEQ ID NO:65.
                                                                                                                                                                                                                                ADQ16646 standard;
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immunoglobulin; complementarity determining region; CDR; peptide mimetic;

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RESULT 33
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erythropoietin;
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                                                                                                                   WO2004050017-A2
                                                                                                                                              Unidentified
                                                                                                                                                                                                                                 TPO mimetic peptide with random
                                                                                                                                                                                                                                                                09-SEP-2004
                                                                                                                                                                                                                                                                                                                        ADQ16615 standard;
                            02-DEC-2002; 2002US-00307724
                                                         17-NOV-2003; 2003WO-US036894.
                                                                                      17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      IEGPTLREWLTSRTP 16
                                                                                                                                                                                                                                                                                                                                                                                               IEGPTLRQWLAARAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frederickson
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                         thrombocytopenia
                                                                                                                                                                                     complementarity determining region; CDR; peptide mimetic; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                        peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%;
73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 8; Pred. No. 0.0016;
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                                                                                                                                                                                                                                   flanking residues SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                      NO:35
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(ALEX-) ALEXION PHARM INC

New immunoglobulin molecule comprising a region, where to complementarity determining regions (CDRs) are replaced or a TPO mimetic, useful for treating thrombocytopenia.

with

EPO mimetic

The invention relates to a novel immunoglobulin molecule or its fragment

Example 1; SEQ ID NO 37; 107pp; English.

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RESULT 34
ADQ16617
ID ADQ16
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thromborytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thromborytopenia. The present sequence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                  immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive; immunotherapy; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                   TPO mimetic peptide with random flanking residues
                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-2004
                                                                                                                WPI; 2004-460973/43.
                                                                                                                                                                                                                  17-NOV-2003; 2003WO-US036894
                                                                                                                                                                                                                                           17-JUN-2004.
                                                                                                                                                                                                                                                                  WO2004050017-A2
                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ16617 standard; peptide; 18
                                                                                                   N-PSDB;
                                                                                                                                                               (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                        02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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                                                                                                   ADQ16618.
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                        Frederickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%;
73.3%;
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Pred.
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                                                                                                                                         Renshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:37
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RESULT 35
ADQ16623
ID ADQ16
XX ADQ16
XX DQ16
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Best Local S
Matches 11
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                                                                  immunotherapy. The immunoglobulin molecule is the composite the immunotherapy, bone marrow treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                   The invention relates to a novel immunoglobulin molecule or its fragmer comprising a region where amino acid residues corresponding to at least portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic are a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunoptherapy. The immunoglobulin molecule is useful for diagnosing or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with EPO mimetic
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   Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bowdish KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-2002; 2002US-00307724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin;
erythropoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO mimetic, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2004-460973/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEGPTLRQWLAARAP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEGPTLREWLTSRTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frederickson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementarity determining region; CDR; peptide mimetic; EPO; thrombopoietin; TPO; immunosuppressive:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treating thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Renshaw
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                                                                                                                                                                                                                                                                                                                                        are replaced
                                                                                                                                                                                                                                                                                                                                                                           its fragment
to at least a
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Best Local Similarity
Matches 11; Consert
                                                              Query Match
Best Local
                                                  Matches
                                                                                                                                                                                                                                                                                                      New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                   Sequence 22
                                                                                                                                    with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents an immunoglobulin heavy chain CDR2 with
                                                                                                                                                                                                                  The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced portion of a two complementarity determining regions (CDRs) are replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-2004
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                                                                                                                                                                                                                                                                             Example 9; SEQ ID NO 128; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   Bowdish KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-2002; 2002US-00307724.
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                                                                                                                          peptide
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                         IEGPTLREWLTSRTPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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IEGPTLROWLAARAKH
                                                                                                     AA;
                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
                                                            67.3%;
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73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain
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                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66; DB Pred. No. 0.00 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2:
                                                               Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                   Renshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₿
                                                   Mismatches
                                                                0
                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
                                                                .0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .0016;
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                                                   Indels
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                                                                                                                                                                                                                                                                                                                      EPO mimetic
                                                   Gaps
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RESULT 37
ADQ16710
ID ADQ16
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AC ADQ16

ADQ16710 standard;

protein;

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ADQ16705
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DT 09-:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 38
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobuiln heavy chain CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2003; 2003WO-US036894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004050017-A2
                                                                                                                                                                                    immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoletin; EPO; thrombopoletin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ16705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; SEQ ID NO 130; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin;
erythropoietin;
                                                                                                                                                                                                                                                                    Modified immunoglobuiln clone 116
                                                                                                                                                                                                                                                                                                                              09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunotherapy;
                                                                                                                                                             .mmunotherapy; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2004-460973/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEGPTLRQWLAARAP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEGPTLREWLTSRTP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inserted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents an immunoglobulin heavy chain CDR2 with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frederickson
                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Renshaw
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                                                                                                                                                                                                                                                                         HC variable region SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPO clone HR2-28 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDRs) are replaced with thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 22
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                                                                                                                                                                                                                                                                            ID NO:125
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RESULT 39
ADQ16704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of Chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents immunoglobulin clone 116 heavy chain variable receives
                                                                                                                                                                                                                                                       immunoglobulin; complementarity determining region; CDR; peptide erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi
                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                        ADQ16704 standard; protein; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2003; 2003WO-US036894
                                                                      Bowdish
                                                                                                                      02-DEC-2002;
                                                                                                                                               17-NOV-2003; 2003WO-US036894
                                                                                                                                                                       17-JUN-2004
                                                                                                                                                                                                WO2004050017-A2
                                                                                                                                                                                                                                                                                               Modified immunoglobuiln clone 116 heavy chain SEQ ID NO:124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variable region.
                                              WPI; 2004-460973/43.
                                                                                               (ALEX-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; SEQ ID NO 125; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                      KS,
                                                                                               ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       IEGPTLRQWLAARAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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                                                                                                                        2002US-00307724
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                      Frederickson
                                                                                                                                                                                                                                                thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.3%;
73.3%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Renshaw M;
                                                                        Renshaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 128
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to at least a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPO mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wior a TPO mimetic, useful for treating thrombocytopenia.

with

EPO

mimetic

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RESULT 40
ABP51695
ID ABP51695
ID ABP51695
ID ABP511
XX ABP511
XX ABP51
XX TPO;
XM TPO;
XM TPO;
XM Compl
XM Homoo
OS Synth
XX MO2000
XX Homo
OS Synth
XX D5-DE
XX 05-DE
PR 04-M2
PR 29-M2
XX UP1;
DR WP1;
DR W
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                     The present invention describes an immunoglobin molecule or its fra (I) comprising a region where amino acid residues corresponding to least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) min that is flanked with proline at its carboxy terminus. (I) has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-2000; 2000US-0251448P.
04-MAY-2001; 2001US-0288889P.
29-MAY-2001; 2001US-0294068P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; SEQ
                                                                                                                                                                                                                                                                                         A novel immunogen molecule comprising a region in which amino ac residues corresponding to at least a portion of the complementar determining region are replaced or fused with an erythropoietin thrombopoetin mimetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-2001; 2001WO-US047656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5G1.1-TPO heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP51695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP51695 standard;
                                                                                                                                                                                                                                     Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALEX-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents immunoglobulin clone 116 heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPO; thrombopoietin; erythropoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-566610/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102
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                                                                                                                                                                                                                                     Fig 13A; 113pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barbas-Frederickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino
and nephrotropic activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haematopoietic
                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody; CDR region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell; haematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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      and can be used
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RESULT 41
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Best Local S
Matches 11
          The invention relates to a novel immunoglobulin molecule or its frag comprising a region where amino acid residues corresponding to at le portion of a two complementarity determining regions (CDRs) are repl with a peptide mimetic selected from an erythropoletin (EPO) mimetic a thrombopoletin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunocherapy. The immunoglobulin molecule is useful for diagnosing treating thrombocytopenia as a result of chemotherapy, bone marrow
                                                                                                                                                                                         New immunoglobulin molecule comprising a region, where to
complementarity determining regions (CDRs) are replaced
or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ16647 standard;
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                                                                                                                                                                                                                                                                                                                                                                        02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-2004
                                                                                                                                                            Example
                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2003; 2003WO-US036894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004050017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin; complementarity determining region;
erythropoietin; EPO; thrombopoietin; TPO; immunosup;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin antibody 5G1.1-TPO heavy chain
                                                                                                                                                                                                                                                                                                                                          (ALEX-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mmunotherapy;
                                                                                                                                                                                                                                                         2004-460973/43.
DB; ADQ16648.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                             PHARM INC
                                                                                                                                                            NO 67; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 472 AA
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73.3%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive
 idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
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   thrombocytopenia
                                                                                                 are replaced
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                                                                                mimetic
                                                                                                                                                                                                               EPO mimetic
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at least a
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RESULT 42
AAB16969
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2-(L4)c-P2-(L4)c-P3 or -(L1)c-P1-(L2)d-P2-(L4)c-P3 or -(L1)c-P1-(L2)d-P2-(L4)c-P3 or -(L1)c-P1-(L2)d-P2-(L4)c-P3 where P1, P2, CC P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, Cc c, d, e, and f = are each independently 0 or 1, provided that at least 1 cof a and b is 1. The composition can have cytostatic, antiasthmatic, CC thrombolytic and immunosuppressive activities. DNAs, vectors and host C enls from the present invention can be used for producing pharmaceutical CC compositions. The compositions are useful for treating cancer, asthma, CC intrombosis, or autoimmune diseases. The use of an Fc domain (rather than CC such as Fc receptor binding, protein A binding, complement fixation, and CC possibly placental transfer. AAA69443 to AAA69256 and AAB16955 to CC AAB18003 represent nucleotide and amino acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPG; TPO; CHA; mimetic; IL-1; TNF; antagonist; Minhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; vascular endothelial growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000
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                                                                                                                                                                                                                                                                                 The present
                                                                                                                                                                                                                                                                                                                Claim 19; Page 203; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                active
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                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified peptide; therapeutic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB16969 standard; peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence represents an immunoglobulin antibody heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
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                                                                                                                                                                                                                                                                                                                                              composition of
e peptides, usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 IEGPTLREWLTSRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                 invention describes composition of matter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
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99US-00428082
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                                                                                                                                                                                                                                                                                                                                                n of matter comprising an Fc don useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                               Cheetham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion;
                                                                                                                                                                                                                                                                                                                                                   an Fc domain and pharmacologically
ancer and autoimmune diseases.
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0.063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 472;
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RESULT 43
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The present invention describes a vehicle-peptide molecule (I) or its comparison (I) can have antiinflammatory, antitumour, immunosuppressive, cc cytostatic, antirheumatic, antiinfertility, hatidiabetic, ophthalmological, cc antianaemic, anorectic, antiinfertility, haemostatic, dermatological and cc antianaemic, anorectic, antiinfertility, haemostatic, dermatological and cc prophylactic agent as well as for screening purposes. (I) is useful for cd diagnosing diseases characterised by dysfunction of their associated cc protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their cc proteins of interest in a biological sample. Additionally, (I) is useful cc retenting inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, cminetic compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic comprising cc compounds are useful for treating conditions that involve an existing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-130313/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 43;
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                                                                                                                                           This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one light diding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/or neurologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic rumour which result in thrombocytopaenia, systemic lupus erythematosus, and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777 represent amino acid and nucleic acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
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cardiovascular; infectious; malignant; neurologic disease;
immunomodulator; cardiant; antimicrobial; cytostatic; neuro
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                                                                                             diseases, as well as anaemia. Accordingly, they exhibit cardiant, antimicrobial, cytostatic and neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2002; 2002US-0368791P
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                                                          useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant; hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune diser; cardiovascular disease; arrhythmia; hyportension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular or neurodegenerative disease or disorder, anemia, cancer, or infection
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Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CENTOCOR INC
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probable arabinosy hemocyanin G-type pyruvate dehydroge cransposase - Cory glutamyl-tRNA synt hypothetical prote hypothetical prote hypothetical prote conserved hypothet myosin I beta, MMI conserved hypothet erythrocyte membra myosin-IC - mouse preprotein translocas myosin I heavy chain myosin I heavy chain myosin I heavy chain myosin I heavy chain myosin I heavy chain myosin I heavy chain myosin Eap protein - Rhi protein - Rhi protein - Rhi protein export (im hypothetical prote hypothetical prote hypothetical prote hypothetical prote protein f32EIO.1 [valine-tRNA (Gln) hypothetical prote two-component hybr MHC class II histo pyruvate dehydroge pyruva

ALIGNMENTS

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C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004 C;Accession: S01317; B36133; S63475 R;Burns, G.; Brown, T.; Hatter, K.; Idriss, J.M.; Sokatch, J.R. Eur. J. Biochem. 1317, 1988 A;Title: Similarity of the El subunits of branched-chain-oxoacid dehydrogenase A;Reference number: S01317; MUID:88329084; PMID:3416875 A;Accession: S01317
                                               A;Gene: bkdAl
C;Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin
C;Keywords: lipoamide; oxidoreductase; phosphoprotein; thiamin pyrophosphate
E;2-410/Product: 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) alpha chain #status p
F;202-251/Domain: thiamin pyrophosphate-binding domain homology <TPB>
F;313/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P09060; EMBL:X13004 R;Madhusudhan, K.T.; Huang, G.; Burns, G.; Sokatch, J. Bacteriol. 172, 5655-5663, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M33715
R;Hester, K.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R. Eur. J. Bicchem. 233, 828-836, 1995
A;Title: Purification of active E1-alpha(2)-beta(2) of Pseudomonas A;Reference number: S63475; MUID:96085147; PMID:8521848
A;Accession: S63475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_{\ell}Alternate names: 2-oxoisovalerate dehydrogenase C_{\ell}Species: Pseudomonas putida
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C;Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable aldehyde oxidoreductase APE0708 - Aeropyrum pernix (strain C;Species: Aeropyrum pernix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-753 < KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Title: Transcriptional analysis of the promoter region;Reference number: A36133; MUID:91008935; PMID:2211503;Accession: B36133
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;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Status: preliminary
;Molecule type: DNA
;Residues: 1-17 <MAD>
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Best Local
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                                                                                                                                                                                                                                           Molecule type: protein Residues: 1-13 <HES>
                                                                                                                                                                                                                                                                                           Status: preliminary
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47.1%;
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Pred. No.
  Score 48.5;
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  DB 1;
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Length 410;
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RESULT G89894

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protein kinase [imported] -

Staphylococcus aureus (strain N315)

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, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state o
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C;Stover, C.K.; Pham, X.Q.;
A;Stover, C.K.; Pham, Y.; Brody,
adman, S.; Yuan, Y.; Brody,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Deinococcus radiodurans (strain C; Species: Deinococcus radiodurans
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A;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                  A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-150 <WHI>
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Best Local S
Matches 8
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                                                          IEGPTLREWLTSRTPH
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LDGSFAREWQTEGTPH
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                                                                                                                                                       49.0%;
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                                                                                                                          Score 48; DB Pred. No. 2.4; 2; Mismatches
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, L.; Utterback,
                                                                                                                                                                                        Length 150;
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T.; Zalewski,
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A;Cross-references: UNIPROT:099UP8;
A;Experimental source: strain N315
C;Genetics:
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89894
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C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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C;Species: Haemophilus influenzae
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Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;

Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,

a, A.; Mizutani-Ui, Y.; Kobayashi, N.; Hayashi, H.; Hiramatsu, K.

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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Pred. No.
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C;Date: 05-Dec-1997 #sequence revision 05-Dec-1997 #text_change 09-Jul-2004
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C;Accession: C69593; S32486
C;Accession: C69593; S32486
C; Bron, S; Brouhllet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chr.
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleriech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanolon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross references: UNIPROT:P37940; GB:Z99116; GB:AL009126; NID:g2634723; A;Experimental source: strain 168 R;Wang, G.F.; Kuriki, T.; Roy, K.L.; Kaneda, T. Eur. J. Biochem. 213, 1091-1099, 1993 A;Title: The primary structure of branched-chain alpha-oxo acid dehydrogen A;Reference number: S32486; MUID:93279308; PMID:8504804
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                                                                                                                                                                                                                                                        A;Cross-references: GB:M97391; GB:M96937; NID:g142610; PIDN:AAA22278.1; A;Experimental source: strain 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4)
N;Alternate_names: branched-chain alpha-oxo acid dehydrogenase
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A; Residues: 1-430 < K
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                                                                                                            ;Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin;Keywords: fatty acid biosynthesis; oxidoreductase; phosphoprotein;143-190/Domain: thiamin pyrophosphate-binding domain homology <TPB>
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K.; Yoshida, F
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EGPTLREWLTSR-TPHS

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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: B64633
                                                           myosin I beta - human
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 19-May-2000 #sequence_revision 19-May-2000 #text
(;Accession: A59253
R;Crozet, F.; Amraoui, A.E.; Blanchard, S.; Lenoir, M.;
Genomics 40, 332-341, 1997
A;Title: Cloning of the genes encoding two murine and ha;Reference number: A59253; MUID:97237053; PMID:9119401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9K9Z0;
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2504
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A;Molecule type: DNA
A;Residues: 1-664 <STO>
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serine/threonine protein kinase BH2504 [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: H33962
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A;Residues: 1-527 <TOM>
A;Cross-references: UNIPROT:025564; GB:AE000600;
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A;Status: preliminary; not A;Molecule type: mRNA
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C; Accession: B64633
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C;Species: Helicobacter pylori
                                           A; Accession: A59253
                                                                                                                                                                          Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
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3; Mismatches
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                                                                                                                                   S.; Lenoir, M.; Ripoll, C.; Vago,
                    conceptual
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C;Superfamily: brush border myosin heavy chain
F;14-683/Domain: myosin motor domain homology •
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                                                                                                                                                                                A;Cross-references: UNIPROT:000159; GB:X98507; A;Experimental source: dev stage adult; tissue
                                                                                                                                                     A;Gene: myo-lb
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Matches
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 308
                                                      1 Similarity
10; Conserv
SVEGSTLREALTHR 321
                        SIEGPTLREWLTSR
                                                      Conservative
                                                                   46.9%;
                                                                    Score 46;
Pred. No.
                                                       Mismatches
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42;
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C;Genetics:
A;Gene: lmo1372
C;Superfamily: [
                                                                                                                                                                                                                                                                                                                      A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maduen, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1246
                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-331 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Glaser, P.; Frangeul, L.; .; Dominguez-Bernal, G.; Du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
C;Accession: AD1246
C;Accession: T. Buchrieger, C.: Amend,
                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q8Y7B4; GB:NC_003210; PIDN:CAC99450.1; PID:g16410788; A;Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                               Science 294, 849-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.; Jones, L.M.; Karst,
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                                                                                                Query Match
Best Local
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234
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                                      EGPTLREWLTSR-TPHS 18
                                                                                                                                                          pyruvate dehydrogenase (lipoamide)
                                                                               Conservative
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64.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.; Amend, A.; Baquero, F.; Berche, P.; urand, L.; Dussurget, O.; Entian, K.D.; l
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                                                                                                                                                              chain; thiamin
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Fsihi, H.
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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1608
                                                                                                                                                                                                                                                                                                                                                                               branched-chain alpha-keto acid dehydrogenase El chain (2-oxoisovalerate dehydrogenase C;Species: Listeria innocua C;Daece: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AH1608
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <GLA>
A;Cross-references: UNIPROT:Q92BY3;
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.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
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     GB:AL592022;
        PIDN: CAC96640.1;
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           PID: 916413882;
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cian, K.D.;
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Voss, H.; Wehland,
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Faihi, H.
              GSPDB
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beta-amyloid-like protein precursor -
C;Species: Drosophila melanogaster
C;Date: 08-Dec-1989 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein At2g42400 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: E84853
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A;Title: A comparative sequence analysis of two human papillomavirus
A;Reference number: S15614; MUID:91188699; PMID:1964523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15618
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
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A; Residues: 1-473 <STO>
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Best Local
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1 Similarity 40.6%;
13; Conservation
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Pred. No. 6.2;
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Pred. No. 14
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                                       fruit fly
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08-Dec-1989 #text_change
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A;Molecule type: protein
A;Residues: 29-49;51-80;84-95;100-117;120-128;130-141;143-176;243-254;256-296;303-336;3
R;Giger, R.J.; Vogt, L.; Zuellig, R.A.; Rader, C.; Henehan-Beatty, A.; Wolfer, D.P.; So;
Eur. J. Biochem. 227, 617-628, 1995
A;Title: The gene of chicken axonin-1. Complete structure and analysis of the promoter.
A;Reference number: $69332; MUID:95172044; PMID:7867620
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                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X79607
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology; cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1002-1036 <GIG>
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A;Title: The axonally secreted cell adhesion molecule, axonin-1. Primary structure, A;Reference number: S22383; MUID:92174898; PMID:1311675
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A;Cross-references: FlyBase
C;Keywords: transmembrane
T13288
mei-41 protein -
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A; Residues: 1-1036 < ZUE1>
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A; Residues: 1-886 < ROS >
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                                                                                                                                                                                 45.9%; ilarity 29.4%; Conservative
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fruit fly (Drosophila melanogaster)
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46.7%;
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Pred. No.
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3; Mismatches
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61;
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
C;Accession: T13288

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A;Reference number: Z1974
A;Accession: T23485
A;Status: preliminary; t)
A;Molecule type: DNA
A;Residues: 1-200 <MIL>
A;Residues: 1-200 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein K08F4.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T23485 R;Hembry, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Hari, K.L.; Santerre, A.; Sekelsky, J.J.; McKim, K.S.; Boyd, J.B.; Hawley, R.S. Cell 82, 815-821, 1995
A;Title: The mei-41 gene of D. melanogaster is a structural and functional homolo A;Reference number: Z11072; MUID:95401271; PMID:7671309
                                                                                                                                                                                         probable glutathione transferase (BC 2.5.1.18) GST3 - Caenorhabditis elegand (Species: Caenorhabditis elegand C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C; Accession: T37464
R; Tawe, W.N.; Eschbach, M.L.; Walter, R.D.; Henkle-Duehrsen, K.
                                                                                                                                                                                                                                                                                      RESULT
T37464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: FlyBase:FBgn0004367
A;Introns: 650/3; 748/3; 2313/3
C;Function:
A;Description: involved in cell cycle checkpoint and meiotic recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: T13288
A; Status: prelimina:
                            A;Cross-references: UNIPROT:016116; EMBL:AF010241; PIDN:AAB65419.1
A;Experimental source: strain Bristol N2
                                                                  A; Molecule type: mRNA
A; Residues: 1-207 < TA
                                                                                                                     A; Reference number: Z21702
A; Accession: T37464
                                                                                                                                                         submitted to the EMBL Data Library, June 1997 A;Description: Paraquat mediates differential gene expression
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A;Cross-ref
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Matches
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                                                                                                  Status: preliminary; translated
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                                                                    1-207 <TAW>
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8; Conserv
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RESULT 23
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C;Accession: C90277

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                              Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: C87021
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                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <STO>
                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; eam, M.A.; Rutherford, K.M.
                                                                                                                                                                                                                                                                                                                                                                                                       serine-threonine protein kinase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 0;C;Accession: C87021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein tmoA [imported] - C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision
                                                                                                                          A;Gene: ML0897
C;Superfamily: Mycobacterium tuberculosis probable serine/threonine-specific protein
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A; Residues: 1-310 < KUR>
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A;Accession: C90277
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                                                                                                                                                            Gene: ML0897
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x.; Thi-Ngoc, H.P.; Redder,
                                                                                                                                                                                                                                                                                                                        Skelton,
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A; Description: Lethal effect
A; Reference number: Z15633
A; Accession: T06371
A; Status: preliminary; trans
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-327 <HEI>
A;Ross-references: UNIPROT:09KTS1; GB:AE004166; GB:AE003852; NID:g9655259; PIDN:AAF9398
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
R;Karaolis, D.K.R.; Johnson, J.A.; Bailey, C.C.; Boedeker, B.C.; Kaper, J.B.; Reeves, P.
Proc. Natl. Acad. Sci. U.S.A. 95, 3134-3139, 1998
A;Title: A Vibrio cholerae pathogenicity island associated with epidemic and pandemic st
A;Reference number: Z16672; MUID:98169509; PMID:9501228
A;Accession: T09435
A;Status: preliminary; translated from GB/EMBL/DDBJ
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B70936
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                      probable serine/threonine-specific protein kinase (EC 2.7.1.-)
C;Species: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, November 1997 A;Description: Lethal effects on root development by
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A; Residues: 3-327 < KAR>
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                        ;Experimental source: cv. Little Marvel
;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                              Cross-references: UNIPROT:Q8L5C7; EMBL:AF034743; NID:g2827991;
                                                                                                                                                                                                                                                                                                                                                    Residues:
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  Species: Mycobacterium
Date: 10-Sep-1999 #sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Pisum sativum (garden pea)
Date: 30-Apr-1999 #sequence_revision
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e: part of
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8; Conserv
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                                                                                                                                                                            EGPTLREWLTSRTPHS 18
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                                                                                                                                        EEPECLEWLNSKEPNS 164
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llarity 50.0%;
Conservative
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        revision
                                                                                                                                                                                                                  Score 43; DB Pred. No. 38; 2; Mismatches
                                                                                                                                                                                                                    2;
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Pred. No. 2
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      10-Sep-1999
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      #text_change
                                                                                                                                                                                                                                                        Length
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          09-Jul-2004
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                                              Mycobacterium
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I.; Sellers,
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ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                              R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Cerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Ku; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      문
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                                                                                                                                                                              polyketide synthase and peptide synthetase mcyE [imported] C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_c]
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DGPTLQEGLNART

number:

Chen, L.; Wood, G.E.; Chen, Y.; Kutyavin, T.; Levy, R.; Li, M.; !

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Krespan,

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Perry,

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Gordon-Kamm

tumefaciens

#text_change 09-Jul-2004

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Agrobacterium

tumefaciens

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gc; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holz Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: B70936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: Mycobacterium tuberculosis
C;Keywords: phosphotransferase
F;17-270/Domain: protein kinase homology <
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A;Experimental source: strain H37Rv
C;Genetics:
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                                                                                                                     A; Map position: linear chromosome C; Superfamily: ornithine-oxo-acid
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-491 < KUR>
                                                                                                                                                                                                                                                                                                                                                             R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: pkn
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                                                                                                                                                                                                    A; Cross-references: UNIPROT: Q8U9P9;
                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                  A; Accession: C98275
                                                                                                                                                                                                                                                                                                         A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                            Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: C98275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polykeitde
                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Agrobacterium tumefaciens ;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001
                                                                                                                                                            Gene: AGR_L_2319
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3 EGPTLREWLTSRT 15
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                                       Similarity
8; Conserv
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66.7%;
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                                                              Score 43;
Pred. No.
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Pred. No.
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44;
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                                           2
                                                                                 Length 491;
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Markelz,
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ckelz, B.
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phosphonate (C;Species: B)
C;Species: B)
C;Date: 21-J;
C;Accession:
probable protein kinase (EC 2.7.1.-) ylop - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: D.-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H69878
C;Accession: H69878
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Poortetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sako, T.; Scanlon,
A;Authors: Schleich, S.; Schroetter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serou
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C;Complex: homotetramer [validated, MUID:96421555]
C;Punction:
C;Punction:
A;Description: EC 3.1.3.- [validated, MUID:96421555]; phosphonate monoester hydrolase;
A;Pathway: glyceryl glyphosate utilization
A;Pathway: glyceryl glyphosate utilization
A;Note: may also function in vivo as phosphodiesterase
C;Superfamily: animal sulfatase
C;Superfamily: animal sulfatase
C;Superfamily: homotetramer; phosphoric monoester hydrolase
C;Seywords: homotetramer; phosphoric monoester status experimental <MAT>
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A;Molecule type: DNA
A;Residues: 1-491 <KUR>
A;Cross-references: UNIPROT:Q8U9P9; GB:AE008689; PIDN:AAL44489.1; PID:g17742095; GSPDB:
A;Experimental source: strain C58 (Dupont)
C;Genetics:_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: mcyE
A; Map position: linear chromosome
C; Superfamily: ornithine-oxo-acid
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A;Residues: 1-514 <DOT>
A;Cross-references: UNIPROT:Q45087; EMBL:U44852; NID:g1177863;
A;Experimental source: strain PG2982
A;Note: part of this sequence, including the amino end of the C;Genetics:
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A;Title: Identification, characterization and cloning of a phosphonate A;Reference number: Z22807; MUID:96421555; PMID:8824203
A;Accession: T44602
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Species: Burkholderia caryophylli
Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:Q45087; EMBL:U44852; NID:g1177863; PIDN:AAC44467.1;
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8; Conserv
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Pred. No.
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   hemocyanin G-type chain - giant octopus (fragment)
C;Species: Octopus dofleini (giant octopus)
C;Apecies: Octopus dofleini octopus)
R;Miller, K.I.; Cuff, M.E.; Lang, W.F.; Varga-Weisz, P.; Field, K.G.; van Holde,
J. Mol. Biol. 278, 827-841, 1998
A;Title: Sequence of the Octopus dofleini hemocyanin subunit: structural and evol
A;Reference number: Z20940; MUID:98277150; PMID:9614945
A;Accession: T30939
A;Accession: T30939
A;Accession: T30939
A;Molecule type: mRNA
A;Besidues: 1-2896 <MIL>
A;Cross-references: UNIPROT:O61363; EMBL:AF020548; NID:g3132879; PID:g3132880; PI
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T30939
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43.9%;

Score 43; DB 2; Pred. No. 1.4e+02; 1; Mismatches 4

Length 1094;

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Gaps

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evolutionar

PIDN: AAC3

8 Similarity

230

GRTLRDWLTRYRP 242 GPTLREWLTSRTP 16 Conservative

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C;Accession: F70697

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

N;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Artle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Tele: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: F70697
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A;Molecule type: DNA
A;Residues: 1-1094 <COL>
A;Cross-references: UNIPROT:P72060; GB:Z80343; GB:AL123456; NID:g3261648; PIDN:CAB02473
A;Experimental source: strain H37Rv
                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable arabinosyltransferase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: Bacillus subtilis probable protein kinase C;Keywords: ATP; phosphotransferase; protein kinase F;9-269/Domain: protein kinase homology <KIN>
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Pred. No.
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A; Molecule type: DNA
A; Residues: 1-371 < HEM>
A; Residues: 1-371 < HEM>
A; Residues: 1-371 < HEM>
A; Cross-references: UNIPROT: P21881; GB:M57435; GB:M31542; NID:g143375; PIDN:AAA62681.1;
A; Cross-references: UNIPROT: P21881; GB:M57435; GB:M31542; NID:g143375; PIDN:AAA62681.1;
A; Cross-references: UNIPROT: P21881; GB:M57435; GB:M31542; NID:g143375; PIDN:AAA62681.1;
A; Cross-references: UNIPROT: P21881; C.; Voshikawa, H.; Darchin, A.
A; Cross-references: UNIPROT: P21881; PA1623; PMID: 384377
A; Cross-references: MSD:MUD: 98044033; PMID: 384377
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A;Note: Odhcy
C;Superfamily:
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                                                RESULT
JC4742
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;Cross-references: GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13331.1;
;Experimental source: strain 168
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Corynebacterium glutamicum
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Pred. No. 49
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RING, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D. Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

R;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: B84271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 170, 91-94, 1996
A; Title: Cloning and characterization of an IS-like element A; Reference number: JC4742; MUID:96200862; PMID:8621097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Corynebacterium glutamicum
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4742
R;Correia, A.; Pisabarro, A.; Castro, J.M.; Martin, J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glutamyl-tRNA synthetase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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A,Note: The authors translated the initiation codon TGT for residue 1
A,Note: The authors translated the codon ATT for residue 125 as Tyr
A,Note: the source is designated as Brevibacterium lactofermentum
                                                                                                                                                                                 A;Gene: gltS
C;Superfamily: glutamine-tRNA ligase; glutamine-tRNA ligase homology
                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-586 <STO>
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A; Residues: 1-436 < COR>
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;Experimental source: ATCC 13869
                                                                                                                  Query Match
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Similarity 50.08;
9; Conservation
                                                                                                                  Similarity
KNPALRDWVAFRMVDTPH
                                             EGPTLREWLTSR---TPH 17
                                                                                             Conservative
                                                                                                                  43.4%;
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                                                                                                                                             Score 42.5;
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Pred. No. 58;
                                                                                                                       Pred.
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C; Date: 1. 2. C. Accession: AH1884
C.Accession: AH1884
C.Accession: AH1884
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Maramura, M.; Tabata Rakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata Nakazaki, N.; Shimpo, S.; Tabata Nakazaki, N.; Shimpo, S.; Tabata Nakazawa, M.; Yasamoto, M.; Yasamoto, M.; Yasamoto, M.; Tabata Nakazawa, M.; Yasamoto, M.; Y

hypothetical protein all0625 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

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                                                           A;Gene: galU
C;Superfamily
C;Keywords: n
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Fitle: Deciphering the biology of Mycobacterium tuberculosis from the complet A; Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain C; Genetics:
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A; Residues: 1-236 < KUR >
                                                                                                                                                                                                                                                                                                                                                                                                           UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) galU [similarity] C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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A; Residues: 1-253 < S'
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A;Experimental source: strain PCC 7120
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;Residues: 1-306 <COL>
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                                                                               Superfamily:
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38;
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R;Stengelin, S.; Stamenkovic, I.; Seed, B.

EMBO J. 7, 1053-1059, 1988

A;Title: Isolation of cDNAs for two distinct human Fc receptors
A;Reference number: S00477; MUID:88296409; PMID:3402431
A;Accession: S00478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenetics 30, 5-12, 1989
A;Title: Identification of multiple isoforms of the low-affinity
A;Reference number: A45877; MUID:89307398; PMID:2526077
A;Accession: A45877
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Eur. J. Immunol. 20, 1367-1377, 1990
A;Title: Distribution, inducibility and biological function of the cloned and expressed A;Reference number: A43543; MUID:90316181; EMID:2142460
A;Accession: A43543.
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JLO119; A45543; Ā60568; A45877; S00478
C;Accession: JLO119; A45543; Ā60568; A45877; S00478
R;Brooks, D.G.; Qiu, W.O.; Luster, A.D.; Ravetch, J.V.
J. Exp. Med. 170, 1369-1385, 1989
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A; Residues: 1-204, 'Y', 206-254, 274-310 <ENG>
A; Cross-references: GB:X52473; NID:g3928171; PIDN:CAA36713.1; PI
A; Cross-references: GB:X52473; NID:g3928171; PIDN:CAA36713.1; PI
R; Engelhardt, W.; Geerds, C.; Frey, J.
Mol. Immunol. 27, 379-382, 1990
Mol. Immunol. 27, 379-382, 1990
A; Title: Organization of human FCRII and FCRII-like (betaFCRII)
A; Reference number: A60568; MUID:90294837; PMID:2141667
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                                                                          A;Introns: 131/1
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Superfamily: Fc gamma receptor III; immunoglobulin
C;Keywords: alternative splicing; glycoprotein; immunoglobulin
F;1-44/Domain: signal sequence #status predicted cSIG>
F;45-310/Product: IgG FC receptor IIb #status predicted cMAT>
F;45-222/Domain: extracellular #status predicted cEXT>
F;45-222/Domain: immunoglobulin homology <INM1>
F;64-115/Domain: immunoglobulin homology <IMM2>
F;145-198/Domain: transmembrane #status predicted <INM>
F;246-310/Domain: intracellular #status predicted <INM>
F;246-310/Domain: intracellular #status predicted <INM>
                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:FCGR2B; FCG2; FCGR2
A;Cross-references: GDB:128183; OMIM:146790
A;Map position: 1q23-1q23
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: the authors suggest that the C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-35,'S',37-204,'Y',206-253,'G',255 <STE>
A; Residues: 1-35,'S',37-204,'Y',206-253,'G',255 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-74,'Q',76-119,'V',121-204,'Y',206-231,'T',233-254,274-310
A;Cross-references: GB:M28696; NID:g184843; PIDN:AAA36051.1; PID:g306929
A;Note: the authors translated the codon CAG for residue 75 has His
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A; Residues: 1-310 < BRO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-38 <EN2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JL0119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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nes: Fc gamma (IgG) receptor
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Score 42;
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PMID:2529342
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C;Species: Homo mapiens (man)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JL0118; A31932; S02297; B45877; S00477; S02296
C;Accession: JL0118; A1932; S02297; B45877; S00477; S02296
R;Brooks, D.G.; Qiu, W.O.; Luster, A.D.; Ravetch, J.V.
J. Exp. Med. 170, 1369-1385, 1989
A;Title: Structure and expression of human IgG FCRII(CD32): functional heterogeneity
A;Reference number: JL0118; MUID:90010791; PMID:2529342
                                                       A;Map position: 1q23-1q23
C;Superfamily: FC gamma receptor III; immunoglobulin homology
C;Superfamily: FC gamma receptor III; immunoglobulin homology
C;Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-317/Product: IgG FC receptor IIa #status predicted <REI>
F;36-216/Domain: extracellular #status predicted <RXT>
F;36-216/Domain: immunoglobulin homology <IMM1>
F;136-189/Domain: immunoglobulin homology <IMM1>
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A;Molecule type: mRNA
A;Residues: 1,'T',3-317 <STU>
A;Residues: 1,'T',3-317 <STU>
A;Cross references: EMBL;Y00644; NID:g31335; PIDN:CAA68672.1; PID:g31336
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A; Residues: 7-317 < STE>
C; Genetics:
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A;Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.
A;Reference number: A45877; MUID:89307398; PMID:2526077
A;Accession: B45877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:J03619; NID:g183619; PIDN:AAA35932.1; PID:g306803
R;Stuart, S.G.; Trounstine, M.L.; Vaux, D.J.T.; Koch, T.; Martens, C.L.; Mellman, I.; NJ. Exp. Med. 166, 1684, 1987
J. Exp. Med. 166, 1668-1684, 1987
A;Title: Isolation and expression of cDNA clones encoding a human receptor for IgG (Fc-A;Reference number: S02297; MUID:88061079; PMID:2824655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: placenta A;Experimental source: placenta A;Note: it is uncertain whether Met-1, Met-3, or Met-7 is the initiator R;Hbbs, M.L.; Bonadonna, L.; Scott, B.M.; McKenzie, I.F.C.; Hogarth, P Proc. Natl. Acad. Sci. U.S. A. 85, 2240-2244, 1988 A;Title: Molecular cloning of a human immunoglobulin G Fc receptor. A;Reference number: S02296; MUID:88176920; PMID:2965389
                                  F;136-189/Domain:
F;217-240/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S00477
A;Status: not compared with conceptual translation
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A; Contents: clone PC23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Stengelin, S.; Stamenkovic, I.; Seed, B.
EMBO J. 7, 1053-1059, 1988
A;Title: IBolation of cDNAs for two distinct human Fc receptors by ligand affinity clon
A;Reference number: S00477; MUID:88296409; PMID:3402431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 7-317 <SEK>
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A;Residues: 3-317 <HIB>
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A;Molecule type: mRNA
A;Residues: 1-317 <BRO>
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Matches
                                                                                                                                                                                                                                                                                                                             Cross-references: GDB:119903; OMIM:146790
241-317/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                   Gene: GDB:FCGR2A
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names: Fc gamma (IgG) receptor II (low affinity) alpha; surface glycoprotein
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Stuart, S.G.; Simister, N.E.; Clarkson, S.B.; Kacinski, B.M.; Shapiro, M.; Mellman, I EMBO J. B, 3657-3666, 1989
A;Title: Human IgG Fc receptor (hFcRII; CD32) exists as multiple isoforms in macrophage A;Reference number: S06946; MUID:90059965; PMID:2531080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P31995; EMBL:X17652; NID:g32073; PIDN:CAA35642.1; PID:g3207 C;Superfamily: Fc gamma receptor III; immunoglobulin homology C;Keywords: immunoglobulin receptor; transmembrane protein F;64-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-430 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein VC2278 [imported] - Vibrio cholerae (strain N16961 serog C;Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-323 <STU>
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                                                                                                                                                                 C; Superfamily:
                                                                                                                                                                                   A; Map position:
                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                              A;Accession: B82096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Homo sapiens (man)
Date: 22-Jan-1993 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                               Matches
                                                                                                                     Query Match
                                                                                                                                                                                                       Gene: VC2278
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119
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                                                                               Similarity 6; Conserv
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IREWIINSIPHS 130
                                     LREWLTSRTPHS 18
                                                                                                                                                                   conserved
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                                                                                 Conservative
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                                                                                                                                                                 hypothetical protein HI0125
                                                                                                   42.9%;
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Pred. No.
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Pred. No.
                                                                                                   Score 42; DB
Pred. No. 69;
                                                                                                                                                                                                                                                   GB:AE004299; GB:AE003852; NID:g9656835; PIDN:AAF954
; strain N16961; biotype El Tor
                                                                                    Mismatches
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MMI beta -

mouse (fragment)

prote

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erythrocyte membrane band 4.2 protein - human
N;Alternate names; pallidin
N;Contains: erythrocyte membrane band 4.2 protein, long spl
C;Species: Homo sapiens (man)
C;Date: 29-Oct-1999 #sequence revision 29-Oct-1999 #text_ch
C;Accession: A39707; A34865; B34865; A34883
R;Koregren, C.; Cohen, C.M.
Proc. Natl Acad. Sci. U.S.A. 88, 4840-4844, 1991
A;Title: Organization of the gene for human erythrocyte mem
A;Reference number: A39707; MUID:91271288; PMID:2052563
A;Accession: A39707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B45438
R;Sherr, E.H.; Joyce, M.P.; Greene, L.A.
J. Cell Biol. 120, 1405-1416, 1993
A;Title: Mammalian myosin I alpha, I beta, and I gamma: new widely expressed A;Reference number: A45438; MUID:93194946; PMID:8449986
A;Accession: B45438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein SPAC1952.06c - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Apate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T37934
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T. submitted to the EMBL Data Library, August 1999
A;Reference number: Z21755
A;Accession: T37934
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-564 <MCD>
A;Residues: 1-564 <MCD>
A;Cross-references: UNIPROT:09UUX1; EMBL:AL109820; PIDN:CAB52570.1; GSPDB:GN00066
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             A; Molecule type: DNA
A; Residues: 1-721 < KOR1>
A; Cross-references: UNIPROT: P16452; GB:L06519; NID:g306738; PIDN:AAA52385.1; PID:g30674
A; Experimental source: cell type erythrocyte; tissue type peripheral blood; tissue lib
R; Sung, L.A.; Chien, S.; Chang, L.S.; Lambert, K.; Bliss, S.A.; Bouhassira, E.E.; Nagel
Proc. Natl. Acad. Sci. U.S.A. 87, 955-959, 1990
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 44
A39707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: strain C;Genetics: C;Geneetics: A;Gene: SPDB:SPAC1952.06C A;Map position: 1
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C:Superfamily: brush border myosin heavy chain I; myosin motor
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Best Local
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Experimental source: strain 972h-;
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l; Mismatches
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Pred. No.
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protein 4.2: a major component of
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72;
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A;Molecule type: mRNA
A;Residues: 1-807 <CRO>
A;Cross-references: UNIPROT:Q9WTI7; GE
A;Experimental source: strain BALB/c;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: myosin-I beta
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-2000 #sequence_revisio
C;Accession: H75634
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H75634
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A;Gene: GDB:EPB42; PA
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A;Map position: 11:44.1
C;Superfamily: brush border myosin heavy
F;14-683/Domain: myosin motor domain homc
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Best Local Similarity
                                                                      Matches
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                                                                                          Local
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                                                                                          Similarity
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                                                                      Conservative
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                                                                                          42.9%;
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70.0%;
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C:Superfamily: protein-glutamine gamma-glutamyltransferase
C:Superfamily: protein-glutamine gamma-glutamyltransferase
C:Keywords: alternative splicing; blocked amino end; glycoprotein; lipoprotein; myristyl
F;2-721/Product: erythrocyte membrane band 4.2 protein, long splice form #status predict
F;2-3,34-721/Product: erythrocyte membrane band 4.2 protein, short splice form #status p
F;298-316/Domain: transmembrane #status predicted <TRM>
F;298-316/Domain: cransmembrane #status predicted <TRM>
F;298-316/Domain: cransmembrane (R-G-D) motif
F;27Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;103,420,447,529,604,705/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;278/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
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A; Molecule type: mRNA
A; Residues: 1-364, 'KRGLPC', 371-379, 'H', 381-405, 'L', 407-721 <SUN1>
A; Residues: GB: M30647; NID:g189433; PIDN:AAA36401.1; PID:g189434
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A; Molecule type: mRNA
A; Residues: 1-3,34-721 < KOR2>
A; Cross-references: GB: M29399; NID: g182083; PIDN: AAA35798.1; PID: g182084
A; Cross-references: GB: M29399; NID: g182083; PIDN: AAA35798.1; PID: g182084
                                                                                                                                                                                                                                                                                                                                                                                                                        R;Crozet, F.; Amraoui, A.E.; Blanchard, S.; Lenoir, M.; Ripoll, C.; Vago, P.; Hamel, Genomics 40, 332-341, 1997
A;Title: Cloning of the genes encoding two murine and human cochlear unconventional A;Reference number: A59253; MUID:97237053; PMID:9119401
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25-OCT-2004
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Branched-chain alpha-keto acid dehydrogenase E1.
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01-MAR-2003
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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HSSP; P12694; IOLX.
GO; GO:0016624; F:oxidoreductase activity,
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001017; Dehydrogenase_E1.
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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Oxidoreductase.
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STRAIN=ATCC 23344;
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Burkholderiaceae; Burkholderia.
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                                                                                                           SEQUENCE
                                                                                                                                                                                                            "Structural flexibility in the Proc. Natl. Acad. Sci. U.S.A. 1
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Q9YE62;
01-NOV-1999
01-NOV-1999
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
  Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haik
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A.
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                      OrderedLocusNames=APE0708;
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
753aa long hypothetical aldehyde oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K96243;
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                                                                                                                                                        MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                   STRAIN=K1
                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                        Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                           Aeropyrum pernix
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Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Willalon D.K., Toshiwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
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Best Local S
Matches
Submitted (JUL-2004) to the EMBI Submitted (JUL-2004) to the EMBI SHEET STATE (SO) GO:0046872; F:metal ion bin InterPro; IPRO01594; Znf_DHHC: Ifam; PF01529; Zf-DHHC; 1.
PRODOM; PD003041; Znf_DHHC; 1.
PROSITE; PS50216; ZF_DHHC; 1.
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25-OCT-2004
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PIR; D72660; D72660; D72660;
HSSP; P19919; 1N62.
GO; GO:0016491; F:oxidoreductase activity;
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR008274; Aldxan_dh_hamm.
InterPro; IPR008674; Aldxan_dh_hamm.
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Name=zgc:91907;
Brachydanio rerio (Zebrafish)
Brachydanio Metazoa; Chordata;
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Pfam; PF02738; Ald Xan dh C2; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 753 AA; 82419 MW; 6836618422F1322D CRC64;
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Actinopterygii; Neopterygii;
Cyprinidae; Danio.
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DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.; "Generation and initial analysis and mouse cDNA sequences.";
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.
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Last sequence up
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Pred. No.
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; Craniata; Vertebrata; Eu
Teleostei; Ostariophysi;
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Q8U0D0;
01-JUN-2002
01-JUN-2002
01-OCT-2003
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01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein PF1669;
OrderedLocusNames=PF1669;
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MEDILINE=229484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sohara M., Matsumoto M., Shimpo S., Tguruoka H., Wada T., Yamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyrh
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      Complete
SEQUENCE
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01-OCT-2003
                                                                                     STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF01757; Acyl_transf_3; 1.
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GO; GO:0016747; F:transferase activity,
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                                                             EMBL; AE010265; AAL81793.1;
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                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota;
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         78E56B3AEFF164CC CRC64;
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01-NOV-1999 (TrEMBLrel. 12, I
01-MAR-2004 (TrEMBLrel. 26, I
Serine/threonine kinase PKN8.
                                                                                                   01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
2-oxoisovalerate dehydrogenase alpha subunit (EC 1.2.4.4) (Branched-2-oxoisovalerate dehydrogenase El component alpha chain) (BCKDP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000001; Prot_kinase; 1.

SMART; SM00028; TPR; 4.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS50005; TPR; 2.

PROSITE; PS50293; TPR_REGION; 1.
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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inouye S., Jain R., Ueki T., Nariya H., Xu C., Munoz-Dorado J., Farez-Vidal E., Inouye M.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ
                                                                                           chain alpha-keto acid dehydrogenase El-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50
ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                 Pseudomonas putida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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STRAIN=DZF1;
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                   Pseudomonadaceae;
                                                                            Name=bkdA1;
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30; GO:0004672; F:protein kinase activity; IE
30; GO:000468; P:protein amino acid phosphor
InterPro; IPR011009; Kinase like.
InterPro; IPR008940; Prenyl trans.
InterPro; IPR001719; Prot kinase.
InterPro; IPR001719; Prot kinase.
InterPro; IPR001719; Prot kinase.
InterPro; IPR001719; TPR-1; I.
Ifam; PF00515; TPR 1; I.
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8; Conserv
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                     Pseudomonas
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114312 MW;
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MW; 7752862DAA25338C CRC64;
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SEQUENCE F
STRAIN=G2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99356017; PubMed=10426958; DOI=10.1038/11563; Aevarsson A., Seger K., Turley S., Sokatch J.R., Hol W.G.J.; "Crystal structure of 2-oxoisovalerate and dehydrogenase and the architecture of 2-oxo acid dehydrogenase multienzyme complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Madhusudhan K.T., Huang G., Burns G., Sokatch J.R.; "Transcriptional analysis of the promoter region of the putida branched-chain keto acid dehydrogenase operon."; J. Bacteriol. 172:5655-5663(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M57613; AAA65614.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methylpropanoyl)dihydrolipoyllysine + CO(2).
-!- COFACTOR: Thiamine pyrophosphate.
-!- SUBUNIT: Heterodimer of an alpha and a beta chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91008935;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                     D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catalyzes the overall conversion of alpha-keto acids to acyl and CO(2). It contains multiple copies of three enzymatic components: branched-chain alpha-keto acid decarboxylase (E1 lipoamide acyltransferase (E2) and lipoamide dehydrogenase (CATALYTIC ACTIVITY: 3-methyl-2-oxobutanoate + (dihydrolipoyllysine-residue (2-methylpropanoyl)transferase] lipoyllysine = [dihydrolipoyllysine-residue (2-methylpropanoyl)transferase] S-(2-methylpropanoyl)dhydrolipoyllysine + CO(2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1080;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Flavoprotein; Oxidoreductase; Thiamine pyrophosphate
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   6:785-792 (1999)
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MEDLINB=22423060; PubMed=12534463;

Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,

Melson K.E., Weinel C., Pouts D.E., Gill S.R., Pop M., Holmes

Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes

Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.

Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,

Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,

Mance I., Chris Lee P., Holtzapple B.K., Scanlan D., Tran K.,
                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                    Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                         2-oxoisovalerate dehydrogenase, alpha subunit.
Name=bkdA1; OrderedLocusNames=PP4401;
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                                                          NCBI_TaxID=160488;
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Q911M2;
Q11MA:
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Q2-0x0150valerate dehydrogenase (Alpha subunit).
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STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

STRAIN=20437337; PubMed=10984043; DOI=10.1038/35023079;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

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MEDLINE=20437337; PubMed=10.984043; DOI=10.1038/35023079;

MEDLINE=2044744, PubMed=10.9840443; DOI=10.1038/35023079;

MEDLINE=2044744, PubMed=10.9840444, PubMed=10.984044, PubMed=10.984044, PubMed=10.984044, PubMed=10.98404, PubMed=10.984044, PubMed=10.98404, PubMed=10.98404, PubMed=10.98404, PubMed=10.98404, PubMed=10.98404, PubMed=10.98404, PubMed=10.98404, PubMed=10.98404, PubMed=10.98404, PubM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB004650; AAG05635.1;
PIR; C83365; C83365.
PIR; S05057; S05057.
HSSP; P09060; 1QS0.
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Pfam; PF00676; E1_dh;
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Hoheisel J., Straetz M., He
Duesterhoeft A., Tuemmler E
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GO; GO:0030077; C:light-harvesting complex (s
GO; GO:0045156; F:electron transporter, trans
GO; GO:004518; P:electron transport; IEA.
GO; GO:0019684; P:photosynthesis, light react
InterPro; IPR005871; Photo_L.
InterPro; IPR00484; Photo_RC.
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01-AUG-1998
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PRINTS; PR00256; REACTNCENTRE.
TIGREAMS; TIGR01157; pufL; 1
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STRAIRSRI / ATCC 13939 / DSM 20539 / NCIB 9279;

STRAIRSRI / ATCC 13939 / DSM 20539 / NCIB 9279;

MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;

White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,

Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,

Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,

Fraser C.M.;
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01-JUN-2003 (TrEMBLrel. 24,
Hypothetical protein DR0948,
OrderedLocusNames=DR0948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000
                                                                                                                                                                                                                                                                                                          Name=pufL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 286:1571-1577(1999).
EMBL; AE001947; AAF10530.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
                                                                                                                                                                                                       STRAIN=IAM14332;
MEDLINE=21822632; PubMed=11832943;
                                                                                                                                                                                                                                                                                                                      Photosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the radioresistant bacterium radiodurans R1.";
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                                                                                                                                                      Nature
                                                                                                                                                                   "Unsuspected
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        NCBI_TaxID=39960;
                                                                                                                                                                                                                                                                     Sphingomonadaceae;
                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
                                                                                                                                                                                                                                                                                              Erythrobacter litoralis
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                                                                                                                                                      ected diversity among marine 415:630-633(2002).
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., Eisen J.A., Fraser C.N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteome;
150 AA;
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16891 MW; 6
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center L subunit (Fragment).
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Last annotation update)
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Pred. No.
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69A7695F09EBF3FB CRC64;
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                                                                                                                                                                  3; DOI=10.1038/415630a;
J.F., Nelson W.C., Preston
M., Delong E.F.;
ine aerobic anoxygenic photo
                                                                                                                 complex (sensu
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RESULT 15
Q9XDVO
ID Q9XDVO
AC Q9XDV
AC Q9XDV
DT 01-NC
DT 01-MA
DE Photo
GN Name-
OK Erryth
OC Bacte
OC Sphin
OX NCBI
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RN [1]
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082989
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Best Local S
Matches 9
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01-NOV-1998
01-NOV-1998
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Q9XDV0;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sphingomonadaceae;
NCBI_TaxID=1042;
[1]
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InterPro; IPR000484; Photo_RC.
Pfam; PF00124; Photo_RC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Pre
Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erythrobacter sp.
Bacteria; Proteobacteria;
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01-NOV-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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SEQUENCE FROM N.A.
                   Sphingomonadaceae;
NCBI_TaxID=94771;
                                            Bacteria; Proteobacteria;
                                                      Erythrobacter sp. MBIC3960
                                                                Name=pufL;
                                                                          01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Photosynthetic reaction
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0030077; C:light-harvesting complex GO; GO:0045156; F:electron transporter, tr GO; GO:006118; P:electron transport; IEA. GO; GO:0019684; P:photosynthesis, light re
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB015708; BAA32995.1; -. HSSP; P02954; 1YST.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MBIC3019;
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                                                                                                                                                                                                                                                                                                              TIGRFAMs;
                                                                                                                                                                                                                                                                                                                        PRINTS; PR00256; REACTNCENTRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Unsuspected diversity among marine aerobic anoxygenic Nature 415:630-633(2002).
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9; Conserve
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9; Conserv
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PS00244; REACTION_CENTER;
                                                                                                                                                                                                             SIEGPTLREWLTSRTP
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                                                                                                                                                                                                                                                                             249 AA;
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                                                                                                                                   PRELIMINARY;
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                                cteria; Alphaproteobacteria; Sphingomonadales;
Erythrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erythrobacter.
                                                                                                                                                                                                                                                                               27702 MW;
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                                                                                      12,
12,
26,
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center L subunit.
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                                                                                                             Created)
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Pred. No.
                                                                                                                                                                                                                                Pred. No. 20;
1; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                         Length 249;
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RESULT 16
Q9RKM5
                                                                        A TO DESCRIPTION OF SECULATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOR READER OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF 
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Nature 415:630-633 (2002).

REMBL; AB027515; BAA78672.1; -.

R HSSP; P02554; 1YST.

R GO; GO:0030077; C:light-harvesting complex (sensu Proteoba GO; GO:0045156; F:electron transporter, transferring elect GO; GO:004518; P:electron transport; IEA.

R GO; GO:001818; P:electron transport; IEA.

R GO; GO:0019684; P:photosynthesis, light reaction; IEA.

R InterPro; IPR005871; Photo L.

R InterPro; IPR000871; Photo RC.

R FIGHERM; PF00124; Photo RC; 1.

R PFANYTS; PR00256; REACTNCENTRE.

R FIGHERM; TIGR01157; PULL; 1.

R PROSITE; PS00244; REACTION CENTER; 1.

SEQUENCE 278 AA; 30735 MW; OBE618844B3C54FB CRC64;
Query Match
                                                                                                                                                                                   Pfam; PF
PRINTS;
SMART; S
                                                                                                                                                                                                                                                                                                                                                                      Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harris D.E., Quail M.A., Kieser H., Collins M., Cronin A., Braser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9RKM5;
01-MAY-2000
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Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative MerR family transcriptional regulator ORFNames=SCD17.06C;
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                                                                    SMART; SM00422; HTH MERR; 1.
PROSITE; PS50937; HTH MERR 2; 1.
Complete proteome; DNA-binding.
SEQUENCE 319 AA; 34841 MW; 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence coelicolor A3(2).";
Nature 417:141-147(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
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L-MAY-2000 (TrEMBLrel. 13, Last sequence update)
L-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                     PR00040; HTHMERR.
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R HSSF; P71584; 106Y.

R HSSF; P71584; 106Y.

R GO; GO:0004574; F:protein serine/threonine kinase activity;

R GO; GO:0004674; F:protein serine/threonine kinase activity;

R GO; GO:0004674; F:protein serine/threonine kinase activity;

R GO; GO:0016740; F:transferase activity; IEA.

Interpro; IPR00199; Kinase like.

Interpro; IPR000719; Prot kinase.

Interpro; IPR002290; Ser_thr_bkinase.

Interpro; IPR002290; Ser_thr_bkinase.

Interpro; IPR002290; Ser_thr_bkinase.

Interpro; IPR002290; Ser_thr_bkinase.

INTERPOSITE; PS0000001; Prot kinase; 1.

BR PROSITE; PS00119; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00119; PROTEIN KINASE ST; 1.

DR PROSITE; PS001108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
         RESULT 18
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Q8GAI0;
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Q9KX10;
01-OCT-2000
Arthrobacter nicotinovorans. Plasmid pAo1.
                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Putative amino acid permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; Y13639; CAA73979.1; -.
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STRAIN=COL;
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R EMBL; AJ507836; CAD47924.1; -.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0005279; F:amino acid-polyamine transporter act

R GO; GO:0006865; P:amino acid transport; IEA.

R GO; GO:0006810; P:transport; IEA.

R InterPro; IPR002293; AA/rel_permease1.

InterPro; IPR004941; Permease region.

Pfam; PF00324; AA permease; Transport.

Plasmid; Transmembrane; Transport.

SEQUENCE 481 AA; 49782 MW; 4EA9FB3BB8B76B64 CRC64;
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MEDILINE=96172783; PubMed=8588735;

Menendez C., Igloi G., Henninger H., Brandsch

"A pA01-encoded molybdopterin cofactor gene (molybdopterin cofactor gene)

nicotinovorans: Charecterization and site-dire
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DOI=10.1128/JB.183.18.5262-5267.2001;
DOI=10.1128/JB.183.18.5262-5267.2001;
Baitsch D., Sandu C., Brandsch R., Igloi G.L.;
"A gene cluster on pA01 of Arthrobacter nicotinovorans involved in degradation of the plant alkaloid nicotine: cloning, purification characterization of 2.6-dibydroxypyridine 3-hydroxylase.";
J. Bacteriol. 183:5262-5267(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98088982; PubMed=9428706;
Menendez C., Otto A., Igloi G., Nick
Bottcher B., Brandsch R.;
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[5]
SEQUENCE FROM N.A.
MEDLINE=97230479; PubMed=9073580;
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"Gene structure and properties of enzymes of the pl
nicotine catabolism of Arthrobacter nicotinovorans.
J. Mol. Biol. 284:1323-1339(1998).
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Igloi G.L., Brandsch R.;
"Sequence of the 165-kilobase catabolic acquence of the 165-kilobase catabolic acquence and identification of a property of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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MEDLINE=99096870; PubMed=9878353; DOI=10.1006/jmbi.1998.2227;
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Brandsch R.;
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Q751J9;
Q5-JUL-2004
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical P0022D06.17)
                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2004) to the EMBL; AC130603; AAT01306.1; EMBL; AC132485; AAU03115.1;
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                                                           Staphylococcus aureus Bacteria; Firmicutes;
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            STRAIN=MW2
                                                                                   OrderedLocusNames=MW1103;
                                                                                               MW1103 protein.
MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
                        SEQUENCE FROM N.A
                                             NCBI_TaxID=196620;
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Bacillales;
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Lancet 359:1819-1827(2002).

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Lancet 359:1819-1827(2002).

Lancet 359:1819-182968.1; -.

RESEP: P71584; 106Y.

RESEP: P71584; 106Y.

RESEP: P71584; F:AFP binding; IEA.

RESO; GO:0005524; F:AFP binding; IEA.

RESO; GO:0006474; F:protein berine/threonine kinase act GO; GO:0016740; F:transferase activity; IEA.

RESO; GO:0016740; F:transferase activity; IEA.

RESO; GO:0016740; F:protein amino acid phosphorylation;

RESEPTO; IPR0011009; Kinase like.

RINTERPTO; IPR001543; PASTA.

RINTERPTO; IPR002790; Ser_thr_pkinase.

RINTERPTO; IPR002790; Ser_thr_pkinase.

RINTERPTO; IPR00271; Ser_thr_pkinase.
Lancet 357:1225-1240(2001).
-!- SIMILARITY: Belongs to the S.
EMBL; AP003361; BAB57382.1; -.
PIR; G89894; G89894.
HSSP; P71584; 106Y.
GO; GO:0005524; F.Penicillin bin GO; GO:0004674; F:protein serine, GO; GO:0016740; F:transferase ac
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SMART; SM00740; PASTA; 3.

SMART; SM00220; STKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN KINASE_TINE;

ATP-binding; Complete proteome; Kinase;

Serine/threonine-protein kinase; Transferase.

SEQUENCE 664 AA; 74363 MW; 26F1386C5DB61828 CRC64;
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STRALN=Mu50 / ATCC 700699;

MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

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P; P71584; 106Y.
GO:0005524; F:AIP binding; IEA.
GO:0008558; F:penicillin binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity;
GO:0016740; F:transferase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (strain Mu50 / ATCC 700699)
Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
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Naimi T.,
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Best Local S
Matches 10
                                                                      InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR002271; Ser thr pkin AS.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR008271; Tyr pkinase.
Pfam; PF03793; PASTA; 2.
ProDom; PF0000001; Prot kinase; 1.
SMART; SM00740; PASTA; 3.
SMART; SM00220; STKC; 1.
SMART; SM002219; TyrKC; 1.
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05-JUL-2004 (TrE
05-JUL-2004 (TrE
05-JUL-2004 (TrE
Protein kinase.
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InterPro;
InterPro;
InterPro;
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-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family EMBL; AP003133; BAB42315.; -.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000658; F:penicillin binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity;

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016468; P:protein amino acid phosphorylation; IEA.
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SMART; SM00740; PASTA; 3.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_TOM; 1.

ATP-binding; Complete proteome; Kinase;

Serine/threonine-protein kinase; Transferase.

Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayasi Cui L., Oguchi A., Aoki K.-I., Nagai Y., Liami H., Hosoyami Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyami Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Whole genome sequencing of meticillin-resistant Staphylococo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR011009; Kinase_like.
InterPro; IPR005543; PASTA.
InterPro; IPR0007719; Prot kinase.
InterPro; IPR002290; Ser thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF03793; PASTA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus (strain N31:
Bacteria; Firmicutes; Bacillales;
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                           IPR005543; PASTA.
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Y., Lian J.-Q., Ito
A., Murakami H., Hoso
no T., Inoue R.-I., K
Goto S., Yabuzaki J.,
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GO; GO:0008658; F:penicillin binding; IEA
GO; GO:0004674; F:protein serine/threoni
GO; GO:0004713; F:protein-tyrosine kinas
GO; GO:0004713; F:protein-tyrosine kinas
GO; GO:0006468; P:protein amino acid phe
InterPro; IPR011009; Kinase like
InterPro; IPR005243; PASTA.
InterPro; IPR005243; PASTA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkinase.
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Holden M.T.G., Feil B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quail M.A., Rabbinowitsch B., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Spratt B.G., Parkhill J.;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Serine/threonine-protein kinase (EC 2.7.1.-).
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Serine/threonine-protein kinase; Transf
SEQUENCE 664 AA; 74377 MW; 3461386C
                                                                                                                                                                                                     ProDom; PD000001; Prot_kinase; 1.

SMART; SM00740; PASTA; 3.

SMART; SM00220; TyrK; 1.

SMART; SM00220; TyrK; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS0011; PROTEIN_KINASE_ST; 1.

PROSITE; PS05011; PROTEIN_KINASE_ST; 1.

ATP-binding; Complete proteome; Kinase;

Serine/threonine-protein kinase; Transferase.

Sequence 664 AA; 74363 MW; 26F1386C5DB61828 CRC64;
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Bacteria; Firmicutes; Bacillales; Stap
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Pfam; PF00069; Pkinase;
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LI, BX571857; CA642231.1; -.

GO:0005524; F;AFP binding; IEA.

GO:0008658; F:penicillin binding; IEA.

GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO:0016740; F:transferase activity; IEA.

GO:0016740; F:protein amino acid phosphorylation; IEA.
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/ MW; 3461386C5DB61828 CRC64;
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RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Peltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Wayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
Spratt B.G., Parkhill J.;
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Pfam; PF00069; Pkinase; 1.

ProDom; PD000001; Prot_Kinase; 1.

PROMART; SM00740; PASTA; 3.

SMART; SM00220; S_TKC; 1.

SMART; SM00229; TyrKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS001107; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Complete proteome; Kinase;
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Q8Y0I5;
01-MAR-2002
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05-JUL-2004 (TrEMBLrel. 27, Last sequence upd
05-JUL-2004 (TrEMBLrel. 27, Last annotation u
Serine/threonine-protein kinase (EC 2.7.1.-)
Name=pknB; OrderedLocusNames=SAR1196;
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Serine/threonine-protein kinase; Transferase.
267 AA: 74363 MW; 26F1386C5DB61828 CRC64;
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Hypothetical

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01-NOV-1995
01-NOV-1995
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                                                                                                                                             entities
or send a
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STRAIN-Rd / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D. Adams M.D., White O., Clayton R.A., Kirkness E.F.

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.

McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation updat
Hypothetical UPF0260 protein HI1355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21881879; PubMed=11823852; DOI=10.1038/415497a; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brotttier P., Camus J.C., Cattolico L., Charlat M., Choisene N., Claudel-Renard C., Cunac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
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Bacteria; Proteobacteria; Betaproteobacteria; Bur
Burkholderiaceae; Ralstonia.
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                EMBL; U32814; AAC230
PIR; F64026; F64026.
TIGR; H11355; -.
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                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
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Bacteria; Proteobacteria;
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                                                                                                                                             s requires a license agreement (Some an email to license@isb-sib.ch).
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Pfam; PF05779; DUF838; 1.
PIRSF006173; UCP006173; 1.
ProDom; PD021710; UCP006173; 1.
Complete proteome; Hypothetical protein.
Complete proteome; Hypothetical protein.
SEQUENCE 154 AA; 18163 MW; 886CE6D467EBAB55 CRC64;
Anopheles gambiae str. PEST.
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Diptera; Nematocera; Culicoidea; Anc
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GO; GO:0030077; C:light-harvesting complex
GO; GO:0045156; F:electron transporter, tr
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0019684; P:photosynthesis, light re
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Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
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01-AUG-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Photosynthetic reaction
                                                                            AgCP2340 (Fragment)
Name=agCG44337; ORF
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PROSITE; PS00244; REACTION_CENTER; 1.
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InterPro; IPR000484; Photo_RC.
Pfam; PF00124; Photo_RC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=IAM12620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=73269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium sanguineum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=pufL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
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                                                                                                                                                                                                                                                                                                                                27
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                                                                                                                                                                                                                                                                                                                                QGPTLNPWLISINPPS
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                                                                                                                      (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 AA; 26840 MW;
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                                                                                ORFNames=ENSANGG00000014770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                48.0%;
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07, Last 1
26, Last 1
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                                                                                                                                                                                                                                                                                                                                   42
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Ler L subunit (Fragment)
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Pred. No.
                                                                                                                           Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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rter, transferring
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17;
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RESULT 30
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EMBL; AY590492; AAT36730.1; -.

HSSP; P00730; 1ARM.

GG; GG:0004182; F:carboxypeptidase A activity; IEA.

GG; GO:0004180; F:carboxypeptidase activity; IEA.

GG; GO:0006508; F:protablese activity; IEA.

GG; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000834; Peptidase_M14.

InterPro; IPR000834; Peptidase_M14.

InterPro; IPR000834; Prot inh_M14A.

InterPro; IPR000834; Prot inh_propept.

Pfam; PF00246; Peptidase_M14; 1.

Pfam; PF00244; Propep M14; 1.

PFAMTYS: DD00725. CRDSTORMS.
                                                                                                                                            Query Match
Best Local
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Best Local
                                                                                                                                 Matches
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Carboxypeptidase A (EC 3.4.17.1).
NameCPA-VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; m.....
Neoptera; Endopterygota;
NCBI_TaxID=7159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
O31703 PRI
O31703; Q7BVS3;
                                                                                                                                                                                   PRINTS; PR00765; CRBÖXYPTÁSEA.

SMART; SM00631; Zn_pept; 1.

PROSITE; PS00132; CARBOXYPEPT_ZN_2; UNKNOWN_1.

PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.

Carboxypeptidase; Hydrolase.

SEQUENCE 417 AA; 47505 MW; E599DB6D4A41B971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=CPA-VI;
Aedes aegypti (Yellowfever mosquito).
Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-PEST;
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6J6D5
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                                                                                                                                Similarity
8; Conserv
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                                                                                                      TLREWLTSRTPHS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR008042; Retrotrans_Pao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282
282 AA;
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                                                                                                                                 Conservative
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            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31558 MW;
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                                                                                                                                            48.0%;
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                                                                              238
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                                                                                                                                 Score 47; DB Pred. No. 52; 2; Mismatches
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Pred. No.
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               PRT;
                                                                                                                                                                                      E599DB6D4A41B97B CRC64;
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               430
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RX MEDLINE=80044033; PubMed=9384377; DOI=10.1038/36786;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Bloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Galamings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Britz C., Fujita M., Fujita Y., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Kleerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Park S.H., Parro V., Pohl T.M., Porcetelle D., Porwollik S.,
RA Park S.H., Parro V., Pohl T.M., Porcetelle D., Porwollik S.,
RA Park S.H., Parro V., Sato T., Scanlan E., Schoeter R.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schoeter R.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schoeter R.,
RA Takemaru K., Takeuchi M., Tanakoshi A., Tarakaka T., Terpstra P.,
RA Takenaru K., Takeuchi M., Tanakoshi A., Tanakaka T., Terpstra P.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RA Yoshikawa H., Danchin A.;
RA Yoshikawa H., Danchin A.;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat molybdopterin biosynthesis protein MoeA.
                                                              Caldwell R.M., Ferrari E.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z9911; CAB13301.1; -.
EMBL; AF012285; AAC24902.1; -.
EMBL; B69659; E69659.
HSSP; P12281; IGBL.
HSSP; P1281; IGBL.
GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=moeA; OrderedLocusNames=BSU14280;
Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                        Henriques A.O., Bryan E.M., Beall B.W., Moran C.P. Jr.; "csel5, cse60, and csk22 are new members of mother-cell-specific sporulation regulons in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hemila H., Palva A., Paulin L., Arvidson S., Palva I., "Secretory S complex of Bacillus subtilis: sequence analysis identity to pyruvate dehydrogenase.";
J. Bacteriol. 172:5052-5063(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome subtilis.";
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                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97144523; PubMed=8990290;
Henriques A.O., Bryan E.M., Beall B.W., Moran C.P. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90368558; PubMed=1697575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:249-256(1997).
                                          InterPro;
                                                                                                                                                                                                                                                                                      Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
IPR001453; MoCF_biosynth
IPR005111; MoeA_C.
IPR005110; MoeA_N.
                                                                                                                                                                                                                                                                                      179:389-398(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of the Gram-positive bacterium Bacillus
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R pfam; pF00793; PASTA; 2.
R pfam; pF00069; Pkinase; 1.
R pfam; pF000001; Prot_kinase; 1.
R Probom; pD000001; Prot_kinase; 1.
JR SMART; SM00740; PASTA; 3.
DR SMART; SM00220; S TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Complete proteome; Kinase; SR
Serine/threonine-protein kinase; Transferase.
Serine/threonine-protein kinase; Transferase.
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QBCSV9
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Q8CSV9;
01-MAR-2003
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008658; F:penicillin binding; IEA.
GO; GO:0008658; F:penicillin binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity;
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR011009; Kinase_like.
InterPro; IPR001719; Prot_kinase.
InterPro; IPR000719; Prot_kinase.
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Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
Zhang Y.-Q., Ren S.-X., Li H.-L., Chen R.-S., Shen Y., Chen Z.,
Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S.,
Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
Yenome-based analysis of virulence genes in a non-biofilm-forming
"Genome-based analysis of virulence genes in a non-biofilm-f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00994; MoCF_biosynth; 1.
Pfam; PF03454; MoeA_C; 1.
Pfam; PF03453; MoeA_N; 1.
ProDom; PD002460; MoCF_biosynth; 1.
TIGRFAMs; TIGR00177; molyb_syn; 1.
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Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Dfam. BP03703, Bacma.
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90
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                                                               IEGPTLREWLTSRTPHS
IEGPTLAEYIHSHGPLS
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106
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                                                                                                                              Score 47; DB Pred. No. 86; 2; Mismatches
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Last annotation update)
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Pred. No.
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Matches 7
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P37940;
01-OCT-1994
01-OCT-1994
25-OCT-2004
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Q7WWY0;
01-OCT-2003
01-OCT-2003
01-MAR-2004
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01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-2094 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
2-oxoisovalerate dehydrogenase alpha subunit (EC 1.2.4.4) (Branched-2-oxoisovalerate dehydrogenase El component alpha chain) (BCKDH
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Bacteria; Proteobacteria; Betaproteobacteria;
Burkholderiaceae; Wautersia.
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Name=trbE; ORFNames=PHG362;
Alcaligenes eutrophus (Ralstonia eutropha).
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93279308; PubMed=8504804; Wang G.-F., Kuriki T., Roy K.L., Kaneda T.; "The primary structure of branched-chain alpha-oxo from Bacillus subtilis and its similarity to other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-bfmBAA; Synonyms-bfmB1a; OrderedLocusNames=BSU24050;
Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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J. Mol. Biol. 332:369-383(2003)
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Gottschalk G.;
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Schwartz E., Henne A., Cramm R., Eitinger
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                                                                                                                             Mizuno M., Ma
Kobayashi Y.;
                                                                                                                                                                                      STRAIN=168 / JH64.
MEDLINE=97124195;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=168 / JH642;
                                                                                                                                                                                                                                                                                                                                                     dehydrogenases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1423;
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                              sporulation genes.
                                                            the Bacillus subtilis
                                                                                           Systematic sequencing
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142:3103-3111(1996)
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                                                                                                                                                        PubMed=8969508;
S., Takemaru K.
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                                                            genome containing the
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tringer T., Friedrich B.,
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STRAIN=168;
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                                                                                                                                                                                                                                  This
                                                                                                                EMBL; M97991; AAA22278.1; -.
EMBL; D84432; BAA12598.1; -.
EMBL; Z99116; CAB14336.1; -.
PIR; C69593; C69593.
                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997).
                                                  Oxidoreductase; Thiamine pyrophosphate
                                                                                           SubtiList;
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                                                               Complete
                                                                                    nterPro;
                                                                                                                                                                                                                                                                                                                    catalyzes the overall conversion of alpha-keto acids to acy and CO(2). It contains multiple copies of three enzymatic components: branched-chain alpha-keto acid decarboxylass (Elipoamide acyltransferase (B2) and lipoamide dehydrogenase CATALYTIC ACTIVITY: 3-methyl-2-oxobutanoate +
                                                                                                                                                                                                                                                       COFACTOR: Thiamine pyrophosphate.
SUBUNIT: Heterodimer of an alpha and a beta chain.
                                                                                                                                                                                                                                                                            methylpropanoy1)transferase[ S-(2-
methylpropanoy1)dihydrolipoyllysine + CO(2).
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                                                                                                                                                                                                                                                                                                  [dihydrolipoyllysine-residue (2-methylpropanoyl)transferase]
lipoyllysine = [dihydrolipoyllysine-residue (2-
                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                P12694; 1DTW.
List; BG10307; bfmBAA.
Pro; 1PR001017; Dehydrogenase_E1.
                                                                       PF00676; E1_dh;
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                                                               Direct protein sequencing; Flavoprotein;
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Pred. No. 4
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Q65HK8;
25-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oxoisovalerate dehydrogenase alpha subunit).
Name=bkdAA; ORFNames=BL01504, BLi02582;
Bacillus licheniformis DSM 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Veith B., Herzberg C., Steckel S., F.
Ehrenreich P., Baeumer S., Henne A.,
Ehrenreich A., Gottschalk G.;
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25-OCT-2004 (TrEMBLrel. 28, Last
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BkdAA (Branched-chain alpha-keto
MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483; Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G. Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khala
                                                                                                                                                      Hypothetical protein HP0906. OrderedLocusNames=HP0906;
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                                                                                                                                                                                                                                                                                                                                                                                                                 licheniformis and comparisons with Genome Biol. 5:R77-R77(2004).
EMBL; AE017333; AAU41456-1; -.
EMBL; CP000002; AAU24096.1; -.
                                              SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
                                                                                                                              Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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                                                                                                                Helicobacteraceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete genome sequence of the industrial bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. Biotechnol. 7:204-211(2004)
                                                                                                   TaxID=210;
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STRAIN=MF3813 TX;
Goldberg C.S., Sullivan B.K., Malc
"Divergence among barking frogs (E
southwestern United States.";
Herpetologica 60:312-320(2004).
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TIGR; HP0906; -.
GO; GO:0009424; C:fla;
GO; GO:0003774; F:mot
Q64K12;
Q64K12;
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae; Telmatobiinae; Eleutherodactylus. NCBI_TaxID=228429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q64K11 PRELIMINARY; PRT; 156 AA. Q64K11; 25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation updat NADH dehydrogenase subunit II (Fragment).
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Nature 388:539-547(1997).
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Herpetologica 60:312-320(2004).
EWBL; AY442949; AAS49141.1; -.
Mitochondrion.
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MADH dehydrogenase subunit II (Fragment).
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EMBL; AY442953; AAS49145.1; -.
EMBL; AY442951; AAS49143.1; -.
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Goldberg C.S., Sullivan B.K., Malone J.H.,
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Amphibia; Batrachia; Anura; Ne
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inae; Eleutherodactylus.
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                                                (TrEMBLrel. 28, Created)
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genase subunit II (Fragment).
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Q82PX5;
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Herpetologica 60:312-320(2004).
EMBL; AY42941; AAS49133.1;
EMBL; AY442948; AAS49140.1;
EMBL; AY442938; AAS49140.1;
EMBL; AY442938; AAS49130.1;
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Telmatobiinae; Eleutherodactylus.
NCBI_TaxID=228429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                southwestern United States.";
Herpetologica 60:312-320(2004).
EMBL; AY442940; AAS49132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=ND2; Eleutherodactylus augusti (barking frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TERMBLrel. 28, Created)
25-OCT-2004 (TERMBLrel. 28, Last sequence update)
25-OCT-2004 (TERMBLrel. 28, Last annotation update)
NADH dehydrogenase subunit II (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q64K25;
25-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
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                                         01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=HuachucaMts30_AZ;
Goldberg C.S., Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q64K25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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a; Hyloidea;
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Best Local S
Matches 8
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Q745Z3;
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation updat
Ribonucleoside-diphosphate reductase alpha chain.
OrderedLocusNames=TTP0162;
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[1]
                                                                          InterPro; IPR000788; Ribonucleo_red.
InterPro; IPR010994; RuvA 2_llke.
InterPro; IPR015829; Sug_transporter.
Pfam; PF02867; Ribonuc_red_lgC; 1.
PRINTS; PR01183; RIBORDTASEM1.
                                                                                                                                                                                                                                                                         Nat. Biotechnol. 22:547-553(2004).

EMBL; AB017222; AAS82492.1; -.

GO; GO:0005371; C:ribonucleoside-diphosphate

GO; GO:0004748; F:ribonucleoside-diphosphate

GO; GO:0006250; P:DNA replication; IEA.
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Jacobi C.,
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SEQUENCE 377 AA; 41307 MW; 0253176AAAEB62F3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15064768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                             PROSITE; PS00216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thermophilus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A., Brueggemann H., Raasch C., Wiezer A., Hartsch T., ang H., Johann A., Lienard T., Gohl O., Martinez-Arias J C., Starkuviene V., Schlenczeck S., Dencker S., Huber J H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; enome sequence of the extreme thermophile Thermus
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                                             SUGAR_TRANSPORT_1; UNKNOWN_1.
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                                                                                                                                                                                              Pfam; P700749; tRNA-SYNT 1c; 1.
Pfam; P703950; tRNA-SYNTTIC C; 1.
PRINTS; PR00987; TRNASYNTHGIU.
TIGRPAMS; TIGR0463; gltx arch; 1.
PROSITE; PS00178; AA TRNA_LIGASE I; FALS
Aminoacyl-tRNA synthetase; ATP-binding;
                                                                                                                                                                                                                                                                                                         EMBL; AE009904; AAL64575.1; -.
HSSP; P00962; INYL.
HAMAP; MF 00022; -; 1.
InterPro; IPR004526; GltX_arch.
InterPro; IPR001035; Ribosomal_L25rel.
InterPro; IPR011035; Ribosomal_L25rel.
InterPro; IPR001412; tRNA-synt_I.
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10-OCT-2003 (Rel. 42, Last sequence up:
25-OCT-2004 (Rel. 45, Last annotation:
Glutamyl-tRNA synthetase (EC 6.1.1.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=IN2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.
                                                                                                                                               SEQUENCE
                                                                                                                                                                                 Protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the hyperthermophilic crenarchaeon aerophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller J.H.;
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PSVRDWVAFRIIDTSKTPH
                                      PTLREWL-----TSRTPH 17
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                                                                      Score 46; DB Pred. No. 1.1e 5; Mismatches
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Pred. No.
 276
                                                                                                                                                                  "HIGH"
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                                                                                                                                               (IGH" region.
767FCEE299A3064C CRC64;
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ing; Complete
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                                                                                           1.1e+02;
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                                                                                                            DB 1;
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                                                                          Indels
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RESULT 45
MY1C_HUMAN
    RRACCOSGEDITA
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MRSSP, 105184; 106Y.

MRSSP, GO:00085524; F:ATP binding; IEA.

MRSSP, GO:00085524; F:penicillin binding; IEA.

MRSSP, GO:0008658; F:penicillin binding; IEA.

MRSSP, GO:0004674; F:protein serine/threonine kinase activity; IEA.

MRSSP, GO:0006468; F:protein amino acid phosphorylation; IEA.

MRSSP, GO:0006468; F:protein amino acid phosphorylation; IEA.

MRSSP, GO:0006468; P:protein amino acid phosphorylation; IEA.

MRSSP, GO:0006468; P:protein amino acid phosphorylation; IEA.

MRSSP, GO:0004674; F:transferase.

MRITERPO; IPR011009; Kinase-like.

MRSSP, GO:0004674; PASTA.

MRSSP, GO:0004674; PASTA, 3.

MRSSP, GO:0004674; PASTA; 3.

MRSSP, GO:000749; PASTA; 3.

MRSSP, SM00740; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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01-OCT-2000
01-OCT-2000
01-MAR-2004
                                                                                                                                                                                                                                                                                                   MY1C HUMAN STANDARD; PRT; 1028 AA. 000159; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last amoutation update) myosin Ic (Myosin I beta) (MMI-beta) (MMID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28:4317-4331(2000).

-!-SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AP001515; BAB06223.1; -.
EPIR; H83962; H83962.
                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9K9Z0
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Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine/threonine-protein kinase; Transferase.
SEQUENCE 664 AA; 73719 MW; E2FF225DCCC6EE52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A
                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                    Name=MYO1C;
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8; Conservative
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                                                                                                                                               Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46;
Pred. No.
                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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1.2e+02;
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Search completed: September Job time: 70.9496 secs
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016461; C:unconventional myosin; TAS.
GO; GO:0016461; C:unconventional myosin; TAS.
GO; GO:0009592; P:detection of sound; TAS.
InterPro; IPR001048; IQ_region.
InterPro; IPR001609; Myosin head.
InterPro; IPR010926; Myosin_tail_2.
Pfam; PF00612; IQ; 3.
Pfam; PF000612; IQ; 3.
Pfam; PF000612; Myosin_tail_2; 1.
Pfam; PF000617; Myosin_tail_2; 1.
PF1MT; PF000617; Myosin_tail_2; 1.
PRINTS; PR00193; MYOSINIEAVY.
PRODOM; PD000355; Myosin_head; 1.
SMART; SM00015; IQ; 2.
SMART; SM00015; IQ; 2.
SMART; SM00015; MYOSINIEAVY.
PRODOM; SM00015; IQ; 2.
SMART; SM00015; IQ; 2.
                                                                                                                                                                                                           Myosin; Repeat.
DOMAIN 19
DOMAIN 699
DOMAIN 723
NP_BIND 105
SEQUENCE 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Kidney;
MEDLINE=97237053; PubMed=9119401; DOI=10.1006/geno.1996.4526;
MEDLINE=97237053; PubMed=9119401; DOI=10.1006/geno.1996.4526;
Crozet F., Amraoui A.E., Blanchard S., Lenoir M., Ripoll C., Vago P.,
Hamel C., Fizames C., Levi-Acobas F., Depetris D., Mattei M.-G.,
Weil D., Pujol R., Petit C.;
"Cloning of the genes encoding two murine and human cochlear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X98507; CAA67131.1; -. PIR; A59253; A59253. HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unconventional type I myosins.";
Genomics 40:332-341(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>;</del>
                                                                                                                                                                                                                                                                                                                      Actin-binding; ATP-binding; Calmodulin-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:7597; MYO1C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
SIMILARITY: Contains 2 IQ domains.
SIMILARITY: Contains 1 myosin-like globular head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Myosins are actin-based motor molecules with ATPase activity. Unconventional myosins serve in intracellular movements. Their highly divergent tails are presumed to bind to membranous compartments, which would be moved relative to actin filaments (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606538; -
                                                                       308 SVEGSTLREALTHR 321
                                                                                                      1 SIEGPTLREWLTSR 14
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722
751
112
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                    2005, 16:21:10
                                                                                                                                                                                                                              Myosin head-like. IQ 1. IQ 2. ATP (Potential).
                                                                                                                                                          Score 46; DB 1;
Pred. No. 2e+02;
                                                                                                                                             Mismatches
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Maximum Match
Listing first
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Match
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1: geneseqp1980s:*
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4: geneseqp2001s:*
5: geneseqp2003s:*
6: geneseqp2003s:*
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW09494 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haematology; thrombocytopenia; TPO; TR; proliferation; bone marrow transfusion; chemotherapy; radiation therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombopoietin receptor binding peptide
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                         AAW09461;
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                                                                           AAW09461 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors on
                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                              \mathbf{L}
                                                                                                                                                                                                                                          1 LAIEGPTLRQWLHGNGRDT 19
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                              LAIEGPTLROWLHGNGRDT 19
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LC, Schatz PJ,
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                                                                                                                                                                                                                                                                                                               100.0%; ilarity 100.0%; Conservative 0
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95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 living cells
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                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cwirla SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wagstrom
                                                                              19
                                                                                                                                                                                                                                                                                                                     <u>,,</u>
                                                                                                                                                                                                                                                                                                                                              Score 106; DB 2;
Pred. No. 1.4e-09;
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                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          Length 19;
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Query Match
Best Local :
Matches
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                       The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mum. Th compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                                                                                Dower WJ,
Mattheakis
                                                           Sequence 19
                                                                                                                                                                                                                                                      Claim 18; Page 89; 106pp; English.
                                                                                                                                                                                                                                                                                                    Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haematology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin receptor binding compound peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                     thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-051883/05.
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19;
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                 Barrett RW, Cwirla SE, I
LC, Schatz PJ, Wagstrom
                                                              AA;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombocytopenia; TPO; TR; proliferation; transfusion; chemotherapy; radiation therapy.
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95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Preferably C-terminus is -C(0)R2 where R2 is selected from hydroxy, lower alkoxy, and -NR3R4, where R3 and R4 are independently selected from hydrogen and lower alkyl, and where the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide forming a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Preferably N-terminus is selected from: -NRR1; NRC(0)R; -NRC(0)OR; -NRS(0)ZR; -NHC(0)NHR; succinimide; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Preferably linkages are selected from: -
CH2OC(0)NR-; phosphonate; -CH2S(0)2NR-; -CH2NR-; -C(0)NR6
; -NHC(0)NH; where R is hydrogen or lower alkyl and R6 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                100.0%;
0;
                Score 106; DB 2;
Pred. No. 1.4e-09;
 Mismatches
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m CR, Wrighton NC;
                             Length 19;
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LAIEGPTLROWLHGNGRDT 19

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RESULT 4
AAB17022
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AC AAB1
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AC AAB1
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Matches 19
                                                                                                                                                                                                                                                                            The present peptide, which binds the thrombopoietin receptor (TR), can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
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                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin receptor binding peptide
                                                                                                                                                                                                                                                      Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dower WJ,
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              TPO-mimetic
                                      31-OCT-2000
                                                                                      AAB17022 standard; peptide; 19
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LC, Schatz PJ, Wagstrom CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                  Page 26; 106pp; English.
                                                                                                                                                                                                     Conservative
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K
             peptide sequence
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                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor; binding peptide; treatment; agonist;
disorder; thrombocytopaenia; chemotherapy;
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95US-00485301.
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                                                                                                                                                                                                                   100.0%; Score 106; DB 2;
100.0%; Pred. No. 1.4e-09;
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              SEQ ID NO:78
                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                               Length 19;
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RESULT 5
AAU25864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
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22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30.
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                                                                                                                                                                                                                            AAU25864 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 221; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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99US-00428082
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                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 106; DB 3; 100.0%; Pred. No. 1.4e-09; ... Mismatches 0;
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Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder;

Human thrombopoietin receptor (TPO-R) activator peptide

#50.

0

17-DEC-2001 AAU25864;

(first entry)

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RESULT 6
AAU25825
ID AAU2
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AC AAU2
DT 17-E
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DE Huma
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KW Pept
KW haen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods CC of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such CC as that due to chemotherapy, radiation therapy or bone-marrow CC transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC in purified or natural biological fluids, in tissue homogenates, and CC in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and CC in sugme-linked inmunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed CC progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
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07-JUN-1996;
15-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19
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                                                               Human thrombopoietin receptor (TPO-R) activator peptide #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 20; 128pp;
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Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
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                                                                                                                                                                                    AAU25825 standard; peptide; 19
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                                                                                                                                                                                                                                                                                                                                                                         19;
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Nanian P,
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95US-00485301.
96WO-US009623.
96US-00699027.
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                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 106; DB 4;
100.0%; Pred. No. 1.4e-09;
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RESULT 7
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AC ABB7
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                                                                                                                                                                                                                                                                                                                                                             Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods CC of activating thrombopoietin receptors in cells comparise contacting the Cells with effective amounts of peptides and peptide mimetics attached to the distribution of the methods are used to treat thrombocytopenia such CC as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC as unique tools for understanding the biological role of thrombopoietin CC (TPO) and to develop other compounds that bind to and activate the TPO cells and fixed cells, in biological fluids, in tissue homogenates, and CC in purified or natural biological fluids, in tissue homogenates, and CC situ staining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed committed committed or in conjunction with additional cytokines
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Best Local
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07-JUN-1995;
07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
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Balasubramanian
                                 TPO mimetic
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                                                                05-APR-2002
                                                                                                                               ABB72908
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                                                                                                                             standard;
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wanian P,
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                             peptide SEQ ID
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                                                                (first entry)
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95US-00485301.
96WO-US009623.
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Wagstrom
                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                      100.0%; Score 106; DB 4; 100.0%; Pred. No. 1.4e-09;
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R, Hendren
                                                                                                                                                                                                                                                                            Mismatches
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Deprince
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                                                                                                                                                                                                                                                                            Gaps
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Modified peptide; mimetic; Fc domain;

fusion; immunoglobulin G;

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RESULT 8
ADJ73060
ID ADJ7
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39; Page 44; 176pp; English.
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                                         ADJ73060 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 106; ilarity 100.0%; Pred. No. 1 Conservative 0; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the present
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                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;

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ADJ52695
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XX ACX ADJ5
XX ACX CH1
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XX CH1
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                              ligand binding region (IBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cyrostatic and neuroprotective activities. This peptide sequence is a TPO mimetic peptide sequence used to make a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; anaemia; immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                 Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 514; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-804237/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2002; 2002US-0368791P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-2003; 2003WO-US009139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003084477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ73060;
                                CH1 deleted
                                                                06-MAY-2004
                                                                                                                                 ADJ52695 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PO mimetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                1 LAIEGPTLROWLHGNGRDT 19
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                     of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Knight DM,
                                                                                                                                                                                                                                                                                                                                                    A
A
                               mimetibody-related peptide SeqID514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                   Conservative
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                               100.0%; Score 106; DB 7; 100.0%; Pred. No. 1.4e-09; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scallon BJ,
                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SeqID 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ghrayeb
                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                       19;
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                                                                                                                                                                                                                                                                                      Gaps
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which encode them, compositions, methods and uses. International Compositions and uses. International Compositions and uses. International Composition and the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, cantibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, ctissue, organ or animal, specifically for modulating, treating, cardiovascular (for example arrhythmia, hypertension or heart commune, cardiovascular (for example arrhythmia, hypertension or heart commune, cardiovascular (for example arrhythmia, hypertension or heart commune), or neurodegenerative (for example multiple sclerosis, dementia conditions, or infectious diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hyportension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia;
dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neurolep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004002417-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancerous condition; infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-2003; 2003WO-US020347
                                                                                                                                06-MAY-2004
                                                        CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
                                                                                            CH1 deleted
                                                                                                                                                                                                      ADJ51656 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2004-082870/08
                                                                                                                                                                                                                                                                                                                                1 LAIEGPTLROWLHGNGRDT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q.
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                LAIEGPTLROWLHGNGRDT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΚA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            A
F
                                                                                            mimetibody-related peptide SeqID514
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knight DM,
                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relates to CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO 514; 129pp; English.
                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                res to CH1 deleted mimetibodies (and the DNA secompositions, methods and uses. The invention
                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                       .0%; Score 106; DB 8; .0%; Pred. No. 1.4e-09;
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                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scallon
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                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                          Length 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nesspor TC
     neuroleptic;
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RESULT 11
AAW33028
ID AAW33
XX
AC AAW33

AAW33028 standard; peptide; 19

AAW33028;

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                                                                                                                                                                                                            This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be considered for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, cardiovasculator, antiallergic, muscular-Gen, cytostatic, haemostatic, cimmunomodulator, antiallergic, muscular-Gen, cytostatic, haemostatic, cantiinflammatory, neuroleptic, ophthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-compositions of the crespiratory-Gen activity acting as a tumour necrosis factor (TNF)-compositions of the compositions of the creatment of diseases or conditions associated with aberrant expression cor activity of the CH1 deleted mimetibody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, cardiovascular, dental or oral, dermatological, ear, nose or throat, obstetric, haematologic, immunological, allergic, infectious, metabolic, gastrolitestinal, gynaecological, hepatic, cobstetric, haematologic, immunological, nutritional, ophthalmologic, sequence is that of a peptide which may be used during the creation of a
                                                                             Matches
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; htroat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; oncological disorder; neurological disorder; nutritional disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder; renal disorder; pulmonary disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and
                                                                                                                                                       Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; SEQ ID NO 514; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-082872/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2003; 2003WO-US020495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-2002;
19-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CENZ ) CENTOCOR INC.
                                                                           19;
                    LAIEGPTLRQWLHGNGRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                         Ŗ,
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002US-0392431P
2002US-0412144P
                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ghrayeb J,
                                                                           0;
                                    19
  19
                                                                                                Score 106; DB 8;
Pred. No. 1.4e-09;
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scallon BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious, neurologic and
                                                                                                                    Length
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                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the DNA sequences
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Best Local S
Matches 18
Agonist; immunoglobulin; Ig; variable domain; heavy chain; light chain; complementarity determining region; CDR; antigenic; thrombopoietin; TPO thrombopoietin receptor; MPL; cytotoxic T-lymphocyte; CTL; epitope; T-helper cell; B-helper cell; synthebody; pharmaceutical; vaccine; proliferation; growth; differentiation; haematopoietic cell; antibody; platelet progenitor cell; immune disorder; thrombocytopenia; disseminated intravascular coagulation; stem cell; transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                               resulting from Chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematologi disorders, esp. thrombocytopenia resulting from chemotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1998
                                                                                                                          Antibody
                                                                                                                                                         20-JAN-2003
                                                                                                                                                                                                                  ABG71749 standard; protein; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 19; Page 89; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-052226/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mattheakis LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                         l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                            μ
                                                                                                                          CDR
                                                                                                                                                                                                                                                                                                                          LAIEGPTLROWLHGNGRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barret RW, Cwirla SE, Duffin DJ, Gates C
LC, Schatz PJ, Wagstrom CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                         containing MPL-TPO binding sequence,
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00478128
95US-00485301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                       95.3%;
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                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                        Score 101; DB 2;
Pred. No. 8.6e-09;
                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment; agonist;
                                                                                                                                                                                                                                                                                                                                                          °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gates CM,
                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haematological
                                                                                                                            TPOVHCDR2
                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 13
AAW66721
ID AAW66
XX
AC AAW66
XX
DT 01-DE

AAW66721 standard;

peptide;

15

01-DEC-1998 AAW66721;

(first entry)

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The invention discloses a variant of an immunoglobulin (Ig) variable CC heavy or light chain domain that comprises at least one complementarity CC determining region (CDR) and framework regions flanking the CDR. The CDR also has added or substituted to it, at least one binding sequence which CC is heterologous to the CDR and is an antigenic, agonistic sequence from a CC thrombopoietin (TPO) receptor binding sequence. The antigenic sequence can be a binding sequence heterologous to the CDR, a cytotoxic T-CC lymphocyte (CTL)-epitope sequence, a T-helper cell sequence, a B-helper Cell sequence or a combination of each. The variant or thrombopoietin CC synthebody, pharmaceutical and vaccine compositions are useful for CC stimulating proliferation, growth or differentiation of haematopoietic CC cells, particularly platelet progenitor cells. The variants are also useful for treating or preventing haematopoietic or immune disorders cresulting from chemotherapy, radiation therapy, or bour marrow CC transfusions (e.g. thrombocytopenia or disseminated intravascular CC computation, amplification and ex vivo expansion of stem cells and CC committed precursor cells for autologous and allogeneic transplantation can swell as for the expansion of stem cells for studying the also useful as diagnostic or analytical reagents for studying the contained within the immunoglobulin CDR consensus variable heavy contained within the immunoglobulin CDR consensus variable heavy
                                                                                                           Best Loc
Matches
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                           sequence
chain dom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New thrombopoietin synthebodies, useful for stimulating proliferation, growth, or differentiation of hematopoietic cells, for treating or preventing hematopoietic or immune disorders, e.g. thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; diagnostic; haemostatic; consensus variable heavy chain domain;
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 75; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soltis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-2001; 2001US-0281183P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-040615/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200278612-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PURD
                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DA,
69
                                                 1 LAIEGPTLROWLHGNGRDT 19
                                                                                                           Similarity
12; Conserv
                                                                                                                                                                                                                                135
MGIEGPTLROWLAARARVT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burch RM,
                                                                                                              Conservative
                                                                                                                                                                                                                             A,
                                                                                                                                                                                                                                                                                           (CONVH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                       59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogert RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "TPO receptor binding agonist peptide"
                                                                                                           1;
                                                                                                                                          Score 63;
Pred. No.
                                                                                                              Mismatches
                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulator; anticoagulant;
CONVH.
                                                                                                                                                                      DB 6;
                                                                                                                                             .078;
                                                                                                              9
                                                                                                                                                                      Length 135
                                                                                                                 Indels
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                                                                                                              Gaps
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В
                                                                                                                                                           The invention relates to peptide compounds composed of two peptide chains CC attached to each of the amino groups of a single Lys in the amide form. CC The compounds are of formula (Pept) (Pept) K(NH2), where Pept is of CC formula: X1.1-E-X2.P-T-L-X3.Y4.Y5-L-X6.X7-X8-X9-X10; and pept is of CC formula: X1.1-E-X2.P-T-L-X3.Y4-X5-L-X6-X7-X8-X9-X10; and pept is of CC acetyllysine; X4 = Gln or Glu; X5 = Trp, L-1-naphthylalanine or Phe; X6 = CC Ala, 5-aminopentanoic acid or 2-aminobutyric acid; X7 = Ala, N-dipentylalanine, or is absent; X8 = Arg, P-amino-phenylalanine, N-CC acetyl-lysine, or is absent; X9, X9' = Ala, beta Ala, N-methyl-alanine, CC are capable of binding to, and activating, the thrombopoietin (TPO) CC receptor. They may be used in vitro as tools for understanding the CC biological role of TPO. They may be used as competitive binders in assays to screen for new TPO receptor agonists. They may be used as reagents for CC detecting TPO receptors in living cells, biological fluids, etc. They may be used to maintain growth and proliferation of TPO-dependent cells and CC for in vitro expansion of megakaryocytes. They may be used to activate TPO receptors in vivo, e.g., to treat blood disorders or thrombocytopaenia associated with bone marrow transfusions, radiotherapy or chemotherapy. The present sequence represents a specific example of CC (Pepl)K(NH2)
                               5
                                                                    Matches
                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombopoietin receptor; haematological disorder; screening; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide compound(s) which can bind and activate thrombopoietin receptor - may be used in treating haematological disorders and in methods for screening for new thrombopoietin receptor agonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assay; megakaryocyte; blood disorder; thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide chain of compound which binds to the thrombopoietin receptor.
                                                                                                                                     Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 61; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-377261/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-DEC-1997;
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                                 w
                                                                  l Similarity
                                 IEGPTLROWLHGNGR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrett RW, Cwirla SE, Gates
manian P, Wagstrom CR, Hendren
   IEGPTLRQWLAARGK 15
                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Epsilon amino group of Lys, in its amide form, attached to another peptide chain identical to the reg (residues 1 to 14) of this peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "thrombopoietin receptor agonist'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= MeGly
                                                                                  58.5%;
73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sarcosine"
                                                                                    Score 62; DB 2;
Pred. No. 0.0097;
                                                                      Mismatches
                                                                                                   DB 2; Length 15
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Deprince RB,
                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                      The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

CC (Id)a-Fl-(K2)b, where: Fl = an Fc domain; X1 and X2 = are each coincipendently selected from -(L1)c-Pl-(L2)d-P2-(L2)d-P2-(L1)c-Pl-(CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)d-P2-(L1)c-Pl-(CC (L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, CC (L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L2)d-P2-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L4)f-P4-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L4)f-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P
                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB17302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide
                                                                                                                                                                                                                                                                                               Sequence 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN
                                                                                                                                                   12;
-
                                                                         ω
                                                                                                                                                                                      Similarity
IEGPTLROWLAARAGGGKB
                                                                      IEGPTLROWL---HGNGRD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical.
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spO; TPO; CTLA4; mimetic; IL-1; INF; antagonist; MMP;
                                                                                                                                                                                  57.1%;
63.2%;
                                                                                                                                                   2
   19
                                                                                                                                                                                      Score 60.5;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boone TC;
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                                                                                                                                                       Mismatches
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RESULT 15

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RESULT 16
ADJ73011
ID ADJ73
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                                                                                                                                                                                                                                                                   The present invention describes composition of matter (I) comprising an CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (L1)a-F1-(K2)b, where: F1 = an Fc domain; X1 and X2 = are each CC (independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, CC (P3, and P4 = are each independently sequences of pharmacologically active CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, CC c, d, e, and f = are each independently 0 or 1, provided that at least 1 CC of a and b is 1. The composition can have cytostatic, antiasthmatic, CC cells from the present invention can be used for producing pharmaceutical CC compositions. The compositions are useful for treating cancer, asthma, CC a fab domain) can provide a longer half-life or incorporate functions CC a Fab domain) can provide a longer half-life or incorporate functions CC a seam; local transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the
                                                                                                                                                            Matches
                                                                                                                                                                               Best
                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; CTLA4; mimetic; IL-1; TWF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB17285 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide; therapeutic agent; fusion; autoimmune disease; cytostatic; antiasthmatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17285;
                                                                                                                                                                                                                            Sequence 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-350702/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
22-OCT-1999;
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                ADJ73011 standard; peptide; 29
                                                                                                                                                                                                                                                          exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 315; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis; pharmaceutical.
                                                                                                                                                                             Local
                                                                                              14
                                                                                                                                                          l Similarity
11; Conserv
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                                                                                                                              AIEGPTLRQWL 12
                                                                                               AIEGPTLROWL 24
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                                                                                                                                                              Conservative
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99US-00428082.
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                                                                                                                                                                                                                                                            얁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheetham J,
                                                                                                                                                                                                                                                         nucleotide and amino acid sequences used the present invention
                                                                                                                                                                             56.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                              0;
                                                                                                                                                                             Score 60;
Pred. No.
                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boone TC;
                                                                                                                                                               Mismatches
                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fc domain; cancer;
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                                                                                                                                                                                              Length 28;
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                                                                                                                                                                        RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel mammalian CDR mimetibodies, specific CC portions or variants thereof. Specifically, it refers to an antibody CC fragment where a protein has been inserted into, or replaces a portion CC of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which CC itself comprises at least one human framework region and at least one CC itself comprises at least one human framework region and at least one CC itself comprises at least one human framework region and at least one CC itself comprises at least one human framework region and at least one CC itself composition (LBR). The present invention describes human CC mimetibodies, including modified immunoglobulins and cleavage products CC that can be useful in gene therapy and the generation of transgenic CC plants and animals. Furthermore, the CDR mimetibody is useful for CC preparing compositions for modulating, treating or reducing the symptoms CC immune, cardiovascular, infectious, malignant and/ or neurologic CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This competites sequence is a TPO mimetic peptide sequence used to make a
                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; anaemia; immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-2004
mimetic; CDR mimetibody; gene therapy; transgenic; immune;
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 465; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heavner GA, Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2002; 2002US-0368791P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ73011;
                                TPO mimetic peptide sequence SeqID 461.
                                                                     06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2003
                                                                                                                                        ADJ73007 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                   of the invention.
                                                                                                                                                                                                                                                                                                                                                                AA,
                                                                                                                                                                                                                                                                                           Conservative
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                                                                     (first
                                                                                                                                                                                                                                                                                       56.6%; Pr
100.0%; Pr
0;
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                                                                     entry)
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                                                                                                                                                                                                                                                                                            Score 60; DB; Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                              DB 7;
0.042;
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                                                                                                                                                                                                                                                                                                                                Length 29;
                                                                                                                                                                                                                                                                                                Indels
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/or neurologic diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is a TPO mimetic peptide sequence used to make a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one ligand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding regionseful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular; infectious; malignant; neurologic disease; anaemia;
immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2002; 2002US-0368791P
                                                                                         mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; anaemia;
                                                                                                                                                                       06-MAY-2004
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 WO2003084477-A2.
                              Synthetic
                                                                                                                                        TPO mimetic peptide sequence SeqID 460
                                                                                                                                                                                                                                     ADJ73006 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CENZ ) CENTOCOR INC
                                                                            .mmunomodulator; cardiant; antimicrobial;
                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                               2 AIEGPTLROWL
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                  AIEGPTLRQWL
                                                                                                                                                                                                                                                                                                                                                                                                                                            A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 461; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                       entry.
                                                                                                                                                                                                                                                                                                                                                                                           56.6%;
                                                                                                                                                                                                                                                                                                                                                 12
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                                                                                                                                                                                                                                                                                                                                                                                             Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             DB 7;
0.042;
                                                                              cytostatic; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 29;
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RESULT 19
ADJ52642
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases, as well as anaemia. Accordingly, they exhibit cardiant, antimicrobial, cytostatic and neuroprotective peptide sequence is a TPO mimetic peptide sequence used mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic of immune, cardiovascular, infectious, malignant and or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or neurologic or 
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                                                                                                                                                                                                                                                 fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 460; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular or neurologic disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ52642 standard;
                                                                                  WO2004002417-A2
                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                    hypotensive;
                                                                                                                                                                                                                                                                                                                                                                                            CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CH1 deleted mimetibody-related peptide SeqID461.
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                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to novel mammalian CDR mimetibodies, specific
                                                                                                                                                                                                                          infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AIEGPTLROWL 12
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                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; nootropic; antibacterial; virucide
                                                                                                                                                                                                                          fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                                                                                                                                                                                             infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 60; DB
%; Pred. No. 0.0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nc and neuroprotective activities. peptide sequence used to make a
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0.042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 29;
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RESULT 20
ADJ52646
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CC which encode them), compositions, methods and uses. The invention may be cc useful for the development of compounds with an immunosuppressive, CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, CC antibacterial, virucide or fungicide activity. In addition, the disclosed CC sequences may prove useful for gene therapy. The CH1-deleted mimetibody CC is useful for diagnosing or treating a disease condition in a cell, CC tissue, organ or animal, specifically for modulating, treating, CC alleviating, preventing the incidence or reducing the symptoms of an CC immune, cardiovascular (for example arrhythmia, hypertension or heart CC failure), or neurodegenerative (for example multiple sclerosis, dementia CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous CC conditions, or infectious diseases of for example bacterial, viral or CC fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
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                                                                                                                                                                                       hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2;
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 28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                          CH1 deleted mimetibody-related peptide SeqID465.
                                                                                                                                                                                                                                                                                                                                          06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                        ADJ52646 standard; peptide; 29
                              27-JUN-2003; 2003WO-US020347
                                                                                              WO2004002417-A2
                                                                                                                              Synthetic
                                                                                                                                             Unidentified
                                                                                                                                                                           viral infection;
                                                                                                                                                                                                                                                                          CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to CH1 deleted mimetibodies (and the DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004-082870/08
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                                                                                                                                                                          fungal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.6%;
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                                                                                                                                                                             infection
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Pred. No.
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0.042;
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RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to CHI deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be cuseful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be
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Matches
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                                                                                                                                                                                                                                                   fungicide; gene therapy; immune disorder; cardiovascular diarrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29
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                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                     ATEST
                                                                                                                                                                                                                                                                                                                   CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                                                                                                                                                                                CH1 deleted mimetibody-related peptide SeqID460
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                                                                                                          08-JAN-2004
                                                                                                                                         WO2004002417-A2
                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                    cancerous condition;
                                                                                                                                                                                                                                                                                                  hypotensive; neuroprotective; nootropic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ52641 standard; peptide; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                     infection; fungal infection.
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100.0%
                                                                                                                                                                                                                                       infectious disease; bacterial
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                                                                                                                                                                                                                                                                                       disease;
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28-JUN-2002; 2002US-0392431P

(CENZ) CENTOCOR INC

27-JUN-2003; 2003WO-US020347

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RESULT 22
ADJ51603
ID ADJ51
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Best Local S
Matches 11
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                                                                                                                                                                            dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antialflammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; NF; cytokine; bone disorder; dermatological disorder; ear disorder; nose disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; neurological disorder; immunological disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder; renal disorder; pulmonary disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovasculor neurodegenerative disease or disorder, anemia, cancer, or infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ51603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ51603 standard; peptide; 29
                   30-JUN-2003; 2003WO-US020495
                                                                                         WO2004002424-A2
                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                           CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CH1 deleted mimetibody-related peptide SeqID461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encode them), compositions, methods and uses. The invention may be for the development of compounds with an immunosuppressive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AIEGPTLROWL 12
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Pred. No.
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RESULT 23
ADJ51602
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Best Local :
                                                                                                                       antiallergic; muscular Gen; cytostatic; antiinflammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynaecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; bostetric disorder; haematologic disorder; immunological disorder; infectious disorder; musculoskeletal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemost
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; SEQ ID NO 461; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-2002; 2002US-0392431P.
19-SEP-2002; 2002US-0412144P.
                                                                                                                                                                                                                                                                                                                                                                                                     dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nutritional disorders.
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                                                               oncological disorder; neurological disorder; nutritional disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CH1 deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CH1 deleted mimetibody-related peptide SeqID460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ51602 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CENTOCOR INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mimetibody; osteopathic; cardiovascular-Gen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
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                                   pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.6%; Score 60; DB 8; 100.0%; Pred. No. 0.042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 24
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or activity of the CH1 deleted mimetibody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, endoorine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, haematologic, immunological, allergic, infectious, musculoskeletal, oncological, neurological, nutritional, ophthalmologic, pediatric, psychiatric, renal or pulmonary disorders. The present sequence is that of a peptide which may be used during the creation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic, immunomodulator, antiallergic, muscular-Gen, cytostatic, antinflammatory, neuroleptic, ophthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-modulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of dieeases or conditions associated with aberrant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New CH1 deleted mimetibody polypeptide and nucleic acid, useful diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic
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19-SEP-2002; 2002US-0412144P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2003; 2003WO-US020495
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                                                                                  dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nutritional disorders.
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   ophthalmological; nephrotropic;
TNF; cytokine; bone disorder; j
                                                                                                                                                                                                                                                                     06-MAY-2004
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                                                            antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
                                                                                                                                              CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
                                                                                                                                                                                                        CH1 deleted mimetibody-related peptide SeqID465.
                                                                                                                                                                                                                                                                                                                                                                                      ADJ51607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which encode them),
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   cytokine; bone disorder; joint disorder; cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                               standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIEGPTLRQWL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIEGPTLROWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8;
0.042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurologic and
                                    necrosis factor;
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RESULT 25
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AC ADJ7
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ADJ73009 standard;

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ADJ73009; 06-MAY-2004

(first entry)

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                                                                                                    Query Match
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                                                                                                                                                                                         or activity of the CH1 deleted mimetibody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, endocrine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, haematologic, immunological, allergic, infectious, musculoskeletal, oncological, neurological, nutritional, ophthalmologic, pediatric, psychiatric, renal or pulmonary disorders. The present sequence is that of a peptide which may be used during the creation of a
                                                                                                                                                                                                                                                                                                                      gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic, immunomodulator, antiallergic, muscular-Gen, cytostatic, antiinflammatory, neuroleptic, ophthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TNF)-modulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2003; 2003WO-US020495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-2002; 2002US-0392431P.
19-SEP-2002; 2002US-0412144P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004002424-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kutoloski KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to CH1 deleted mimetibodies (and the DNA sequences h encode them), compositions, methods and uses. The invention may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004-082872/08
15 AIEGPTLROWL 25
                            2 AIEGPTLRQWL 12
                                                                    11;
                                                                                       Similarity
                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 465; 123pp; English.
                                                                                                                                                                              of the
                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pulmonary disorder.
                                                                                                                                                                               invention.
                                                                                       100.0%;
                                                                                                        56.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ghrayeb J,
                                                                    0,
                                                                                     Score 60;
Pred. No.
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scallon BJ,
                                                                                       DB 8;
0.042;
                                                                     0;
                                                                                                      Length 29;
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RESULT 26
ADJ73010
ID ADJ73
XX
ADJ73
XX
AC ADJ73
XX
DT 06-M2
XX
DT 06-M2
XX
DT 06-M2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one ilgand binding region (LBR). The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic that can be useful in gene therapy and the generation of transgenic preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/or neurologic cardiant, antimicrobial, cytostatic and neuroprotective activities. This
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; anaemia; immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding regiouseful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO mimetic peptide sequence SeqID
               mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; anaemia; immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAR-2003; 2003WO-US009139.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 463; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2002; 2002US-0368791P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2003
                                                                               TPO mimetic
                                                                                                                 06-MAY-2004
                                                                                                                                                                             ADJ73010 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide sequence is a TPO mimetic peptide sequence used to make
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-804237/75
                                                                                                                                                                                                                                                                17
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                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                  AIEGPTLRQWL 12
                                                                                                                                                                                                                                                                                                                                                                                               31
                                                                                                                                                                                                                                                              AIEGPTLROWL 27
                                                                                                                                                                                                                                                                                                                                                                                                                             of the
                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                               peptide sequence
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                              56.6%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                              Score 60;
Pred. No.
                                                                              SeqID 464.
                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                              0.0
                                                                                                                                                                                                                                                                                                                                               .045;
                cytostatic; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                             Length 31;
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RESULT 27
ADJ52644
ID ADJ52
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Query Match
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Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel mammalian CDR mimetibodies, specific portions or variants thereof. Specifically, it refers to an antibody fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which itself comprises at least one human framework region and at least one light diding region [LBR]. The present invention describes human mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic plants and animals. Furthermore, the CDR mimetibody is useful for preparing compositions for modulating, treating or reducing the symptoms of immune, cardiovascular, infectious, malignant and/or neurologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, cardiant, antimicrobial, cytostatic and neuroprotective activities. This peptide sequence is a TPO mimetic peptide sequence used to make a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 464; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
             Unidentified.
Synthetic.
                                                                             fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-804237/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2002; 2002US-0368791P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-2003; 2003WO-US009139
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                                                                                                                                                                                                                              06-MAY-2004
                                                                                                                                                                                                                                                                                           ADJ52644 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CENZ ) CENTOCOR INC
                                                                                                                                                             CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                              CH1 deleted
                                                                                                                                               hypotensive; neuroprotective; nootropic; antibacterial; virucide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                infection;
                                                                                                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                           2 AIEGPTLROWL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GA,
                                                                                                                                                                                                                                                                                                                                                                           AIEGPTLRQWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knight DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                              mimetibody-related peptide SeqID463.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                              (first entry)
                                                              fungal
                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.6%; Score 60; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scallon
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7;
0.045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC which encode them), compositions, methods and uses. The invention may be considered them, compositions, methods and uses. The invention may be consecuted them, compositions, methods and uses. The invention may be considered them, cardiant, hypotensive, neuroprotective, nootropic, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, cardiovascular, ordinant, hypotensive, neuroprotective, nootropic, cardiovascular, virucide or fungicide activity. In addition, the disclosed consequences may prove useful for gene therapy. The CH1-deleted mimetibody consumed the constant for treating a disease condition in a cell, cardiovascular (for example activity in a cell, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia conficience or infections diseases or discorders, anaemia, cancerous conditions, or infectious diseases or discorders, anaemia, cancerous conditions, or infectious diseases of cor example multiple sclerosis, dementia conficiency or infectious diseases or discorders, anaemia, cancerous conditions, or infectious diseases of for example multiple sclerosis, dementia conficiency or infectious diseases of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Кeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004002417-A2
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                                                                     fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple solerosis; dementia; Albheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavner GA,
                       Unidentified
                                                                                                                                                         CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                         CH1 deleted mimetibody-related peptide SeqID464.
                                                                                                                                                                                                                            06-MAY-2004
                                                                                                                                                                                                                                                                                              ADJ52645 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CENZ ) CENTOCOR INC.
                                                         viral intection;
                                                                                                                                       hypotensive; neuroprotective; nootropic; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                    AIEGPTLROWL 12
                                                                                                                                                                                                                                                                                                                                                                                  AIEGPTLROWL 27
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                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Residue is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8;
0.045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC which encode them), compositions, methods and uses. The invention may be CC useful for the development of compounds with an immunosuppressive, CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, CC antibacterial, virucide or fungicide activity. In addition, the disclosed CC sequences may prove useful for gene therapy. The CH1-deleted mimetibody CC is useful for diagnosing or treating a disease condition in a cell, CC tissue, organ or animal, specifically for modulating, treating, CC tissue, organ or animal, specifically for modulating, treating, CC immune, cardiovascular (for example arrhythmia, hypertension or heart CC failure), or neurodegenerative (for example multiple sclerosis, dementia CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous CC conditions, or infectious diseases or disorders, anaemia, cancerous CC or Michiner or infectious diseases or disorders, anaemia, cancerous CC conditions, or infectious diseases or disorders, anaemia, cancerous CC conditions, or infectious diseases or disorders, anaemia, cancerous CC conditions, or infectious diseases or disorders, anaemia, cancerous CC conditions, or infectious diseases if or example bacterial, viral or CC cused during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder gastrointestinal disorder; gynaecological disorder; hepatic disorder;
                                                                                                                CH1 deleted mimetibody; osteopathic; cardiovascular-Gen; dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUN-2003; 2003WO-US020347.
                                                         ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                  antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
                                                                                                                                                                                                                                     06-MAY-2004
                                                                                                                                                                                                                                                                                                              ADJ51606 standard; peptide; 31 AA.
                                                                                                                                                                                                                                                                           ADJ51606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                mimetibody-related peptide SeqID464.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60; DB; Pred. No. 0.0.0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8;
0.045;
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                                                            ADJ51605
                                                                          RESULT 30
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Matches 11
                                                                                                                                                                                                                                                                                        respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
modulator or cytokine-agonist. The methods and compositions of the
present invention are useful for the diagnosis, prevention and/or
treatment of diseases or conditions associated with aberrant expression
or activity of the CHI deleted mimeribody, such as a bone or joint,
cardiovascular, dental or oral, dermatological, ear, nose or throat,
endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
obstetric, haematologic, immunological, altergic, infectious,
musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
pediatric, psychiatric, renal or pulmonary disorders. The present
sequence is that of a peptide which may be used during the creation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     obstetric disorder; haematologic disorder; immunological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; oncological disorder; nutritional disorder; ophthalmologic disorder; pediatric disorder; psychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an osteopathic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2003; 2003WO-US020495.
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              ADJ51605
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19-SEP-2002; 2002US-0412144P
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                                           ADJ51605 standard; peptide; 31
                                                                                                                                                                                                                                                   Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-082872/08
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                                                                                                                                                      2 AIEGPTLROWL 12
                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                  of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders.
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                    Score 60;
Pred. No.
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antiinflammatory, neurolaptic, ophthalmological, nephrotropic or respiratory-Gen activity acting as a tumour necrosis factor (TMP)-modulator or cytokine-agonist. The methods and compositions of the present invention are useful for the disgnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CH1 deleted mimetibody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, endocrine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, haematologic, immunological, allergic, infectious, musculoskeletal, oncological, neurological, nutritional, ophthalmologic, pediatric, psychiatric, renal or pulmonary disorders. The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiallargic; muscular Gen; cytostatic; antiinflammatory; neuroleptic; ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; gynacological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; allergic disorder; infectious disorder; musculoskeletal disorder; infectious disorder; musculoskeletal disorder;
                                                                                                                                                                                                                                                                                                        which encode them), compositions, methods and uses. The invention mauseful for the development of compounds with an osteopathic, cardiovascular-den, dermatological-den, auditory, endocrine-den, gastrointestinal-den, gynaecological-den, hepatotropic, haemostatic, immunomodulator, antiallergic, muscular-den, cytostatic, antiallergic, muscular-den, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and nutritional disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; SEQ ID NO 463; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-082872/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kutoloski
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19-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CENZ ) CENTOCOR INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to CH1 deleted mimetibodies (and the DNA sequences
31
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0392431P.
2002US-0412144P.
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                                                                                                                                                                                                                                                                                                                                                                                                        invention may
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Query Match Best Local Similarity

56.6%; 100.0%;

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                                     conditions involving a megakaryocyte and/or platelet deficiency, e.g. CC disease conditions involving thrombocytopaenia such as aplastic anaemia, CCC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia. CCC maintaining the ribbility or storage life of platelets and/or CCC maintaining the viability or storage life of platelets and/or CCC megakaryocytes and its derived cells. The compounds demonstrate an CCC improved ability to bind to and/or trigger transmembrane signal through, CCC i.e. activating, the mpl receptor the compounds demonstrate an CCC thrombopoletic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity. CCC i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity. CCC platelet precursors. Further, certain of the compounds also exhibit CCC superior therapeutic properties, such as improved plasma half-life, CCC represents a preferred TMP of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that binds to the c-mpl (mpl) receptor, and which stimulates the production or platelets and/or the production of platelets precursors, is new. Further disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The pharmaceutical composition of the invention is useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombocytopaenia in an animal, and for increasing megakaryocytes or platelets in a patient. The TMP of the invention is useful for treat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001; 2001US-0328666P.
10-OCT-2002; 2002US-00269806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombocytopaenia; aplastic anaemia; autoimmune autoimmune haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemostatic; antianaemic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin mimetic peptide (TMP8), seq
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Best Local
                                                                                                                        autoimmune haemolytic anaemia, Hughe's syndrome and lupoid thrombocytopaenia. The TMP of the invention is also useful for maintaining the viability or storage life of platelets and/or megakaryocytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thromobopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombocytopaenia in an animal, and for increasing megakaryocytes or platelets in a patient. The TMP of the invention is useful for treating conditions involving a megakaryocyte and/or platelet deficiency, e.g. disease conditions involving thrombocytopaenia such as aplastic anaemia, autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, autoimmune becomplished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that binds to the c-mpl (mpl) receptor, and which stimulates the production of platelets and/or the production of platelet precursors, is new. Further disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The pharmaceutical composition of the invention is useful for treating that the pharmaceutical composition of the invention is useful for treating that the pharmaceutical composition of the invention is useful for treating the pharmaceutical composition of the invention is useful for treating the pharmaceutical composition of the invention is useful for treating the pharmaceutical composition of the invention is useful for treating the pharmaceutical composition of the invention is useful for treating the pharmaceutical composition of the invention is useful for treating the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production
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platelet precursors. Further, certain of the compounds also exhibit superior therapeutic properties, such as improved plasma half-life, biological activity and in vivo circulation time. The current seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production
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The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that CC binds to the c-mpl (mpl) receptor, and which stimulates the production of CC platelets and/or the production of platelet precursors, is new. Further CC disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The CC platelets in an animal, and for increasing megakarycytes or CC platelets in a patient. The TMP of the invention is useful for treating CC conditions involving a megakarycyte and/or platelet deficiency, e.g. CC disease conditions involving thrombocytopaenia such as aplastic anaemia, CC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, Hughe's syndrome and lupoid thrombooytopaenia. The TMP of the invention is also useful for megakarycytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior and in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane signaling; mpl receptor; thrombopoietin mimetic pept TMP; c-mpl receptor; platelet precursor; megakaryocyte; thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia; autoimmune haemolytic anaemia; Hughe's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-2004
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73.3%;
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A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP] 1-(L, 1) nTMP 2], is new. TMP1 and TMP2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x 2-x 1 0, x 2-x 1 1, x 2-x 1 2, x 2-x 1 3, x 2-x 1 4, x 1-x 1 0, x 1-x 1 7, x 1-x 1 2, x 2-x 1 2, x 2-x 1 2, x 2-x 1 4, x 1 - x 1 0, x 1-x 1 1, x 1 - x 1 2, x 1 1 2, x 1 2, x 1 2, x 1 2, x 1 2, x 1 3, and x 1 2, x 1 4, x 1 1 1, x 1 2, x 1 2 1, x 1 2 1, x 1 2 1, x 1 3, and x 1 2, x 1 3, x 1 2, x 1 3, and x 1 3, x 1 3, x 1 3, x 1 3, x 1 3, x 1 1, x 1 3, x 1 1, x 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1 1, x 1
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immunodeficiency virus; anti-HIV;
ressive; anti-inflammatory; linker.
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73.3%;
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Best Local S
Matches 13
The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)aF1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P2-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          auroimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombogis: pharmacoutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N, Q or G; X 1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising 1 to 20 amino acids, and n = 0 or 1. The compounds bind to and activate the c-Mp1 receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  composition of matter comprising an Fc domain and pharmacologically e peptides, useful for treating cancer and autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 324; 608pp; English.
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68.4%;
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       The present invention describes an immunoglobin molecule or its fragment ((1) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus (I) has attianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of proliferation, differentiation or growth of for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with corresponding to a portion of CDR is replaced with an EPO mimetic, or which has one or
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04-MAY-2001;
29-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a Fab domain) can provide a longer half-life or incorporate function such as Fc receptor binding, protein A binding, complement fixation possibly placental transfer. AAA6943 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                        A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis
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                                                                                                                                                                                                                               Claim
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DB; ABQ73366.
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                                                                                                                                                                                                                             Fig 5; 113pp; English.
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; 2001US-0288889P.
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                         The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet production. (I) with a region where amino acid residues corresponding to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
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(I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoletin (EPO) or thrombopoletin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has antianaemic, haemostatic and nephrotropic activities, and can be used as a stimulator of proliferation, differentiation and maturation of haematopoletic cells, and a stimulator of haematopolesis. (I) is useful for stimulating proliferation, differentiation or growth of promegakaryocytes or megakaryocytes, where (I) is contacted with promegakaryocytes or megakaryocytes, which results in increased platelet promediction. (I) with a region where amino acid residues corresponding to
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haemostatic; nephrotropic; haematopoietic cell; haematopoiesie.
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73.3%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
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RESULT 39
ADQ16619
ID ADQ16
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The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a portion of CDR is replaced with an EPO mimetic, or which has one or more of its CDRs fused to an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with haematopoietic stem cells or their progenitors. (I) is useful for diagnostics or therapeutics, in cell isolation strategies, and for treating patients suffering from deficiency in cell populations caused by disease, disorders or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73377 and ABB51669 to ABP51696 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                            New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive; immunotherapy; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bowdish KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                        Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-2002; 2002US-00307724
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                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 39; 107pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%;
91.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renshaw M;
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0.035;
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                                                                                                                                                                                                                                                with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic peptide with flanking
                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least portion of a two complementarity determining regions (CDRs) are replaced
                                                                                                                                                                                                                                                                                                                                                                                                                        New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with or a TPO mimetic, useful for treating thrombocytopenia.
                                      ADQ16646 standard;
                                                                                                                                                                                                           Sequence 18
                                                                                                                                                                                                                                     The present sequence residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; BPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                               Example 6; SEQ ID NO 61; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bowdish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-DEC-2002; 2002US-00307724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunotherapy; thrombocytopenia.
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                                                                                                                                                                      Similarity
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                                                                                                      IEGPTLROWLAARAR 17
                                                                                                                               IEGPTLROWLHGNGR 17
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                                    peptide; 18
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73.3%;
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Pred. No.
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Best Local S
Matches 11
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                                                                                                                                                                                          Haemostatic; antianaemic; immunosuppressive; platelet; transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide; TMP; c-mpl receptor; platelet precursor; megakaryocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4;
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erythropoietin;
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  WO2003031589-A2
                                                      Homo sapiens
                                                                                                               lupoid
                                                                                                                                      thrombocytopaenia; aplastic anaemia; autoimmune autoimmune haemolytic anaemia; Hughe's syndrome
                                                                                                                                                                                                                                                                                                          TMP peptide TMP1.
                                                                                                                                                                                                                                                                                                                                                              01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004-460973/43
                                                                                                             thrombocytopaenia; linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LAIEGPTLROWL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALEXION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPIEGPTLROWL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementarity determining region; CDR; peptide mimetic; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents a TPO mimetic peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ູເດ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59; DB Pred. No. 0.03 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                      thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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to at least a
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RESULT 43
ADQ16705
ID ADQ16
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X S X F X B X B X B X B X B X
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 83; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel thrombopoietin mimetic peptides which bind to mpl receptor, which stimulate the production of platelets and/or the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-403101/38
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                                                                           immunoglobulin; complementarity determining region; CDR; peptide mimetic; erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                       Modified
                                                                                                                                                                               09-SEP-2004
                                                                                                                                                                                                                                                               ADQ16705 standard;
                                                                                                                                                                                                                     ADQ16705;
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                                                        .mmunotherapy;
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                                                                                                                                     immunoglobuiln
                                                                                                                                                                                                                                                                                                                                                                                                    IEGPTLROWLHGNGRDT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursors, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                               İEGPTLROWLAARALET
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0328666P.
2002US-00269806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002WO-US032552
                                                                                                                                                                               (first entry)
                                                          thrombocytopenia.
                                                                                                                                                                                                                                                             protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hartley
                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.7%;
64.7%;
                                                                                                                                     clone 116
                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                       HC variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7;
0.044;
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                                                                                                                                            SEQ
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                                                                                                                                            ij
                                                                                                                                            NO:125
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Synthetic

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RESULT 44
ADQ16704
ID ADQ16
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Query Match
Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004050017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-460973/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2003; 2003WO-US036894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUN-2004
                                                                                                                                                                                                                              erythropoietin; EPO; thrombopoie immunotherapy; thrombocytopenia.
                                                                                                                                                                                                                                                                                                                09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                   ADQ16704 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowdish KS,
              WPI; 2004-460973/43
                                                                                           02-DEC-2002; 2002US-00307724
                                                                                                                      17-NOV-2003; 2003WO-US036894.
                                                                                                                                                17-JUN-2004
                                                                                                                                                                           WO2004050017-A2
                                                                                                                                                                                                                                                         immunoglobulin;
                                                                                                                                                                                                                                                                                  Modified immunoglobuiln clone 116 heavy chain SEQ ID NO:124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ALEX-) ALEXION PHARM INC.
                                                                  (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence represents immunoglobulin clone 116 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LAIEGPTLROWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                       LPIEGPTLROWL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frederickson S,
                                       Frederickson S,
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                          complementarity determining region; CDR; peptide mimetic; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.7%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                      225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 59; DB 8
Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Renshaw
                                         Renshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                         Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are replaced with EPO mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 128;
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RESULT 45
ABP51695
ID ABP51
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thromborytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents immunoglobulin clone 116 heavy chain.
                                                                                                            A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or
                                                                                                                                                                                                                                                                 05-DEC-2000; 2000US-0251448P
04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; SEQ
                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                              Bowdish
                                                                                                                                                                                                                                                                                                                           05-DEC-2001; 2001WO-US047656
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP51695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP51695 standard;
                                                                    Example 4;
                                                                                                                                                                                                                                       (ALEX-)
                                                                                                                                                                                                                                                                                                                                                       13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                     WO200246238-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5G1.1-TPO heavy chain amino
                                                                                                                                                                                 2002-566610/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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3
                                                                                                                                                                                                                                          ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                    ABQ73374.
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                                                                    Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                              Barbas-Frederickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO 124; 107pp; English.
                                                                  13A; 113pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.7%;
91.7%;
                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                               Renshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO:67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPO mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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least a portion of replaced or fused w

The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at

comprising a region where amino acid residues corresponding st a portion of the complementary determining region (CDR) as laced or fused with biologically active peptides e.g. a pepti

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Search completed: September 1, Job time: 88.3453 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, CC that is flanked with proline at its carboxy terminus. (I) has CC antianaemic, haemostatic and nephrotropic activities, and can be used as CC a stimulator of proliferation, differentiation and maturation of CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful CC promegakaryocytes or megakaryocytes, where (I) is contacted with CC promegakaryocytes or megakaryocytes, which results in increased platelet CC production. (I) with a region where amino acid residues corresponding to CC a portion of CDR is replaced with an EPO mimetic, or which has one or CC more of its CDRs fused to an EPO mimetic, is useful for increasing the CC production of red blood cells, where (I) is contacted with haematopoietic stem cells or their progenitors. (I) is useful for diagnostics or therapeutics, in cell populations caused by disease, CC disorders or treatments related to the suppression of haematopoiesis. ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 472 AA;
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A;Cross-references: UNIPROT:P49222; GB:U04055
A;Note: authors translated the codon TAC for residue 129 as R,Rybicki, A.C.; Schwartz, R.S.; Qiu, J.J.; Gilman, J.G. Mamm. Genome 5, 438-445, 1994
A;Fitle: Molecular cloning of mouse erythrocyte protein 4.2: A;Reference number: I48901; MUID:95003352; PMID:7919657
A;Accession: I48901
A;Status: preliminary.
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C;Date: 18-1
C;Accession
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A; Cross-refe:
C; Superfamil:
C; Keywords:
F; 2/Modified
                                                                                                                                                                                   A;Cross references: UNIPROT:P16452; GB:L06519; NID:g306738; PIDN:AAA52385.1; PID:g306740 A;Experimental source: cell type erythrocyte; tissue type peripheral blood; tissue lib h R;Sung, L.A.; Chien, S.; Chang, L.S.; Lambert, K.; Bliss, S.A.; Bouhassira, E.E.; Nagel, Proc. Natl. Acad. Sci. U.S.A. 87, 955-959, 1990 A;Title: Molecular cloning of human protein 4.2: a major component of the erythrocyte me A;Reference number: A34865; MUID:90138995; PMID:1689063 A;Accession: A34865; MUID:90138995; PMID:1689063 A;Accession: A34865 MRNA A;Residues: 1-364, 'KRGLPC', 371-379, 'H', 381-405, 'L', 407-721 <SUN1> A;Cross-references: GB:M30647; NID:g189433; PIDN:AAA36401.1; PID:g189434
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Proc. Natl. Acad. Sci. U.S.A. 88, 4840-4844, 1991
A;Title: Organization of the gene for human erythrocyte membrane
A;Reference number: A39707; MUID:91271288; PMID:2052563
A;Accession: A39707
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: A39707; A34865; B34865; A34883
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Genomics 21, 478-485, 1994
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A;Residues: 1-352,'A',354-620,'S',622-691 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-721 <KOR1>
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;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
;Accession: A54741; I48901
;Residues: 1-3,34-364, 'KRGLPC',371-379,'H',381-405,'L',407-721 <SUN2>;Cross-references: GB:M30646; NID:g189435; PIDN:AAA36402.1; PID:g189436; Experimental source: isolate Sickle cell patient; cell type reticulocyte; Note: parts of this sequence were determined by protein sequencing; Korsgren, C.; Lawler, J.; Lambert, S.; Speicher, D.; Cohen, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: protein-glutamine gamma-glutamyltransferase; Keywords: blocked amino end; lipoprotein; myristylation; 2/Modified site: myristylated amino end (Gly) (in mature
                                                                                                                                Molecule type:
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C;Date: 21-NO. C;Date: 21-NO. C;Caccession: S13178
C;Accession: S13178
R;Beck, J.; Ripka, S.; Siegner, A.; Schiltz, E.; Summark; R;Beck, J.; Ripka, S.; Siegner, A.; Schiltz, E.; Summark; R;Beck, J.; Ripka, S.; Siegner, A.; Schiltz, E.; Summark; R; Ripka, S.; Siegner, A.; Schiltz, E.; Summark; R; R; Siegner, A.; Schiltz, E.; Summark; R; R; Siegner, A.; Schiltz, E.; Summark; R; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Summark; R; Siegner, A.; Schiltz, E.; Summark; R; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; Schiltz, E.; Siegner, A.; A;Reference number: S13178; MUID:91006137; A;Accession: S13178

A;Status: preliminary

6-methylsalicylic acid synthase - Penicillium C;Species: Penicillium griseofulvum C;Date: 21-Nov-1993 #sequence_revision 01-Sep-

griseofulvum

#text_change

gene

of.

Penicillium

patulum

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-973 <KUR>
A;Cross-references: UNIPROT: (08YPC5; GB:BA000019; PIDN:BAB75972.1; PID:g17133408; GSPDB:GA;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Superfamily: protein-glutamine gamma-glutamyltransferase
C;Cayloroduct: erythrocyte membrane band 4.2 protein, long splice form #status predict
F;2-3,34-721/Product: erythrocyte membrane band 4.2 protein, short splice form #status p
F;298-316/Domain: transmembrane #status predicted <TRM>
F;298-316/Domain: transmembrane #status predicted <TRM>
F;518-520/Region: cell attachment (R-G-D) motif
F;27Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;103,420,447,529,604,705/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;278/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
                                                                                                                                                                                                                                                                                                                         C;Raccession: AB2340
C;Raccession: AB2340
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz,
R;Kaneko, T.; Nakamura, S.; Sugimoto, M.; Takaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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A;Map position: 15q15-15q15
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A;Cross-references: GB:M29399; NID:g182083; PIDN:AAA35798.1; PID:g182084
C;Comment: This protein is a major constituent of the erythrocyte membrane.
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A; Residues: 1-3,34-721
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                                                                                                                                                                               A;Gene: alr4273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein alr4273 [imported] - Nostoc sp.
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Best Local S
Matches 9
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Best Local
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                                                                                      Similarity
8; Conserv
                                            PTLROWLHGNG
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72.78;
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75.0%;
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                                                                                                                Score 50;
Pred. No.
                                                                                           Mismatches
                                                                                                                DB
13;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <STO>
A;Cross-references: UNIPROT:Q9AC48; GE
C;Genetics:
A;Gene:CC0018
A;Gene:CC0018
C;Superfamily: Molybdenum cofactor Mol
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A;Residues: 1-1774 <BEC>
A;Cross-references: UNIPROT:P22367; GB:X55776; NID:g3211; PIDN:CAA39295.1; PID:g3212
C;Superfamily: Streptomyces hygroscopicus probable polyketide synthase module 4; 3-oxoac
homology; [acy1-carrier-protein] S-malonyltransferase homology <Oxio-
C;Keywords: carrier protein
C;Keywords: 3-oxoacy1-[acy1-carrier-protein] synthase I homology <Oxio-
F;54-455/Domain: 3-oxoacy1-[acy1-carrier-protein] S-malonyltransferase homology <AMT>
F;56-844/Domain: [acy1-carrier-protein] S-malonyltransferase homology <AMT>
F;1412-1605/Domain: short-chain alcohol dehydrogenase homology <SAD2>
                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87251
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A; Residues: 1-419 < ART>
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Nucleic Acids Res. 14, 4987-4999, 1986
A;Tille: Analysis of the nucleotide sequence of the ereB
A;Reference number: A24381; MUID:86259072; PMID:3523438
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004
C;Accession: B87251
C;Accession: B87251
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C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
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C;Species: Escherichia coli
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                                                                                                            cofactor Molybdenum
     44.3%;
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Pred. No.
          Score 47;
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RESULT

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glutamate-1-semialdehyde 2,1-aminomutase C;Species: Cenarchaeum symbiosum

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Cenarchaeum symbiosum

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C;Geneti
A;Gene:
                                                                                                                A;Note: bldKB
C;Function:
A;Description: involved i
C;Keywords: oligopeptide
                                                                                                                                                                                             A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-602 <NOD> A;Cross-references: UNIPROT:P72407; EME A;Experimental source: strain M145
                                                                                                                                                                                                                                                                                                                                           oligopeptide ABC transport protein bldKB [imported] - C;Species: Streptomyces coelicolor C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #te C;Accession: T45278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
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E83151
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A; Accession: T45278
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A;Experimental source: strain PAO1
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A; Residues: 1-391 <STO>
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llarity 64.3%;
Conservative
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50; MUID:20437337; PMID:10984043
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L.L.; Coulter, S.N.; Folger,
 187
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                                                         ; Score 46.5; D; Pred. No. 27; 3; Mismatches
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A.; Larbig, K.; Lim,
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A;Title: Genomic analysis reveals chromosomal variation A;Reference number: Z20994; MUID:98422450; PMID:9748430 A;Accession: T31313
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A;Title: Identification and organization of carbon dioxide fixation genes in Xanthobacto A;Reference number: S13573; MUID:91172133; PMID:1900916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription activator LysR-type CbbR - Xanthobacter flavus C;Species: Xanthobacter flavus C;Species: Xanthobacter flavus C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text_change C;Accession: A36925; S13578; S35408 R;van den Bergh, E.R.B.; Dijkhulzen, L.; Meijer, W.G.
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A; Residues: 1-434 <SCH>
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                hypothetical protein BH1379 [imported] C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision C;Accession: C83822 R;Takami, H; Nakasone, K; Takaki, Y;
                                                                                                                  RESULT 11
C83822
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A36925
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                                                                                                                                                                                                                                                                                                                                                   A;Gene: cbbR
A;Start codon: GTG
C;Superfamily: transcription activator LysR-type
C;Keywords: DNA binding; transcription regulation
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A; Residues: 1-150 <MEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reference number:
Accession: A36925
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Best Local
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10; Conserv
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mber: A36925; MUID:94012468; PMID:8407781
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sone, K.; Takaki, Y.;
28, 4317-4331, 2000
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41.2%;
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52.6%;
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Pred. No.
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Pred. No. 20;
2; Mismatches
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                    Maeno,
                                                                                                Bacillus halodurans (strain C-125)
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                    G.;
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                      Sasaki,
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                      N.; Fuji,
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A;Molecute 'JE'.
A;Residues: 1-235 <STO>
A;Cross-references: UNIPROT:Q9KD40;
A;Cross-references: strain C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kivisaar, M.; Kasak, L.; Nurk, A.

Gene 98, 15-20, 1991

A;Title: Sequence of the plasmid-encoded catechol 1,2-dioxygenase-expressing
A;Reference number: JN0143; MUID:91192610; PMID:2013408
                                                                                                                                                                                                                                       R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
                                                                                                                                                                                                                                                                                               hypothetical protein hpcE-2 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: C90453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Genome: plasmid
C;Superfamily: catechol 1,2-dioxygenase
C;Keywords: aromatic hydrocarbon catabolism; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P31019; GB:M57500; NID:g145127; PIDN:AAC64900.1;
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A; Residues: 1-302 <KIV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Pseudomonas sp.
C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 09-Jul-2004
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                                                                                                                                                                 A;Description: Sulfolobus solfataricus A;Reference number: A99139 A;Accession: C90453
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                                                                                                                                                                                                                           submitted to GenBank, April 2001
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                                                                                                              A;Residues:
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Best Local S
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Best Local :
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                 Query Match
                                                                      Genetics:
                                                                                           Cross-references: UNIPROT:Q97V63; GB:AE006641; NID:g13816109; PIDN:AAK42882.1; GSPDB:6
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Score 45;
Pred. No.
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A;Cross-references: UNIPROT:Q8YF91; GB:AE008917; PIDN:AAL52812.1; PID:g17983650; GSPDB:
A;Experimental source: strain 16M
C;Genetics:
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella A;Reference number: AD3252; PMID:11756688
A;Accession: AI3455
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A;Description: Sequence of A. thaliana BAC T10P11 from chromosome IV.
nuclear protein SR-25 - mouse
C;Species: Mus musculus (house mouse)
C;Bate: 09-Jun-2000 #sequence_revision
C;Accession: JC7219
                                                                                RESULT 16
JC7219
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A; Accession: T01086
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
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A;Map position: I
C;Superfamily: probable transcription repressor
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A; Note: T10P11.10
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Best Local
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57.1%;
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                       #text_change 09-Jul-2004
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A; Experi
C; Geneti
A; Gene:
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A splicing factors. C; Keywords: nucleus; RNA processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Sasahara, K.; Yamaoka, T.; Moritani, M.; Tanaka, M.; Iwahana, H.; Yoshi Biochem. Biophys. Res. Commun. 269, 444-450, 2000 A;Title: Molecular cloning and expression analysis of a putative nuclear A;Reference number: JC7219; MUID:20175222; PMID:10708573
                                                                                                                                                                                                                                            glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - C;Species: Leishmania mexicana (c;Species: Leishmania mexicana C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004 C;Accession: B48445; S25142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BH3822 [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Ju
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F84127
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                                                                                                                                                                           R;Hannaert, V.; Blaauw, M.; Kohl, L.; Allert, S.; Opperdoes, Mol. Biochem. Parasitol. 55, 115-126, 1992
A;Title: Molecular analysis of the cytosolic and glycosomal cap. Reference number: A48445; MUID:93063042; PMID:1435864
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                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <HAN>
                                                                                                                                                                                                                                                                                                              B48445
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A;Molecule type: DNA
                                                                                                                                                          A; Accession: B48445
                                                             ,Cross-references: UNIPROT:Q01558; EMBL:X65220; NID:g9552; Superfamily: glyceraldehyde-3-phosphate dehydrogenase; Keywords: oxidoreductase
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#sequence_revision
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                                                                                                  PIDN:CAA46323.1; PID:g9553
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IEGPTLRQWLHGNG 16

A.; Davis, P.; Davies, R.M.; Dowd, L.; White,

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Farrar,

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A;Cross-references: UNIPROT:P3:
C;Genetics:
A;Gene: BnC2
A;Introns: 95/1; 222/2; 362/3
C;Superfamily: glycinin
C;Keywords: seed; storage prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 19, 1049-1055, 1992
A;Title: Molecular analysis of a cruciferin storage protein A;Reference number: $25090; MUID:92379259; PMID:1511129
A;Accession: $25091
A;Status: translation
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S25091
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
probable sulfatase [imported] - Salmonella enterica subsp. er C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_char C; Accession: AI0506
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Picks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Brassica napus (rape)
C;Date: 04-Feb-1998 #sequence_revision
C;Accession: S25091
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A;Map position: I
C;Superfamily: Molybdenum cofactor Molybdenum cofactor precursor Z
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A;Cross-references: UNIPROT:Q8YGY6; GB:AE008917; PIDN:AAL52200.1; PID:g17982982; GSPDB:A;Experimental source: strain 16M
C;Genetics:
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A; Residues: 1-496 < BRE>
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Best Local
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                                                                      A;Molecule type: mRNA
A;Residues: 1-1712 <1801>
A;Cross-references: UNIPROT:P08572; EMBL:J04210; EMBL:X05610;
R;Hostikka, S.L.; Kurkinen, M.; Tryggvason, K.
FEBS Lett. 216, 281-286, 1987
                                                                                                                                                                                                                                                                       collagen alpha 2(IV) chain precursor - human
N;Alternate names: procollagen alpha 2(IV) chain
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence revision 03-Oct-1995 #text change 09-Jul-2004
C;Date: 07-Jun-1990 #sequence revision 03-Oct-1995 #text change 09-Jul-2004
C;Accession: A32024; S00007; S02624; S00246; S17678; S16911; B32117; S16877;
R;Hostikka, S.L.; Tryggvason, K.
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A; Title: The complete primary structure of the alpha2 chain of A; Reference number: A32024; MUID:89066769; PMID:3198637
A; Accession: A32024
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         A; Reference number: S00007; MUID: 87219158; PMID: 3582677
                                                  A; Title: Nucleotide sequence coding for the
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                                ated region.
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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: A10506
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T49773
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                                                                                                                                                                                                                                                         submitted to the Protein S
A; Reference number: Z25022
A; Accession: T49773
                                                                                                                                                                                                                                                                                                                                            N;Alternate names: protein B:
C;Species: Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: STY0046
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A; Residues: 1-571 < PAR>
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A; Residues: 1-972 < SCH>
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                                                                                                                                  A; Map position:
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59
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                                                          8; Conserv
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 TLTOWSRGNATOT 71
                             TLROWLHGNGRDT 19
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61.5%;
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                                                                          Score 44;
Pred. No.
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Pred. No.
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                                                        DB 2; L. 1.1e+02; 5;
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63;
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                                                                                                                                                                                                                                                                                                                                 #text_change 09-Jul-2004
                                                                                        Length 972;
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                                                                                                                                                                                                                                                                                                      B.;
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Salmonella
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human type IV

collagen alpha-2 chain cDNA

GB:M20753;

NID:g29550;

DIG

human

type

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S00165; S39

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A; Action type: mRNA
A; Molecule type: mRNA
A; Residues: 1-470, 'P', 472-682, 'G', 684-1043 <OBE>
A; Cross-references: EMBL: X05562; NID: g30075; PIDI
A; Cross-references: EMBL: X05562; Kuehn, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X12784; GB:M36963; NID:g30072; PIDN:CAA31275.1; PID:g30073 R;Soininen, R.; Huotari, M.; Hostikka, S.L.; Prockop, D.J.; Tryggvason, K. J. Biol. Chem. 263, 17217-17220, 1988
A;Title: The structural genes for alpha1 and alpha2 chains of human type IV collager A;Reference number: A92690; MUID:89034231; PMID:3182844
A;Accession: B32117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The genes for the alpha1(IV) and alpha2(IV) chains A;Reference number: S02738; MUID:89030632; PMID:2846280 A;Accession: S16911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hostikka, S.L.; Tryggvason, K. FEBS Lett. 224, 297-305, 1987
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A; Residues: 1254-1398, 'V', 1400-1712 < HOS2>
                                                                                                                                   A; Molecule type: protein
A; Residues: 37-247 <SIE1>
A; Note: the sequence from Fig. 4 is
R; Eble, J.A.; Golbik, R.; Mann, K.;
EMBO J. 12, 4795-4802, 1993
A; Title: The alpha-1-beta-1 integrir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-33 < SOI1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, June 1987 A;Reference number: S17678 A;Accession: S17678
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A;Residues: 1-682,'G',684-1043 <BRA>
A;Cross-references: EMBL:X05562; NID:g30075; PIDN:CAA29076.1; PID:g30076
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A;Residues: 1347-1350;1377-1383;1426-1432;1465-1471;1529-1535;1625-1630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:J04217; NID:g180759; PIDN:AAA53097.1; PID:g553233; EMBL:J05039
A;Note: this sequence was submitted to the EMBL Data Library, October 1988
R;Siebold, B.; Qian, R.Q.; Glanville, R.W.; Hofmann, H.; Deutzmann, R.; Kuehn, K.
Eur. J. Biochem. 168, 569-575, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-33 < POE>
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                      A; Molecule type: protein A; Residues: 407-570 < EBL
                                                                                                             A;Title: The alpha-1-beta-1 integrin recognition site of the A;Reference number: S39614; MUID:94038963; PMID:8223488
                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S00165; MUID:88029476; PMID:3117548
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Construction of a model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:J04217; EMBL:J05039; NID:g180759; PIDN:AAA53097.1; Soininen, R.; Huotari, M.; Ganguly, A.; Prockop, D.J.; Tryggvason, K. Biol. Chem. 264, 13565-13571, 1989
.Title: Structural organization of the gene for the alpha-1 chain of human Reference number: S16876; MUID:89340433; PMID:2701944
.Accession: S16877
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Residues: 1-33 <SOI2>
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                                                                                   Accession: S39615
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R.S.; Benson,
V.A.; Lovello,
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                                                                                                                                                                                                                inconsistent
Kuehn, K.
K.T.; van
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A;Residues: 1040,'I',1042-1398,'V',1400-1418,'M',1420-1635,'V',1637-1712 <KIL>
A;Residues: 1040,'I',1042-1398,'V',1400-1418,'M',1420-1635,'V',1637-1712 <KIL>
A;Cross-references: EMBL:M24766; NID:g537328; PIDN:AAA52043.1; PID:g537329
A;Cross-references: EMBL:M24766; NID:g537328; PIDN:AAA52043.1; PID:g537329
A;Siebold, B.; Deutzmann, R.; Kuehn, K.

Eur. J. Biochem. 176, 617-624, 1988
A;Tille: The arrangement of intra- and intermolecular disulfide bonds in the carboxy
A;Reference number: S02550; MUID:89005112; PMID:2844531
A;Accession: S02550
A;Molecule type: protein
A;Residues: 1480-1535;1545-1614;1617-1662,'H',1664-1700,'G';1705-1708;1710-1712 <SIE
A;Molecule type: protein
A;Rolecule type: protein
A;Note: the sequence form Fig. 7 is inconsistent with that shown in Fig. 11 in havin
A;Note: the sequence form Fig. 7 is inconsistent with that shown in Fig. 11 in havin
A;Note: the sequence form Fig. 7 is inconsistent with that shown in Fig. 11 in havin
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A;Note: the sequence in Fig. 11 in havin
A;Note: the sequence in
F;68-1455/Region: interrupted helical
F;362-364/Region: cell attachment (R-G-D) motif
F;784-796/Region: cell attachment (R-G-D) motif
F;888-870/Region: cell attachment (R-G-D) motif
F;889-891/Region: cell attachment (R-G-D) motif
F;889-891/Region: cell attachment (R-G-D) motif
F;970-972/Region: cell attachment (R-G-D) motif
F;1059-1071/Region: cell attachment (R-G-D) motif
F;1228-1230/Region: cell attachment (R-G-D) motif
F;1452-1454/Region: cell attachment (R-G-D) motif
F;1452-1390/Region: cell attachment (R-G-D) motif
F;1452-1390/Region: cell attachment (R-G-D) motif
F;1459-1930/Region: cell attachment (R-G-D) motif
F;1459-1930/Region: cell attachment (R-G-D) motif
F;1479-1930/Region: cell attachment (R-G-D) motif
F;1486-1712/Domain: carboxyl-terminal repeat <CT1>
F;1495-1930/Region: collagen IV carboxyl-terminal repeat <CT2>
F;1495-1930/Region: collagen IV carboxyl-terminal repeat <CT2>
F;1495-1530/Region: collagen IV carboxyl-terminal repeat <CT2>
F;1495-15
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A;Introns: 15/2; 33/3; 1347/1; 1380/1; 1429/1; 1468/1; 1532/1; 1527/3 #status incomplet.
A;Introns: 15/2; 33/3; 1347/1; 1380/1; 1429/1; 1468/1; 1532/1; 1527/3 #status incomplet.
A;Note: the alpha 1(IV) and alpha 2(IV) chain genes are encoded on opposite strands with C;Complex: Type IV collagen is a heterotrimer of two alpha 1(IV) chains (see PIR:CGHU4B) domains (with disulfide and desmosine cross-links), dimeric associations among trimer crupted helical domain (with disulfide and desmosine cross-links).
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A;Residues: 1486-1574, I', 1576-1712 <MYE>
A;Residues: 1486-1574, I', 1576-1712 <MYE>
A;Cross-references: EMBL:J02760; NID:g180425; PIDN:AAA58422.1; PID:g180426
C;Comment: Prolines and lysines at the third position of the tripeptide repeating ed and subsequently O-glycosylated.
C;Genetics:
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A;Title: Partial structure of the human alpha-2(IV) collagen chain A;Reference number: S01450; MUID:88085168; PMID:3692475
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Hoppe-Seyler's Z. Physiol. Chem. 362, 943-951, 1981
A;Title: Pepsin fragments of human placental basement-membrane
A;Reference number: S16908; MUID:82005835; PMID:6792033
A;Accession: B58517
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A;Residues: 490-492,'X',494-496;675-677,'G',679-680,'G',682,684-685,'P'
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A;Title: Isolation and characterization of pepsin-solubilized human basement membrane
A;Reference number: S16910; MUID:84053346; PMID:6416291
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A;Residues: 490-492,'X',494-501,'P',503-507;952-957,'X',959-966,'X',968;984-986,'X'
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A;Cross-references:
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A;Molecule type: genomic RNA
A;Residues: 1-3430 <CAS>
A;COSS references: UNIPROT:P06935; GB:M10103; GB:M12294; NID:g336167; PIDN:AAA48498.1;
A;Cross-references: UNIPROT:P06935; GB:M10103; GB:M12294; NID:g336167; PIDN:AAA48498.1;
A;Oross-references: UNIPROT:P06935; GB:M10103; GB:M12294; NID:g336167; PIDN:AAA48498.1;
A;Oross-references: UNIPROT:P06935; GB:M10103; GB:M12294; NID:g336167; PIDN:AAA48498.1;
A;Cross-references: UNIPROT:P06935; GB:M10103; GB:M12294; NID:g336167; PIDN:AAA48498.1;
A;Cross-references: UNIPROT:P0695; GB:M10294; NID:g336167; PIDN:AAA48498.1;
A;Cross-references: UNIPROT:P0695; GB:M10294; NID:g336167; PIDN:AAA48498.1;
A;Cross-references: UNIPROT:P07040; Membrane-associated glycoprotein NV2 precursor #status predicted <NV2
F;105-123/Product: membrane-associated glycoprotein NV2 #status predicted <NV3
F;275-790/Domain: nonterminal signal sequence #status predicted <NV3
F;286-239/Product: membrane-associated glycoprotein V3 precursor #status predicted <NV3
F;291-787/Product: membrane-associated glycoprotein V3 precursor #status predicted <NV3
F;188-2109/Product: monstructural protein NV4 #status predicted <3NV>
F;189-1702/Region: nucleotide-binding motif A (P-loop)
F;178-1787/Region: nucleotide-binding motif B
F;1786-3427/Product: nonstructural protein NV5 #status predicted <NV4
F;2580-3427/Product: nonstructural protein NV5 #status predicted <NV5>
F;189-1796,2994,1289,1659,1966,2336,2459,2489,2573,2739,2759,2864,2902/Binding site: c
C;Species: Kunjin vill.
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #sequence_revision 30-Sep-1989 #sequence_revision 30-Sep-1989
C;Accession: A28697
R;Coia, G; Parker, M.D.; Speight, G.; Byrne, M.E.; Westau J. Gen. Virol. 69, 1-21, 1988
A;Title: Nucleotide and complete amino acid sequences of Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight Speight 
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C;Species: West Nile virus
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A25256
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F;1504-1590,1537-1593/Disulfide bonds: (F;1549-1555,1658-1665/Disulfide bonds: #
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A;Title: Primary structure of the West Nile flavivirus genome A;Reference number: A25256; MUID:86124703; PMID:3753811
A;Accession: A25256
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N;Contains: capsid protein C; envelope protein E; I
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G.
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AG0147
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A; Residues: 1-296 < KUR>
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71.4%;
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F;216-290/Product: membrane protein M #status predicted <MPM>
F;291-791/Product: envelope protein E #status predicted <EPE>
F;292-1143/Product: nonstructural protein NS1 #status predicted <NS1>
F;1144-1374/Product: nonstructural protein NS2a #status predicted <N2A>
F;1375-1505/Product: nonstructural protein NS2b #status predicted <N2A>
F;166-2124/Product: nonstructural protein NS2b #status predicted <NS3>
F;1699-1706/Region: nucleotide-binding motif A (P-loop)
F;1786-1791/Region: nucleotide-binding motif B
F;1790-1793/Region: DEAH motif
F;2125-2273/Product: nonstructural protein NS4a #status predicted <N4A>
F;2274-528/Product: nonstructural protein NS4a #status predicted <N4B>
F;2529-3433/Product: nonstructural protein NS5 #status predicted <N85>
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C;Keywords: ATP; capsid protein; envelope protein; membrane protein; nonstructural prote
F;2-123/Product: capsid protein C #status predicted <CPC>
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A;Residues: 1-3433 <COI+
A;Residues: 1-3433 <COI+
C;Superfamily: yellow fever virus genome polyprotein
C;Superfamily: yellow fever virus genome polyprotein
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 bel A;Accession: H82539
A;Status: preliminary
                                                                                                                                                                                                                                                                     protein-L-isoaspartate O-methyltransferase XF2585 [imported] - Xylella fast C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004 C;Accession: H82539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Genome sequence of Yersinia pestis, the causative A; Reference number: ABO001; MUID:21470413; PMID:11586360
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0147
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Pred. No. 4.5e+02;
3; Mismatches 5;
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Pred. No. 37;
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A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Uunqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrando, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marxino, C.L.; Warques, M.V.; Wartins, E.A.; Machins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M., de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.; de Silva, A.M.; Silva Jr., W.A.; da Silva, A.R.; Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, A.J. Salva, 
fatty-acid desaturase homolog yocE - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Accession: B69901
C;Accession: B69901
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber (C.; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
C.; Bron, S.; Broulllet, S.; Emtian, K.D.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Galizzi, A.; Lapidus, A.; Lardino Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Forsman, M.; Haeggstroem, B.; Lindgren, L.; Jaurin, B. J. Gen. Microbiol. 136, 589-598, 1990
A.Title: Molecular analysis of beta-lactamases from four species A.Reference number: A45822; MUID:90362045; PMID:2391494
A;Accession: A45822
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A;Residues: 1-313 <FOR>
A;Cross-references: UNIPROT:P35391; GB:M34178; NID:g153182;
C;Superfamily: Beta-lactamase I
C;Keywords: hydrolase
F;93/Active site: Ser #status predicted
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A; Residues: 1-218 < SIM>
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Superfamily:
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8; Conserv
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EEPELSRWVPGEKRDT
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87.5%;
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Pred. No. 31;
0; Mismatches
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Pred. No. 47;
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         Fujita, Y.; Fuma, S.; Galizzi, A.; Gallex
H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
o, M.; Kurita, K.; Lapidus, A.; Lardinois,
.; Levine, A.; Liu, H.; Masuda, S.; Maueel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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M.; Cho
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                                                 A; Status: preliminary
A; Molecule type: DNA
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y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scamlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Tognoni, A.; Tosato, V.; Uchiyama, A.; A; Winters: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: B69901
A; Kocession: B69901
A; Molecule type: DNA
A; Residues: 1-352 < KUN>
A; Cross-references: UNIFROT:034653; GB:Z99114; GB:AL009126; NID:92634230; PIDN:CAB13810
R.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimi C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89894
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A; Residues: 1-481 <BEV>
A; Cross-references: UNIPROT:065676; EMBL:AL023094

A; Cross-references: cultivar Columbia; BAC clo
                                                                                                                                                                                                         protein kinase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89894
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A; Accession: T05270
A; Molecule type: DNA
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R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, ewes, H.W.; Mayer, K.F.X.; Schueller, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable serine/threonine-specific protein kinase (EC 2.7.1.-) T4L20.80 - Arabidopsis C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
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C;Superfamily: Fatty acid (acyl-CoA) desaturase
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C;Keywords: phosphotransferase
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A; Introns: 179/2; 216/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the Protein Sequence Database,
A;Reference number: Z15406
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Best Local S
Matches 10
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7; Conserve
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Similarity 50.0%;
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Pred. No. 53;
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Pred. No.
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A;Cross-references: UNIPROT:Q99UP8; GB:BA000018; PID:g13701020; PIDN:BAB42315.1; GSPDB:
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                        A;Cross-references: FlyBase:FBgn0000382
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;6-101/Domain: SH2 homology <SH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P29349; GB:M94730; NID:g157144; PID:g157145
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:109964, NCBIP:10996)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: corkscrew encodes a A; Reference number: A43254; A; Accession: A43254
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                                                                                                                                                                      A;Reference number: A71250;
A;Accession: E71376
                                                                                                                                                                                          A;Title: Complete genome sequence of Treponema pallidum, A;Reference number: A71250; MUID:98332770; PMID:9665876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: FlyBase:csw
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A; Residues: 1-841 < PER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine-phosphatase (EC 3.1.3.48) corkscrew - fruit fly (Drosophila melanogast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;583/Active site: Cys (phosphocysteine intermediate) #status predicted;589/Binding site: substrate phosphate (Arg) #status predicted
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;252-634/Domain: protein-tyrosine-phosphatase homology <PTP>
;583/Active site: Cys (phosphocysteine intermediate) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Title: corkscrew encodes a putative protein tyrosine;Reference number: A43254; MUID:92346711; PMID:1638629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Drosophila melanogaster;
Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004;
Query Match
                                                                       Molecule type: DNA
;Residues: 1-1023 <COL>
:Cross-references: UNIPROT:083069; GB:AE001187; GB:AE000520; NID:g3322273; PIDN:AAC6501
;Experimental source: strain Nichols
                                                                                                                                                Status: preliminary; nucleic acid sequence not shown; translation not
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Best Local :
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40.6%;
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43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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Length 1023;
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                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-106 <KUR>
                                                                                                                                                                                            A; Authors: Yoo, H.; Tao, ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                     A,Experimental source: strain C58 (Dupont) C;Genetics:
                                                                                                                                     A; Reference number: A; Accession: AC3086
                                                           A;Cross-references: UNIPROT:Q8U7Y8; GB:AE008689; PIDN:AAL45105.1; PID:g17742774; GSPDB:6
                                                                                                                                                      A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                         AC3086
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C; Accession: AC3086
C; Accession: AC3086
C; Accession: AC3086
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; R; Wood, D.W.; Setubal, J.C.; Guenthner, D.; I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; I ; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
Bs-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvar,
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 bel A;Accession: E82797
                                                                                                                                                                                C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AC3086
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A;Residues: 1-104 <SIM>
A;Cross-references: UNIPROT:Q9PG01; GB:AE003899; GB:AE003849; NID:g9105351; PIDN:AAF8331
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                                                                                                                                                                                                                                            sarcosine oxidase delta subunit [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
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4; Mismatches
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Kutyavin, T.; Levy,
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M.; McClell
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P.; Jung, M.;

Krespan, W.; Perry, M.; Gordon-Kamm,

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A;Gene: AGR L_1105
A;Map position: linear chromosome
C;Superfamily: Corynebacterium sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: linear chromosome C; Superfamily: Corynebacterium sp
                                                                                                                                                                                                                                                        R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83161
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C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
밁
                                                                                                                                                                    A;Cross-references: UNIPROT:Q9HXC7; GB:AE004805; GB:AE004091; NID:g9950055; PIDN:AAG072:
A;Experimental source: strain PAO1
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A; Residues: 1-218 <STO>
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A;Residues: 1-106 <KUR>
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A;Reference number: A97359; MUID:21608551; PMID:11743194
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EGPVLMHCKHGNNR 138
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RESULT 38

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A; Nolecule type: DNA
A; Rolecule type: DNA
A; Coss-references: UNITROT: (927T0; GB: AB001647; GB: AB001363; NID: 94376920; PIDN: AAD187
A; Coss-references: UNITROT: (927T0; GB: AB001647; GB: AB001363; NID: 94376920; PIDN: AAD187
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C;Species: bovine herpesvirus 4
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000
C;Accession: T44657
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Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255; PMID:10684935
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C;Genetics:
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
                                                                                                                                                  glyceraldehyde-3-P dehyrogenase [imported] - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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A; Residues: 1-273 < LOM>
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A; Accession: T44657
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A;Experimental source: strain AR39, HL cells
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A; Residues: 1-335 < REA>
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                                                                                                                   C; Accession: E86568
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RESULT 42
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C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text change 09-Tml-2004
C;Accession: $43339, $1250
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A;Residues: 1-249,'A','251-335 <LIW>
A;Residues: 1-249,'A','251-335 <LIW>
A;Cross-references: EMBL:X73034; NID:g297453; PIDN:CAA51515.1; PID:g297454
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; oxidoreductase
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A;Cross-references: UNIPROT:Q9Z7T0; GB:BA000008; NID:g8978996; PIDN:BAA98831.1; GSPDB:GN
A;Experimental source: strain J138
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A;Accession: E86568
A;Status: preliminary
A; Reference number: A30754
A; Accession: A30754
A; Molecule type: DNA
                                                                                                                                                                      C;Date: 19-May-1989 #sequence_revision 31-Dec-1990 #text_change C;Accession: JT0361; A30754 R;Jobling, M.G.; Ritchie, D.A. Gene 66; 245-258, 1988 A;Title: Nucleotide sequence of a plasmid determinant for resist A;Reference number: JT0361; MUID:89006266; PMID:3049247 A;Accession: JT0361
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C;Date: 07-Sep-1994 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S43339; S36592
R;Liaud, M.F.; Valentin, C.; Brandt, U.; Bouget, F.Y.; Kloareg, B.; Cerff, Plant Mol. Biol. 23, 981-994, 1993
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A;Description: The evolutionary origin of red algae as deduced from the nuclear
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                                                                 R;Jobling, M.G. submitted to GenBank, September 1988
                                                                                                                               A;Molecule type: DNA
A;Residues: 1-339 <JO1>
                                                                                                                                                                                                                                                                                                                              hypothetical protein terA - Alcaligenes C;Species: Alcaligenes sp.
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A;Residues: 1-335 <LIA>
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;Superfamily:
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, i Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                      R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Map position: 1
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
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A; Accession: F96826
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C; Superfamily:
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A;Cross-references: UNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F309.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                    A; Gene: T8K14.5
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                                                                                                       A; Cross-references:
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                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                           A;Status: preliminary
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C,Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                       UNIPROT: Q9SAJ6; GB: AE005173; NID: g4835756; PIDN: AAD30223.1;
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5; Mismatches
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Pred. No.
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Conway, A.B.; Conway, A.R.; Creasy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                      Shinn, P.; Southwick, A.M.; Sun,
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73;
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Maiti, R.; Marziali,
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; Dewar, K.;
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RESULT 45
S51837
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C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: chloroplast; gluconeogenesis; glycolysis; oxidoreductase
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Matches 5
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;Molecule type: mRNA
;Residues: 1-433 «MEY»
;Cross-references: UNIPROT:Q37264; EMBL:L32561; NID:g1100224; PIDN:AAD10214.1; PID:g110
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Best Local Similarity 35.7%;
Matches 5; Conservative
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Similarity 35.7%;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence 1
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Hypothetical protein YPO0843.
Name=YPO0843; OrderedLocusNames=PBPRB0156;
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Q76H55;
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SEQUENCE
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InterPro; IPR009061; Putativ_DNA_bind.
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR378675; CAG22029.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         serotype Typhimurium DT104.";
J. Clin. Microbiol. 42:1807-1812(2004).
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Ishihara R., Sameshima T.,
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Cestaro A., Malacrida G., Simionati B.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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., Akiba M., Nakazawa
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003524; F:ATP binding; IEA.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0004672; F:protein kinase activity; IE
GO; GO:0004648; P:protein amino acid phosphor
InterPro; IPR011009; Kinase like.
InterPro; IPR001932; PP2C-1Ike.
InterPro; IPR001932; PP2C-1Ike.
InterPro; IPR008266; Tyr Dkinase_AS.
Pfam; PP00481; PP2C; 1.
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01-JUN-2003
01-JUN-2003
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Q8CSV9;
01-MAR-2003
01-MAR-2003
01-MAR-2004
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SEQUENCE
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DNA Res. 9:189-197(2002).
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OrderedLocusNames=bll2800;
Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M., "Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATCC 12228)."; Mol. Microbiol. 49:1577-1593 (2003).
                                                                                                                                                                                                                                                  Protein kinase.
OrderedLocusNames=SE0895;
Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales;
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SMART; SM00331; PP2C SIG; 1.
SMO331; PP2C SIG; 1.
SMOSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00109; PROTEIN_KINASE_TYR;
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Sasamoto S., Watanabe A., Idesawa K., Iriguchi M.
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N
STRAIN=USDA110;
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Bradyrhizobiaceae; Bradyrhizobium.
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                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=ATCC 12228;
                                                                                                                                        PubMed=12950922;
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HSSP; P71584; 10
GO; GO:0005524;
GO; GO:0008658;
GO; GO:0004674;
GO; GO:0006468;
GO; GO:0006468;
                                                                                                             metabolites.";

Proc. Natl. Acad. Sci. U.S.A. 98:12215-

EMBL; AP005021; BAC67716.1; -.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0015074; P:DNA integration; IEA.
                                                                                                                                                                                                                                                                                                                                    STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Keda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22608306; PubMed=12692562; Ikeda H., Ishikawa J., Hanamoto A., Shinos Sakaki Y., Hattori M., Omura S.; "Complete genome sequence and comparative microorganism Streptomyces avermitilis.";
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01-JUN-2003
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SMART; SM00740; PASTA; 3.
SMART; SM00220; S TKC; 1.
SMART; SM00220; S TKC; 1.
FROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Complete proTeome; Kinase;
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InterPro; IPR005543; PASTA.
InterPro; IPR00719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PP03793; PASTA; 2.
Pfam; PF00069; Pkinase; 1.
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01-OCT-2003 (TrEMBLrel.
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SEQUENCE 667 AA; 75411 MW; 479877B4531CDD97 CRC64;
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GO:0008658; F:penicillin binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity;
GO:0016740; F:transferase activity;
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                                   GO:0006310; P:DNA recombination; lerPro; IPR011010; DNA_brk_join_enz.
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57.1%;
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                                                                                                                                                                                                                                                                                                         ability of producing
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Pred. No. 25;
4; Mismatches
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                                        STRAIN=GMI1000;

MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;

Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N

Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.",

"Mature 415:497-502(2002).
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Complete proteome
SEQUENCE 690 AA
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
PROBABLE PHAGE PHI-105 ORF25-LIKE PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Katayose Y.; "Oryza sativa nipponbare(GA3) genomic DNA, clone:OSJNBb0066M12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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l protein OSJNBb0066M12.35.
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A Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,

A Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,

A Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,

A Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,

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Utterback T.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,

A Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,

A Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,

Bender C.L., White O., Fraser C.M., Collmer A.;

"The complete genome sequence of the Arabidopsis and tomato pathogen

"Fseudomonas syringae pv. tomato DC3000.";

Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).

EMBL; AE016869; AA054502.1;

-. REMBL; AE016863; AA054939.1;

-. REMBL; AE016863; AA058222.1;

EMBL; AE016863; AA058222.1;

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Complete proteome.
SEQUENCE 407 AA; 45951 MW; CC223
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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GO:0004803; F:transposase activity;
GO:0006313; P:DNA transposition; IE.
erPro; IPR002559; Transposase_11.
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proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
EMBL; AE016857; AA053902.1; -.
EMBL; AE016869; AA057203.1; -.
TIGR; PSPT00358; -.
TIGR; PSPT03734; -.
MEDLINE-22334015; PubMed=12928499; DOI=10.1073/pnas.1731982100; Buell C.R., Joardar V., Lindebberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Dugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Melson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Felblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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GO; GO:0004803; F:transposase activity;
GO; GO:0006313; P:DNA transposition; IE
InterPro; IPR002559; Transposase_11.
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Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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   Sung L.A., Chien S., Chang L.-S., Lambert K. Bouhasaira E.E., Nagel R.L., Schwartz R.S., "Molecular cloning of human protein 4.2: a n erythrocyte membrane.";
Proc. Natl. Acad. Sci. U.S.A. 87:955-959(19)
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                                                                                                                                                                                                                                                  "Complete amino acid sequence and homologies membrane protein band 4.2.";
Proc. Natl. Acad. Sci. U.S.A. 87:617-617/1007
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Mammalia; Eutheria;
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                                                                                                                                                TISSUE=Reticulocytes;
MEDLINE=90138995; Pub
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Korsgren C., Lawler J., Lambert S
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Qiu J.J.-H., Nagel R.L., Rybicki A.C.; Yawata Y., Ata K., Kanzaki A. "An alamine-to-threonine substitution in protein 4.2 cDNA is associated with a Japanese form of hereditary hemolytic anemi (protein 4.2 Nippon)."; Blood 79:1846-1854(1992).
                                                                                                                                                                                                                                                                                                                                                                                    Br. J. Haematol. 89:762-770117537.

-i- FUNCTION: Probably plays an important role in the erythrocyte shape and mechanical properties.

-i- SUBUNIT: Oligomer. Interacts with the cytoplasmic SLC4A1/band 3 anion transport protein.

-i- SUBCELLULAR LOCATION: Membrane-associated (cytoplasmic cytoplasmic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human erythrocyte protein 4.2, a h is N-myristylated.";
J. Biol Char
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MEDLINE=93271204; PubMed=8499466; DOI=10.1016/0005-2736(93)90156-T;
Dotinas E., Speicher D.W., Guptaroy B., Cohen C.M.;
"Structural domain mapping and phosphorylation of human erythrocyte
                                                                 This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A novel mutation in the erythrocyte protein 4.2 gene of Japanese patients with hereditary spherocytosis (protein 4.2 Fukuoka)."; Br. J. Haematol. 88:527-533(1994).
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Takaoka Y., Ideguchi H., Matsuda
Fukumaki Y.;
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PTM: Both cAMP-dependent kinase (CAPK) and another kinase present in the red-blood cells seem to be able to phosphorylate EPB42.

DISEASE: Defects in EPB42 are a cause of hereditary spherocytosis (HS) [MIM:17070], a hematologic disorder leading to chronic hemolytic anemia and characterized by numerous abnormally shaped erythrocytes which are generally spheroidal. Absence of band 4.2 associated with spur or target erythrocytes has also been
                                                                                                                                      site may of band 4
                                                                                                                         SIMILARITY: Belongs to the transglutaminase family.
                                                                                                                                                                   MISCELLANEOUS:
                                                                                                                                                                              associated with reported.
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GO; GO:0005856; C:cytoskeleton; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005524; F:ATP binding; TAS.
GO; GO:0005200; F:structural constituent
InterPro; IPR00102; GlutransfG.
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Name=Epb42; Synonyms=Epb4.2;
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Direct protein sequencing; Disease mutation; Erythrocyte maturation;
Hereditary hemolytic anemia; Lipoprotein; Myristate; Phosphorylation
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Phosphoserine (by PK
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  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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TRPALP -> KRGLPC (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A -> T (in HS; Nippon/Fukuoka)
/FTId=VAR_007482.
R_-> Q (in HS; Tozeur).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> H (in Ref. 3).
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QGEPSQRSTGLAGLYAAPAASPVFIKGSGMD
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Reticulocytes;
MEDLINE=9500352; PubMed=7919957;
Rybicki A.C., Schwartz R.S., Qiu J.J.-H., Gilman J.G.;
Rybicki A.C., Schwartz M.S., Qiu J.J.-H., Gilman J.G.;
"Molecular cloning of mouse erythrocyte protein 4.2: a
"Molecular cloning of mouse erythrocyte protein 4.2: a
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                                                                                                                                       SITE
                                                                                                                                                                                                              InterPro; IPR001102; GlutransfG.
InterPro; IPR008958; Transglut C.
InterPro; IPR002931; Trnsglunase_like.
Pfam; PF00807; Transglut C; 2.
Pfam; PF01841; Transglut core; 1.
Pfam; PF00868; Transglut_N; 1.
                                                                                                                                                                                                                                                                                                                                  EMBL; U03487; AAA62275.1; -.
EMBL; U04055, AAA67916.1; -.
EMBL; U04056; AAA67917.1; -.
EMBL; L35933; AAA39875.1; -.
EMBL; L35933; AAA39875.1; -.
EMBL; A54741; A54741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Karacay B.B.K., Enzhong X.E.X., Chang L.-S.L.S.;
"Murine erythrocyte protein 4.2 gene: similarity and dif-
structure and expression from its human counterpart.";
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (Store send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95048323; PubMed=7959722;
Koregren C., Cohen C.M.;
"CDNA sequence, gene sequence, and properties of n
"CDNA sequence, implicated in the murine pallid
4.2), the protein implicated in the murine pallid
Genomics 21:478-485(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=BALB/c, and
                                                                                                                                                                     PROSITE; PS00547; TRANSGLUTAMINASES; 1.
Cell shape; Cytoskeleton; Erythrocyte m
Myristate; Phosphorylation; Structural
                                                                                                                                                                                                                                                                                                         MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Probably plays an important role in the erythrocyte shape and mechanical properties. SUBUNIT: Oligomer. Interacts with the cytoplasmic SLG4Al/band 3 anion transport protein. SUBCELLULAR LOCATION: Membrane-associated (cytoplasmic subcellular controls)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of band 4.2.
SIMILARITY: Belongs to the transglutaminase factorion: Was originally (Ref.2) thought to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erythrocyte membranes) and cytoplasmic.
MISCELLANEOUS: The substitution of an Ala for a Cys in the site may be responsible for the lack of transglutaminase
                                                                                                                                                                                                                                                                                                      MGI:95402; Epb4.2
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                               247
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223
297
449
527
    76608
    ₩;
              Band 3 binding (By similarity).

N-myristoyl glycine (By similarity).

Phosphoserine (By similarity).

Y -> H (in Ref. 2, AAA67917).

K -> N (in Ref. 2, AAA67917).

C -> S (in Ref. 2, AAA67917).

K -> R (in Ref. 2, AAA67917).

S -> R (in Ref. 2, AAA67917).

S -> R (in Ref. 2, AAA67917).

S -> C (in Ref. 2, AAA67917).
    3F6BCEF23DD385A6
                                                                                                                                                      arity.
                                                                                                                                                                                    maturation; Lipoprotein;
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                                                                                                                                                                     protein.
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oe pallidin.
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d mutation.";
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SETARIN-C57BL/6J; TISSUE=Embryo;

STRAIN-C57BL/6J; TISSUE=Embryo;

MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Alpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Alphins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Alphins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Alphins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

XX Alphins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

XX Alphins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Alphins R.F., Jordan N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Alphins R.F., Mozen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Alphins R.F., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Alphins R.F., Mozen B., Ketteman M., Madan A., Gabbs R.A.,

XX Alphins R.F., Touchman J.W., Green E.D., Dickson M.C.,

XX Alphins R.F., Touchman J.W., Green E.D., Dickson M.C.,

XX Alphins R.F., Schalsk U., Smailus D.E., Schmerch A., Schein J.E.,

XX Alphins R.F., Schmerch A., Schmerch A., Schein J.E.,

XX Alphins R.F., Schmerch A., Schmerch A., Schmerch A., Schmerch A., Sc
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Query Match
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HSSP; P00488; 1EXO.

GO; GO:0018149; P:peptide cross-linking; IE

InterPro; IPR001102; GlutransfG.

InterPro; IPR002114; HPr SerP S.

InterPro; IPR002918; Transglut C.

InterPro; IPR002938; Transglut C: 2.

Pfam; PF00927; Transglut C: 2.

Pfam; PF01841; Transglut Core; 1.

Pfam; PF01841; Transglut N; 1.
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25-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC066806; AAH66806.1; -. EMBL; BC066194; AAH66194.1; -.
                                                              PROSITE; PS00589; PTS HPR SER; UNKNOI PROSITE; PS00547; TRANSGLÜTAMINASES; SEQUENCE 691 AA; 76697 MW; EC3E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc.
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Mammalia; Eutheria;
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                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
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STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249
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                                                                                                                                                              TGc;
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Rodentia;
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47.2%;
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28, Last annotation update)
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      Score 50;
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                                                                                                                          UNIKNOWN_1.
                                                                  WASES; 1.
EC3E1623482D8E12 CRC64;
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RESULT 14
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PIL; AB340; AB2340.

GO; GO:0005524; F.ATP binding; I
GO; GO:0005524; F.ATP

Pfam; PF01590; GAF; 1.

Pfam; PF02518; HATPase_C; 1.

SMART; SM00065; GAF; 4.

SMART; SM00387; HATPase_C; 1.
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Q8YPC5;
01-MAR-2002
01-MAR-2002
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01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete
SEQUENCE
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                                                                   Beck J., Ripka S., Siegner A., Schiltz E "The multifunctional 6-methylsalicylic a Penicillium patulum. Its gene structure polyketide synthasss.";
                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
6-methylsalicylic acid synthase (EC 2.3.1.165)
penicillium patulum (Penicillium griseofulrum)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; l
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; mitosporic Trichocomaceae; 
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Kishida Y., Kohara M., Matsumoto M.,
Nakazaki N., Shimpo S., Sugimoto M.,
Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                              SEQUENCE FROM N.A.,
STRAIN=DSM 62862;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=103690;
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                                                                                                                                                         MEDLINE=91006137; PubMed=2209605;
                                                                                                                                                                                                                                    NCBI_TaxID=5078;
                                                                                                                                                                                                                                                                                                                                                                                                                       MSAS_PENPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 8:205-213(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genomic sequence of the filamentous nitrogen-fixing
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polyketide synthase...
Sur. J. Biochem. 192:487-498(1990).
-!- FUNCTION: This multifunctional enzyme is a polyketide synthase.
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be A., Iriguchi M., Ishikawa
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Cyanobacteria; Nostocales;
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72.7%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                      Schiltz E.,
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M., Matsuno A
M., Takazawa
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acid synthase gene of
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atsuno A., Muraki A.,
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PIR; S13178; S13178.

InterPro; IPR001227; Ac_transferase.

InterPro; IPR00981; Ac_like.

InterPro; IPR00994; Ketoacyl_synth.

InterPro; IPR006163; Pp_bind.

InterPro; IPR006162; Ppantne_S.

Pfam; PF00698; Acyl_transf_1; 1.

Pfam; PF00109; Ketoacyl-synt; 1.

Pfam; PF002801; Ketoacyl-synt; 1.

Pfam; PF02801; Ketoacyl-synt; 1.
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
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DOMAIN
                                                                   MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a; Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Pre Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  066272
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                                                                                                                                      SEQUENCE FROM N.A. STRAIN=IAM14332;
                                                                                                                                                                                                                                                                                                Name=pufL;
    EMBL; AB010981; BAA25791.1; -.
                         "Unsuspected diversity among marine Nature 415:630-633(2002).
                                                                                                                                                                                              NCBI_TaxID=39960;
                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                           Erythrobacter litoralis.
                                                                                                                                                                                                                                                                                                                  Photosynthetic reaction
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SUBUNIT: Homomultimer.
INDUCTION: In the late logarithmic growth phase.
SIMILARITY: Contains 1 acyl carrier domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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PSS00606; B KETOACYL SYNTHASE; 1.
PS00012; PHOSPHOPANTETHEINE; 1.
ps00012; PHOSPHOPANTETHEINE; 1.
psounthesis; Direct protein sequencing;
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center L subunit (Fragment).
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Pred. No. 1e+C
4; Mismatches
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Beta-ketoacyl synthase (By similarity).
Malonyltransferase (By similarity).
Phosphopantetheine (By similarity).
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1e+02;
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SEQUENCE
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EMBI; AB015708; BAA32995.1; -.

HSSP; P02954; 1YST.

GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. GO; GO:0045156; F:electron transporter, transferring electron. GO; GO:0006118; P:electron transport; IEA.

GO; GO:0019694; P:photosynthesis, light reaction; IEA.

InterPro; IPR005871; Photo_L.

InterPro; IPR005871; Photo_RC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erythrobacter sp.
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Erythrobacter.
Q9XDV0 PRELIMINARY;
Q9XDV0;
01-NOV-1999 (TrEMBLrel. 12,
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InterPro; IPR000484; Photo_RC.
Pfam; PP00124; Photo_RC.
PRINTS; PR00256; REACTNCENTRE.
TIGRFAMS; TIGR01157; pufL; 1.
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GO; GO:00330077; C:light-harvesting complex (sensu Proteobacte...

GO; GO:0045156; F:electron transporter, transferring electron...

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0019684; P:photosynthesis, light reaction; IEA.

GO; GO:0019684; P:photosynthesis, light reaction; IEA.
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PRINTS; PR00256; REACTNCENTRE.
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9; Conserv
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Eisen J.A., Fraser C.M.,
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PS00244; REACTION_CENTER;
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                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11832943; DOI=10.1038/415630a; T., Heidelberg J.F., Nelson W.C., Pre J.A., Fraser C.M., Delong E.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27214 MW; 52B268713E199ABD CRC64;
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81.8%;
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Pred. No. 18;
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Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Holmes M.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DoBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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EMBL; AB027515; BAA78672.1; -.

HSSP; P02954; 1YST.

GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte...

GO; GO:0045156; F:electron transporter, transferring electron...

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0019684; P:photosynthesis, light reaction; IEA.
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Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Erythrobacter.
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01-MAR-2004 (TrEMBLrel.
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01-OCT-2003 (TrEMBLrel. 2
Hypothetical protein.
OrderedLocusNames=PP4765;
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Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Pre
Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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01-JUN-2003
GO; GO:0015036; F:disulfide oxidoreductase activity; IEA GO; GO:0006118; P:electron transport; IEA. InterPro; IPR000759; Adrndx reductase.

InterPro; IPR001327; FAD_pyr_redox.
                                                                                                            EMBL; AE016791; AAN70335.1; TIGR; PP4765; -.
                                                                                                                                                             Fraser C.M.;
"Complete genome sequence and comparative a metabolically versatile Pseudomonas putida Environ. Microbiol. 4:799-808(2002).
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InterPro; IPR000484; Photo_RC.
Pfam; PF00124; Photo_RC; 1.
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    PS00244; REACTION_CENTER;
    278 AA; 30735 MW; 0BE
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InterPro; IPR000205; NAD_BS.
InterPro; IPR00100; Pyr_redox.
Pfam; PP03486; HI0933_like; 1.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00348; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
PRO050m; PD018041; HI0933_like; 1.
Pr0Dom; PD018041; HI0933_like; 1.
Complete proteome; Hypothetical proSEQUENCE 412 AA; 43682 MW; 1F4F
                                                                                            InterPro; IPR007815; Erythro_esteras.
Pfam; PF05139; Erythro_esteras; 1.
Antibiotic resistance; Hydrolase; Plasmid; Serine_esterase.
                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation between Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                   Escherichia coli.
Plasmid pIP1527.
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05-JUL-2004
                                                                                                                              EMBL; X03988; CAA27626.1;
PIR; A24381; ESECRM.
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia
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                                                                                    SEQUENCE
                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      Arthur M., Autissier D., Courvalin P.; "Analysis of the nucleotide sequence of the ereB
                                                                                                                                                                                                                                                                                                                                           MEDLINE=86259072;
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Pred. No. 31;
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32;
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RESULT 21 Q7SFQ9 ID Q7SFQ9

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Sordariomycetidae; Sordariales;
NCBI_TaxID=5141;
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GO; GO:0046673; F:metal ion transporter;
GO; GO:0030001; P:metal ion transport; I
InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR002523; Mg2+_transptCorA.
Pfam; PF01544; CorA; 1.
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STRAIN=OR74A;
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Name=NCU09091.1;
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                           EMBL; AP006532; BAC99
Hypothetical protein
                                                               Sasaki T., Matsumoto T., Katayose Y.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases EMBL; AP006532; BAC99962.1; -.
                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta;
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Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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8887 MW;
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F163E46DB01AEF57 CRC64;
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CG11077-pA (RES5125p).
ORFNames=CG11077;
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
Glycoside hydrolase family 2
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"Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautotroph Nitrosomonas europaea.";
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                             InterPro; IPR002196; Glyco hydro 24.
Pfam; PF00959; Phage lysozyme; 1.
Bacteriolytic enzyme; Complete protec
SEQUENCE 154 AA; 17326 MW; BB5511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC 19718 / IFO 14298;
MEDLINE-22586410; PubMed-12700255;
DOI-10.1128/JB.185.9.2759-2773.2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
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53.8%;
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Q688F0;
25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chow Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R., Chen Y.-L., Chang C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H., Hsiang J.-N., Hsu C.-H., Lung J.-J., Kau P.-I., Lee M.-C., Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003846; AAF59393.1; --
EMBL; AY071482; AAL49104.1; --
FlyBase; FEBEN003990; CG11077
GO; GO:0016021; C:integral to membrane;
GO; GO:0005778; C:peroxisomal membrane;
GO; GO:0005748; GO:005778; C:peroxisomal membrane;
InterPro; IFR007248; Mpw17_PMP22.
Pfam; PF04117; Mpv17_PMP22; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsid
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein O
Name=OSJNBa0035I01.11;
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Genome Biol.
                                                                                                                                                    Hypothetical protein. SEQUENCE 392 AA; 4
                                                                                                                                                                                                                 "Oryza sativa BAC OSJNBa0035I01
Submitted (SEP-2004) to the EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                 EMBL; AC137000; AAU10721.1;
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4 EGPT--LRQWLHGNGRD
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    Brokstein P., Ho
Chavez C., Dorsett

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(TIEMBLrel. 28, Last sequence up
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1 protein OSJNBa0035101.11.
                                                                  Conservative
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                                                                                      . 88
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EMBL/GenBank/DDBJ databases
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                                                                                      Score
Pred.
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., Park S.,
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ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; S TKC; 1.

SMART; SM00219; TYKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ROSITE; PS00108; PROTEIN KINASE ST; 1.

Kinase; Serine/threonine-protein kinase.
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GO; GO:0016301; F.Kinase activity; IEA.
GO; GO:0004674; F.protein serine/threonine kinase activity;
InterPro; IPR011009; Kinase_like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=P0046G12.38;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                    Hypothetical protein BLL2800.
Name=BLL2800; OrderedLocusNames=PBPRA2520;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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                                          high pressure adaptations."; submitted (MAR-2004) to the EMBL/GenBank/DDBJ
                                                                                                                   Valle G.;
                                                                                                                                  Vezzi A., Campanaro S., D
Cestaro A., Malacrida G.,
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=74109;
                                                                                                                                                                                                                                                                                  Photobacterium profundum (Photobacterium sp. (Bacteria, Proteobacteria, Gammaproteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6LP74;
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"Oryza sativa nipponbare(GA3)
                                                                                                                                                                                                                                                                  Vibrionaceae;
                                                                                          "Genome analysis of Photobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
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8; Conserva
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                                                                                                                                                                                                                                                                Photobacterium.
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66.7%;
                                                                                                                                            D'Angelo M.,
., Simionati
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Last annotation updat
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Pred. No. 43;
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genomic DNA,
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RESULT 28
EP42_BOVIN
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O46510;
28-FEB-2003
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SWART; SM00331; PP2C; 1.

SWART; SM00331; PP2C_SIG; 1.

SWART; SM00220; S_TKG; 1.

SWART; SM00219; TYCK; 1.

PROSITE; PS00101; PROTEIN KINASE DOW; 1.

PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.

Complete proteome; Hypothetical Protein.

Complete Scoteme; Hypothetical Protein.

Complete Scoteme; Hypothetical Protein.
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR008271; Tyr_pkinase.
Pfam; PF00069; Pkinase; 1.
Pfam; PF00069; Pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular basis of bovine red-cell Japanese black cattle.", Biochem. J. 332:183-187(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity;
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; F:protein maino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR011932; PP2C-like.
                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Japanese black;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=EPB42; Synonyms=BEP42;
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25-JAN-2005
                                                                                                                                                                                                                                                                                                    (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98244826; PubMed=9576866;
                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Band 4.2 probably plays an important role in the regulation of erythrocyte shape and mechanical properties. The major membrane binding for band 4.2 is the cytoplasmic domain of the erythrocyte anion transporter, band 3 (By similarity).
SUBCUNIT: Oligomer (By similarity).
SUBCULIULAR LOCATION: Cytoplasmic surface of erythrocyte membranes
                                                                                                                                                                                                                                     MISCELLANEOUS: The substitution site may be responsible for the of band 4.2.
                                                                                                                                                                                                                 SIMILARITY: Belongs to the transglutaminase family.
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FUNCTION: Band 4.2 probably plays
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3 (Rel. 41, Last seq
5 (Rel. 46, Last ann
e membrane protein b
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ane protein band 4.2 (Erythrocyte protein
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HSSP; Q08188; 119M.
GO; GO:0018149; P:peptide cross-linking; IE
InterPro; IPR001102; GlutransfG.
InterPro; IPR002114; HPT_SerP_S.
InterPro; IPR002931; Transglut C:
InterPro; IPR002931; Transglut C; 2.
Pfam; PF01841; Transglut Core; 1.
Pfam; PF01841; Transglut Core; 1.
Pfam; PF01841; Transglut N; 1.
SMARPT. SMOAA60; Transglut N; 1.
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MOD_RES
SEQÜENCE
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PROSITE; PS00547; TRANSGLUTAMINASES; FALSE_NEG
Cell shape; Cytoskeleton; Erythrocyte_maturation
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InterPro; IPR008958; Transglut C.
InterPro; IPR002931; Transglumase_like.
Pfam; PF00927; Transglut C; 2.
Pfam; PF01841; Transglut_core; 1.
Pfam; PF00868; Transglut_N; 1.
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                                                                                                                                                                                                                                    MEDLINE=98244826; PubMed=9576866; Matsumoto M., Inaba M., Ono Ki.; "Molecular basis of bovine red-cell japanese black cattle."; japanese black cattle."; Biochem. J. 332:183-187(1998).
                                                                                                                                                                                                                                                                                                                                                                                       Erythrocyte protein
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01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                              046509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell shape; Cytoskeleton; Erythrocyte maturation; Lipoprotein; Myristate; Phosphorylation; Structural protein.
                                                                                                                                                                                                                                                                                                                  Bovinae; Bos.
NCBI_TaxID=9913;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                             Name=BEP42;
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249
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                                                                                      SM00460; TGc; 1.
E; PS00589; PTS_HPR_SER;
CE 687 AA; 76616 MW;
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686
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76485 MW;
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N-myristcyl glycine (By similarity)
Phosphoserine (By similarity).
; 71CDB6BCC82F2F7D CRC64;
                                                       Score 48; DB
Pred. No. 76;
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                                                                                        UNKNOWN 1.
599708868B355D2D CRC64;
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RESULT

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RESULT 32 055838 ID 05583

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Best Local S
Matches 10
                                                                                            Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Duell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,

Overton II L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,

Overton II, L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,

Fadrosh D.W., Tallon L.J., Koo H., Ziemann V., Hsiao J., Blunt S.,

Fadrosh D.W., Tallon L.J., Koo H., Ziemann V., Feldblyum T.V.,

Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,

Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,

White O., Salzberg S.L., Fraser C.M.;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q75174;
Q75174;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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Q84FF9;
                                                                                                                                                                                   EMBL; AC133398; AAR01777.1;
Hypothetical protein.
SEQUENCE 182 AA: 10077.
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Interpro; IPR003961; FN_III.
SMART; SM00060; FN3; 2.
SEQUENCE 1916 AA; 199157 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group). Enukaryota; Viriddiplantae; Etreptophyta; Enspermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat.)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat.)
Hypothetical protein OSJNBa0083F15.8.
Name=OSJNBa0083F15.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Hartzell P.L., Youder
Submitted (DEC-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myxococcus xanthus.
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cystobacterineae; Myxococcaceae;
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70
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8; Conserv
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                                                TLROWLHGNGRDT 19
THRPWLHGDGANT
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55.6%;
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Last annotation update)
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Pred. No.
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     RESULT 33
MOAA_CAUCR
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Best Local S
Matches 9
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"Phylogeny of the genus Flavivirus.";
J. Virol. 72:73-83(1998).
EMBL, AFO13414; AACS802.1;
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003968; F:RNA-directed RNA poly
GO; GO:0019079; P:viral genome replicat
InterPro; IPR000208; Flavi NS5.
R InterPro; IPR007095; RNA_pol_DS_PS.
R InterPro; IPR007094; RNA_pol_PSvir.
R Pfam; PF00972; Flavi_NS5; 1.
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01-JUN-1998
01-OCT-2003
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAINATCC 19089 / CB15;
MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Vamathevan J.J.,
Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
Bracer C.M...
Bracer C.M...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOAA CAUCR STANDARD; PRT; 349
G9AC48;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence updat
25-OCT-2004 (Rel. 45, Last annotation upd
Molybdenum cofactor biosynthesis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
NON_TER
SEQUENCE
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STRAIN-Oita 36;
MEDLINE-98080391; PubMed-9420202;
Finno G., Chang G.J., Tsuchiya K.R.,
     This
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NCBI_TaxID=64294;
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                                                                                                                                          "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- FUNCTION: Together with moaC, is involved in the conversion
guanosine derivative (GXP) into molybdopterin precursor Z (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=moaA; OrderedLocusNames=CC0018;
                                                                                                                                                                                                                                            Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caulobacteraceae; Caulobacter.
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                                          COFACTOR: Binds 1 3Fe-4S cluster (By similarity). PATHWAY: Molybdenum cofactor biosynthesis; first step. SIMILARITY: Belongs to the radical SAM superfamily. Mc
                                                                                                                        similarity)
     SWISS-PROT
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344
344 AA;
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  entry
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39610 MW;
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copyright.
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RNA polymerase activity;
replication; IEA.
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No.
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     is
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InterPro; IPR006638; Elp3/MiaB/NifB.
InterPro; IPR00385; MoaA_NifB_PqqE.
InterPro; IPR010505; Mob_Synth_C.
InterPro; IPR007197; Radical_SAM.
Pfam; PF04055; Mob_Synth_C; 1.
Pfam; PF04055; Radical_SAM; 1.
SMART; SM00729; Elp3; 1.
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Q9HX67;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2003 (TrEMBLrel. 2
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SEQUENCE
                                                                               between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAINATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Mestbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
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PIR; B87251; B87251.
                                                                                                                                                                            "Complete genome sequence of Pseu opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004813; AA07336-1; -.
PIR; E83151; E83151.
InterPro; IPR004792; HI0933_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudomo
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OrderedLocusNames=PA3949;
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                         Score 47;
Pred. No.
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46F4B0A76BAEC200 CRC64;
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STRAIN-Nippombare;

MCCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K.,

MCCombie W.R., de la Bastide M., Santos L., Zutavern T., Miller B.,

Kuit K., Nascimento L., Baker J., Santos L., Zutavern T., Miller B.,

Cunnius D.M., Katzenberger F., Muller S., Bell M., Balija V., Shah R.,

King L., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC092749; AAM08549.1; -.

EMBL; AC092749; AAM08549.1; -.

TELECOPIC TERECOGRAPHIC LIVE
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Q7G676;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
Q5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Q5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNAb0078C13.19 (Putative gag-pol).
Name=OSJNAb0078C13.19; ORFNAmes=OSJNBb0023M11.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7G676
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InterPro; IPR009057; Homeodomain_like.
InterPro; IPR005162; Retrotrans gag.
InterPro; IPR008916; Retrov_capsid_C.
Pfam; PP03732; Retrotrans_gag; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein OSJNBb0023M11.3.
Name=OSJNBb0023M11.3;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                SEQUENCE FROM N.A.

McCombie W.R., de la Bastide M., Spiegel L., Preston R.,

Kuit K., Nascimento L., Zutavern T., Balija V., Bell M.,

Miller B., Katzenberger F., Muller S., King L., Sullivan

Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI TaxID=39947;
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The Rice Chromosome 10 Sequentin-depth view of structure, chromosome 10.";
Science 300:1566-1569(2003).
                                                                                                               SEQUENCE
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                                                                                                                  FROM N.A.
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                                                                                        Consortium;
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                                                            of rice
                                                                                                                                                                                                                         Ferraro K.,
Baker J.,
P., Yang C.,
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RESULT
Q7T918
                                                              DR EMBL; AB114858; BAC79364.1; ---

DR HSSP; Q9Q4T1; IBBF.

DR GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IF

DR GO; GO:0008524; F:ATP binding; IEA.

DR GO; GO:0008026; F:ATP-dependent helli

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003724; F:RNA helicase activity

R GO; GO:0003724; F:RNA helicase activity

R GO; GO:0003724; F:RNA helicase activity

R GO; GO:0003724; F:RNA helicase activity

R GO; GO:0003795; F:structural molecule

R GO; GO:0019079; P:viral genome replic

InterPro; IPR0011545; DEAD.

InterPro; IPR0011545; DEAD.

InterPro; IPR0011545; DEAD.

InterPro; IPR001356; Flavi_DEAD.

InterPro; IPR000336; Flavi_DEAD.

InterPro; IPR000336; Flavi_NS2A.

InterPro; IPR000752; Flavi_NS2A.

InterPro; IPR000753; Flavi_NS2A.

InterPro; IPR000753; Flavi_NS4A.

InterPro; IPR001528; Flavi_NS4A.

InterPro; IPR001528; Flavi_NS4A.

InterPro; IPR001528; Flavi_NS4A.

InterPro; IPR001528; Flavi_NS4B.

InterPro; IPR
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Best Local
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A., McCombie W.R., Me
Buell C.R., Wing R.A., McCombie W.R., Me
Submitted (MAY-2003) to the EMBL/GenBank
EMBL/AC123594; AAM74436.1; -
EMBL/AC123594; AAM74436.1; -
InterPro; IPR00916; APETOTIANS Gag.
InterPro; IPR008916; Retrov_capsid_C.
Pfam; PF03722; Retrotrans_gag; 1.
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01-OCT-2003
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    Pfam;
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G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0019031; C:viral envelope; IEA.
G0; G0:0019031; C:viral envelope; IEA.
G0; G0:0005524; F:ATP binding; IEA.
G0; G0:0006726; F:ATP-dependent helicase activity; IEA.
G0; G0:0016787; F:hydrolase activity; IEA.
G0; G0:0013723; F:RNA binding; IEA.
G0; G0:0003724; F:RNA belicase activity; IEA.
G0; G0:0003724; F:RNA-directed RNA polymerase activity; IEA.
G0; G0:0003968; F:sRNA-directed RNA polymerase activity; IEA.
G0; G0:0005198; F:structural molecule activity; IEA.
G0; G0:0019079; P:viral genome replication; IEA.
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PF01003; Flavi_capsid; I.
PF07652; Flavi_DEAD; 1.
PF00869; Flavi_glycoprot; 1.
PF02832; Flavi_glycop_C; 1.
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8; Conserv
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EMBL/GenBank/DDBJ
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Pred. No.
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J databases.
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Q93IU2
ID Q93IU
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Pfam; PF01005; Flavi_NS1; 1.
Pfam; PF01005; Flavi_NS2A; 1.
Pfam; PF01002; Flavi_NS2A; 1.
Pfam; PF011350; Flavi_NS4A; 1.
Pfam; PF011350; Flavi_NS4B; 1.
Pfam; PF011350; Flavi_NS5; 1.
Pfam; PF00179; Flavi_NS5; 1.
Pfam; PF01570; Flavi_NS5; 1.
Pfam; PF01728; FtaJ; 1.
Pfam; PF001728; FtaJ; 1.
Pfam; PF001728; FtaJ; 1.
Pfam; PF001496; PEDVidase_S7; 1.
ProDDom; PD001496; Flavi_GlycoprotE; 1.
ProDDom; PD001496; Flavi_S1; 1.
                                                  Q93IU2
Q93IU2;
Q93IU2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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SEQUENCE
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Q7MP20; PREMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLEL 26, Last annotation update)
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SMART; SM00490; HELICC; 1.
ATP-binding; Helicase; Hydrolase; Polyprotein.
ATP-binding; Helicase; Hydrolase; Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

PubMed=1465995; DOI=10.1101/gr.1295503;

Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,

Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F;

Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F;

"Comparative genome analysis of Vibrio vulnificus, a marine
Streptomyces coelicolor. Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=VV0544;
Vibrio vulnificus (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP005332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome
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495 AA;
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ome; Hypothetical
AA; 57275 MW; 2
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64.3%;
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Gammaproteobacteria; Vibrionales;
Actinobacteridae; Actinomycetales;
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Pred. No. 6e+0
1; Mismatches
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Pred. No. 9
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2C121F9AC6051DB4
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PIR; T45278; T45278.

GO; GO:0005215; F:transporter act
GO; GO:0006810; P:transport; IEA.

InterPro; IPR000914; SBP bac 5; 1.

SEQUENCE 602 AA; 65851 MW; 50
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EMBL; AL939122; CAC44320.1; -...
GO; GO:0005215; F:transporter act
GO; GO:0006810; P:transport; IEA.
InterPro; IPR00914; SBP bac 5.
Pfam; PF00496; SBP bac 5; 1.
Complete proteome; Lipoprotein.
SEQUENCE 600 AA; 65533 MW; 90
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01-FEB-1997
01-FEB-1997
01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                   Nodwell J. R., McGovern
Submitted (AUG-1996) to
-!- SIMILARITY: Belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor. Bacteria; Actinobacteria;
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Nature 417:141-147(2002).
-i- SIMILARITY: Belongs t
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=M145;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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    EGPT-LRQWLHGNG 16
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llarity 64.3%;
Conservative
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                                                 Score 46.5; I
Pred. No. 1.2e
3; Mismatches
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EMBL/GenBank/DDBJ databases.
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Last sequence update)
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. 1.1e+02;
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RESULT
Q8RSL6
RESULT 43
Q6H5Y4
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01-JUN-2002
01-JUN-2002
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  Q6H5Y4
Q6H5Y4;
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Tauch A., Schluter A., Bischoff N., Goesmann A., Meyer F., Puhler A.;
"The 79,370-bp conjugative plasmid pB4 consists of an IncP-lbeta
backbone loaded with a chromate resistance transposon, the strA-strB
streptomycin resistance gene pair, the oxaccillinase gene blaNPS-1, an
a tripartite antibiotic efflux system of the resistance-nodulation-
division family.";
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINB=21167756; PubMed=11133989; DOI=10.1074/jbc.M008414200;
Chen S.-C., Yeh C.-H., Yeh M.-S., Huang C.-J., Liu T.-Y.;

"Biochemical Properties and cDNa Cloning of Two New Lectins from plasma of Tachypleus tridentatus. Tachypleus plasma lectin 1 and plasma. 276.9631.9639(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Galactose-binding protein.
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EMBL; AJ431260; CAD24344.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 85 AA; 9445 MW; DC06B2B012
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Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
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EMBL; AP005394; BA025865.1; -.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serime/threonine kinase activ

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

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STRAIN=1021;

STRAIN=1021;

STRAIN=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;

MEDLINE=21396507, PubMed=11481430; DOI=10.1073/pnas.161294398;

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

-i- FUNCTION: Together with moaC, is involved in the conversion of

guanosine derivative (GXP) into molybdopterin precursor Z (By
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Molybdenum cofactor biosynthesis protein A.
Name=moaA; OrderedLocusNames=R01864; ORFNames=SMc00144;
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Submitted (JUN-2002)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYrKC; 1.
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Ehrhartoideae; Oryzeae; Oryza.
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28-FEB-2003
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
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R HAMAP; MF 01225; -; 1.

R InterPro; IPR006638; Elp3/MiaB/NifB.

R InterPro; IPR000385; Moaa_NifB_PqqE.

R InterPro; IPR001505; Mob synth C.

R InterPro; IPR007197; RadIcal_SAM.

R Pfam; PF06463; Mob synth C; 1.

R Pfam; PF046463; Mob synth C; 1.

R Pfam; PF04055; RadIcal_SAM; 1.

R Pfam; PF04055; RadIcal_SAM; 1.

R SMART; SM00729; Elp3; 1.

R SMART; SM00729; Elp3; 1.

R PROSITE; PS01305; MOAA_NIFB_PQQE; 1.

M JFe-48; Complete proteome; Iron; Iron-sulfur; Metal-binding; Molybdenum cofactor biosynthesis.
                                aminotransferase family.

EMBL; AF083072; AAC62704.1; -.

PIR; T31313; T31313.

HSSP; P24630; 4GSA.

GO; GO:0030170; F:pyridoxal phosphate bindi
GO; GO:0008483; F:transferase activity; IE
GO; GO:0016740; F:transferase activity; IE
InterPro; IPR005814; Aminotrans 3.
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                                                                                                                                                                                     "Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
J. Bacteriol. 180:5003-5009(1998).
-!- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                             MEDLINE=98422450; PubMed=9748430; Schleper C., DeLong E.F., Preston Swanson R.V.;
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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PATHWAY: Molybdenum cofactor biosynthesis; first step.
SIMILARITY: Belongs to the radical SAM superfamily. MoaA family.
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07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                               The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-051883/05
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Mattheakis LC, Schatz PJ, Wagstrom
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                                                                                                                                                                                 Sequence
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                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemotherapy,
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RESULT 2
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07-JUN-1995;
                          The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of <a href="R000 Da">R000 Da</a>, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mum. The compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
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Mattheakis
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bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                             Page 89; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrett RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transfusion;
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95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Preferably N-terminus is selected from: -NRR1; NRC(0)R; -NRC(0)OR; -NRS(0)2R; -NHC(0)NHR; succinimde; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-
; -NHC(O)NH; where R is hydrogen or lower alkyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lower alkyl"
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PJ, Wagstrom
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m CR, Wrighton NC;
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                                                                                                                    The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting
                                                                                                                                                                                                                                   Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
                                                                                                                                                                                                                                                                                            Dower WJ, Barrett RW, Cwirla SE, I
Mattheakis LC, Schatz PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1996
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                                                                                      Sequence 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietin receptor binding
                                                                                                                                                                                                   Claim 30; Page 91; 106pp; English
                                                                                                                                                                                                                         thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone marrow
                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO
                                                                                                            receptors on living cells
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CADGPTLREWISEC 14
                      CADGPTLREWISFC 14
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                                           Conservative
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95US-00485301.
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                                                    100.0%;
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                                          Score 85; DB 2;
Pred. No. 6.9e-07;
; Mismatches 0;
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Pred. No. 6.9e-07;
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RESULT 4
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haematology;
bone marrow
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Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy;
                                                                        Thrombopoietin
                                                                                                                          11-MAR-1998
                                                                                                                                                                           AAW33031;
                                                                                                                                                                                                                          AAW33031 standard; peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14 AA;
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LC, 'Schatz
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chemotherapy; radiation therapy.
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Wagstrom CR, V
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6.9e-07;
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Wrighton NC;
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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                                                                                                                                                                                signal
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                                                                                                                                                                                                                                                                                                                       Thrombopoietin receptor binding peptide.
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14; Conserv
                                                                                                                                                                                      transduction; receptor activation;
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LC, Schatz
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n; receptor activation; cell culture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
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Mattheakis LC, Schat
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thrombopoietin dependent
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Mattheakis
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07-JUN-1995;
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LC, Schatz
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Wagstrom CR, Wrighton
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Peptides and peptide mimetics which thrombopoietin receptor - useful in

bind to and activate the treatment of haematological

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RESULT 8
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The present peptide, which binds the thrombopoietin receptor (Tused to treat disorders which are susceptible to treatment with thrombopoietin agonist, preferably haematological disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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Mattheakis
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LC, Schatz
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RESULT 9
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                                                                                               The present peptide, which binds the thrombopoietin receptor (TR), can used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bon marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
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07-JUN-1995;
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PJ, Wagst
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RESULT 10
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RESULT 11
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          AAW33032 standard; peptide;
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LC, Schatz
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Wrighton NC;
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RESULT 12
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AAB17014;

31-OCT-2000

(first entry)

AAB17014 standard; peptide;

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TPO-mimetic peptide sequence SEQ ID NO:70

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Mattheakis
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                                                                                                                                    resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate th mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
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07-JUN-1995;
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                                                                                                Sequence 14 AA;
                                                                                                                                                                                                                                                            Claim
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                                                                                                                          cell lines
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                                                                                                                                                                                                                                                          30; Page 91; 106pp; English.
                                                 14;
 1 CADGPTLREWISFC 14
               1 CADGPTLREWISFC
                                                             Similarity
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95US-00485301.
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Schatz
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PJ, Wagstrom
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1, -(L2)d-P2, -(L1)c-P1, -(L2)d-P2-(L3)e-P3, (X1-P1-(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1-(L2)d-P3-(L4)f-P4 where P1-(L4)f-P4 where P1
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  Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
                                                                                                                                                     17-DEC-2001
                                                                                                                                                                                                                                                             AAU25826 standard; peptide; 14 AA
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22-OCT-1999;
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                                                                                         thrombopoietin
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                                                                                         receptor (TPO-R) activator peptide
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Pred. No. 6.9e-07;
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Pepl

17-DEC-2001 AAU25852;

(first

entry)

Peptide mimetic; human; thrombopoietin receptor;

TPO-R; TPO; cytokine;

Human thrombopoietin receptor (TPO-R) activator peptide #38.

RESULT 14

AAU25852 standard; peptide;

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Matches
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Best Local
                                                                                                                                                                                                                of activating thrombopoletin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoletin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                             situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELGA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                                                                                            Sequence
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Balasubramanian P, Wagstrom CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAU25815-AAU26049 represent peptides and peptide mimetics
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CADGPTLREWISFC 14
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strom CR, Hendren
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Pred. No. 6.9
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RESULT 15
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                 Human thrombopoietin receptor (TPO-R) activator peptide
                                                     17-DEC-2001
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Wanian P,
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Deprince RB,
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                                                                                                             ABB72900
                                                                                                                              RESULT 16
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07-JUN-1995;
07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemostatic; thrombocytopenia; chemotherapy, radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting with peptides and peptide mimetics attached to hydrophilic polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Col 20; 128pp; English.
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                                                                                                                                                                                                                                                                                                             Sequence 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLAX )
                                                                                               ABB72900 standard;
                                                                                                                                                                                                                                                14;
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                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                 CADGPTLREWISFC
                                                                                                                                                                                 CADGPTLREWISFC
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nanian P,
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A
                                                                                                                                                                                                                                                  Conservative
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95US-00485301.
96WO-US009623.
96US-00699027.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RW, Cwirla S: Wagstrom CR,
                                                                                                 peptide;
                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                 Score 85;
Pred. No.
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R, Hendren
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                   6.9e-07;
                                                                                                                                                                                                                                                                                     DB 4;
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Deprince RB,
                                                                                                                                                                                                                                                                                  Length 14;
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                                                                                                                                                                                                                                                       Gaps
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05-APR-2002 TPO mimetic

(first

entry) CI DES

0

peptide

NO:70

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The present invention describes a vehicle-peptide molecule (I) or its CC multimers. (I) can have antiinflammatory, antiitumour, immunosuppressive, CC cytostatic, antirheumatic, antiinfertility, haemostatic, ophthalmological, CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and neuroprotective activities. (I) can be used as a therapeutic or CC prophylactic agent as well as for screening purposes. (I) is useful for CC diagnosing diseases characterised by dysfunction of their associated CC protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their CC proteins of interest in a biological sample. Additionally, (I) is useful CC retains of interest in a biological sample. Additionally, (I) is useful CC retains of interest in a biological sample. Additionally, (I) is useful CC composens of interest in a biological sample. Additionally, (I) is useful CC retains of interest in a biological sample. Additionally, (I) is useful CC composens of the composens of the composens of the composens of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition o
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 39; Page 44; 176pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic retinopathy, obesity, sleep disorders and infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-130313/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fanconi's syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory and autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC
                                                                                                                                                                                        14;
                                                                                                                                                                                                                                          Similarity
                                                                                              CADGPTLREWISFC
CADGPTLREWISFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the present invention
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100.0%; I
tive 0;
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                                                                                                                                                                                        Score 85; DB 5;
Pred. No. 6.9e-07;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                       Length 14;
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RESULT 17 ADJ73051

CH1 deleted mimetibody-related

peptide SeqID505

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06-MAY-2004

(first entry)

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                                                                                                                                                                                                                                                                                                                                          This invention relates to novel mammalian CDR mimetibodies, specific CC portions or variants thereof. Specifically, it refers to an antibody CC fragment where a protein has been inserted into, or replaces a portion of, one or more CDR regions, such that each CDR mimetibody comprises at least one portion of a heavy chain or light chain variable region, which CC itself comprises at least one human framework region and at least one CC ligand binding region (LBR). The present invention describes human CC mimetibodies, including modified immunoglobulins and cleavage products that can be useful in gene therapy and the generation of transgenic CC plants and animals. Furthermore, the CDR mimetibody is useful for CC preparing compositions for modulating, treating or reducing the symptoms CC of immune, cardiovascular, infectious, malignant and/ or neurologic CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This captile sequence is a TPD mimetic peptide sequence used to make a
                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mimetic; CDR mimetibody; gene therapy; transgenic; immune; cardiovascular; infectious; malignant; neurologic disease; anaemia; immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding regionseful for preparing a composition for treating e.g., immune,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                 Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 505; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2002; 2002US-0368791P
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                                                              ADJ52686;
                                                                                           ADJ52686 standard;
                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                      1 CADGPTLREWISEC 14
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                               sequence is a TPO mimetic peptide sequence ody of the invention.
                                                                                                                                                                                                                                                                                                 A
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                                                                                                                                                                                                                                     Conservative
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                                                                                          peptide;
                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                    Score 85;
Pred. No.
                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                     6.9e-07;
                                                                                                                                                                                                                                                                      DB 7;
                                                                                                                                                                                                                                                                    Length 14;
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RESULT 19
ADJ51647
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                                                                                                                                                                                                                                                                                   Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                         useful for the development of compounds with an immunosuppressive, cardiovascular, cardiant, hypotensive, neuroprotective, nootropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, treating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases of disorders, anaemia, cancerous conditions, or infectious diseases of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant; hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New CH1-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                               Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which encode them),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to CH1 deleted mimetibodies (and the DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2;
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CH1 deleted minetibody; osteopathic; cardiovascular-Gen; dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
                                                                                                         ADJ51647;
                                               CH1 deleted
                                                                            06-MAY-2004
                                                                                                                                        ADJ51647 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection;
                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                     1 CADGPTLREWISFC 14
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                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                       CADGPTLREWISFC 14
                                                                                                                                                                                                                                                                                                                                                 AA
                                             mimetibody-related
                                                                                                                                                                                                                                                                                 Conservative
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                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compositions, methods and uses. The invention may
                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ghrayeb J,
                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                   Score 85; DB 8;
Pred. No. 6.9e-07;
                                           peptide SeqID505
                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scallon BJ,
                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                  Length 14;
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CC which encode them), compositions, methods and uses incompositions of compounds with an osteopathic, cardiovascular-den, dermatological-den, auditory, endocrine-den, compounds extra encoderation or cardiovascular-den, dermatological-den, auditory, endocrine-den, communomodulator, antiallergic, muscular-den, cytostatic, communomodulator, neuroleptic, ophthalmological, nephrotropic or communomodulator, neuroleptic, ophthalmological, nephrotropic or communomodulator, neuroleptic, ophthalmological, nephrotropic or communomodulator or cytokine-agonist. The methods and compositions of the compression of the compression of the compression of the compression of the compression of the compression of the compression of cardiovascular, dental or oral, dermatological, ear, nose or throat, compression, metabolic, gastrointestinal, gynaecological, hepatic, communological, allergic, infectious, metabolic, gastrointestinal, gynaecological, hepatic, communological, allergic, infectious, metabolic, gastrointestinal, allergic, infectious, psychiatric, renal or pulmonary disorders. The present compression of a peptide which may be used during the creation of a
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                                                                             Matches
                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic; aphthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor; TWP; cytokine; bone disorder; joint disorder; cardiovascular disorder; dental disorder; oral disorder; dermatological disorder; ear disorder; nose disorder; throat disorder; endocrine disorder; metabolic disorder; gastrointestinal disorder; graecological disorder; hepatic disorder; obstetric disorder; haematologic disorder; immunological disorder; allergic disorder; haematologic disorder; musculoskeletal disorder; ophthalmologic disorder; pediatric disorder; pulmonary disorder; psychiatric disorder; renal disorder; pulmonary disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-2002; 2002US-0392431P
19-SEP-2002; 2002US-0412144P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                           Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nutritional disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-082872/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2003; 2003WO-US020495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004002424-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kutoloski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; SEQ ID NO 505; 123pp; English.
                                                                             14;
                          1 CADGPTLREWISFC
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                                                                                                Similarity
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                                                                           100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knight DM,
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                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gynecologic, infectious, neurologic and
                                                                                                  Score 85;
Pred. No.
                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scallon BJ,
                                                                                                    6.9e-07;
                                                                                                                      DB 8;
                                                                                                                    Length 14;
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RESULT 20 AAW09456 ID AAW09456 standard; protein; 18

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Query Match
Best Local Similarity
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                  The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of <a lequence 10 a, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mum. The compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintrain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW09456;
                                                                                                                                                                                                                                                                Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
                                                                                                                                                                                                                                                                                                             WPI; 1997-051883/05.
                                                                                                                                                                                                                                                                                                                                          Mattheakis
                                                                                                                                                                                                                                                                                                                                                      Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin receptor binding compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-1997
                                                                                                                                                                                                                    Claim 18; Page 89; 106pp; English
                                           Sequence
                                                                                                                                                                                                                                                 thrombocytopenia resulting from chemotherapy,
                                                                                                                                                                                                                                                                                                                                                                                    (GLAX )
                                                                                                                                                                                                                                                                                                                                                                                    GLAXO
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LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombocytopenia; TPO; TR; proliferation; transfusion; chemotherapy; radiation thera
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                                                                                                                                                                                                                                                                                                                                                                                                              95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US008998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Preferably C-terminus is -C(O)R2 where R2 is selected from hydroxy, lower alkoxy, and -NR3R4, where R3 and R4 are independently selected from hydrogen and lower alkyl, and where the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide forming a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Preferably N-terminus is selected from: -NRR1; NRC(0)R; -NRC(0)OR; -NRS(0)ZR; -NHC(0)MIR; succinimide; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 13 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Preferably linkages are selected from: -
CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .18
                                                                                                                                                                                                                                                                                                                                       Schatz PJ, Wagstrom
100.0%;
                                                                                                                                                                                                                                                                                                                                                      Cwirla SE,
Score
Pred.
                                                                                                                                                                                                                                                                                                                                       m CR, Wrighton
No.
DB 2;
9e-07;
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                                                                                                                                                                                                                                                                                                                                          Gates
            Length
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RESULT 22
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AC AAB1:
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                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombopytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin
                                                 AAB17020 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                         Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 19; Page 89; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                             to maintain the
ll lines
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                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                           CADGPTLREWISFC
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LC, Schatz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor binding
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95US-00485301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor;
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                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cwirla SE, Duffin DJ, Gates CM, PJ, Wagstrom CR, Wrighton NC;
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                                                                                                                                                                                                                                                                                                Score 85;
Pred. No.
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                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                   DB 2;
9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment;
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                                                                                                                                                                                                                                                                                                                          Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemotherapy, etc.
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RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p), and p4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EFO; TFO; CTLA4; mimetic; IL-1; TWF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; thrombolial growth factor; matrix metalloproteinase; asthma; thrombolial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPO-mimetic peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes composition of matter (I) comprising FC domain, pharmacologically active peptides, and linkers. Where (I) (X1)a-F1-(X2)b, where: F1 = an FC domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, (L4)f-P4 where P1, (L2)d-P2-(L3)e-P3-(L4)f-P4 (L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-
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                                17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18
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                                                                                                                                            AAU25820 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical.
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                                (first entry)
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99US-00428082
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                                                                                                                                         peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 85;
Pred. No.
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ABB72906;

ABB72906 standard; peptide; 18 AA.

05-APR-2002

(first entry)

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Matches
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                 transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understranding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                                                                                                                                                                                                                                                                                                       Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2000; 2000US-00516704.
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                                                                     Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 65-66; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yin Q;
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                  Local
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14;
                    Similarity
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anian P,
                                                                         AΑ;
Conservative
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95US-00485301.
96WO-US009623.
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                  100.0%;
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                  Score 85;
Pred. No.
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     Mismatches
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                  DB 4;
9e-07;
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                                   Length 18;
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TPO mimetic

peptide SEQ ID

NO:76

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                                                                                                                                                                                                                                       CC multimers. (1) can have antiinflammatory, antitumour, immunosuppressive, CC cyrostatic, antirheumatic, antiinfertility, haemostatic, ophthalmological, CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and neuroprotective activities. (1) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (1) is useful for CC diagnosing diseases characterised by dysfunction of their associated CC protein of interest, for identifying normal or abnormal proteins of CC interest, as a part of diagnostic kit to detect the presence of their CC proteins of interest in a biological sample. Additionally, (1) is useful CC proteins of interest in a biological sample. Additionally, (1) is useful CC retating inflammatory and autoimmune diseases, tumour growth, cancer, cc infertility, and neurological degenerative diseases. (1), comprising EPO-CC minetic compounds are useful for treating disorders characterised by low cred blood cell levels such as anaemia. The TPO-mimetic comprising CC compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing compounds are useful for treating conditions that involve an existing conditions that involve an existing conditions that involve an existing compounds are useful in thrombocytopaenia, aplastic anaemia, metastatic cumour which result in thrombocytopaenia, aplastic anaemia, metastatic cancer which result in thrombocytopaenia, systemic lupus erythematosus, cancer and conditions that involve an expected megastaryocyte/platelet et deficiency or an expected megastaryocyte/platelet compounds and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly and anomaly an
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 39; Page 44; 176pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-130313/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a vehicle-peptide molecule (I) or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-2001; 2001WO-US014310
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CADGPTLREWISFC
                                               CADGPTLREWISEC 14
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                                                                                              Score 85; DB 5; Length 18; Pred. No. 9e-07; Indels
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CC plants and animals. Furthermore, the CDR mimetibodies symptoms or variants thereof. Specifically, it refers to an antibody CC fragment where a protein has been inserted into, or replaces a portion CC of, one or more CDR regions, such that each CDR minetibody comprises at least one portion of a heavy chain or light chain variable region, which CC ligand binding region (LBR). The present invention describes human CC mimetibodies, including modified immunoglobulins and cleavage products CC that can be useful in gene therapy and the generation of transgenic CC plants and animals. Furthermore, the CDR mimetibody is useful for CC preparing compositions for modulating, treating or reducing the symptoms CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator, CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This compositions is a TPO mimetic peptide sequence used to make a CC mimetibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 25
ADJ73058
RESULT 26
ADJ52693
ID ADJ5
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AC ADJ5
XX
AC ADJ5
XX
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region, useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2002; 2002US-0368791P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAR-2003; 2003WO-US009139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO mimetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ73058 standard; peptide; 18
06-MAY-2004
                            ADJ52693;
                                                        ADJ52693 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 512; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-804237/75
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                                                                                                                                                                                                            Local
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                                                                                                                                                                                                         Similarity
                                                                                                                                  CADGPTLREWISFC
                                                                                                                                                     CADGPTLREWISFC
                                                                                                                                                                                                                                                        18
                                                                                                                                                                                           100.0%; Score 85; ilarity 100.0%; Pred. No. Conservative 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide sequence SeqID 512
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(first entry)
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                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ghrayeb
                                                                                                                                                                                                              9e-07;
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                                                                                                                                                                                                                         Length 18;
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RESULT 27
ADJ51654
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                     cardiovascular, cardiant, hypotensive, neuroprotective, notropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CH1-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypotensive; neuroprotective; nootropic; antibacterial; virucide; fungicide; gene therapy; immune disorder; cardiovascular disease; arrhythmia; hypertension; heart failure; neurodegenerative; multiple sclerosis; dementia; Alzheimer's disease; anaemia; cancerous condition; infectious disease; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New CHI-deleted mimetibody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, or neurodegenerative disease or disorder, anemia, cancer, or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which encode them), compositions, methods and uses. The invention useful for the development of compounds with an immunosuppressive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to CH1 deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heavner GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2002; 2002US-0392431P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUN-2003; 2003WO-US020347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kutoloski KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CENZ ) CENTOCOR INC.
               CH1 deleted mimetibody-related peptide SeqID512
                                               06-MAY-2004
                                                                                                           ADJ51654 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deleted mimetibody-related peptide SeqID512
                                                                                                                                                                                                                                                                                                                                                           during the creation of a mimetibody of the invention.
                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                CADGPTLREWISFC 16
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A
                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 512; 129pp; English
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fungal infection.
                                                                                                                                                                                                                                                             100.0%; £
100.0%; E
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ghrayeb
                                                                                                                                                                                                                                                             Score 85; DB
Pred. No. 9e-
0; Mismatches
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                                                                                                                                                                                                                                                      DB 8; L-
, 9e-07;
0;
                                                                                                                                                                                                                                                                                          Length 18;
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RESULT 28

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This invention relates to CH1 deleted mimetibodies (and the DNA sequences CC which encode them), compositions, methods and uses. The invention may be CC useful for the development of compounds with an osteopathic, cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen, CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic, CC immunnomodulator, antiallergic, muscular-Gen, cytostatic, cantiniflammatory, neuroleptic, ophthalmological, nephrotropic or CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-CC modulator or cytokine-agonist. The methods and compositions of the CR reatment of diseases or conditions associated with aberrant expression CC or activity of the CH1 deleted mimetibody, such as a bone or joint, CC cardiovascular, dental or oral, dermatological, ear, nose or throat, CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic, obstetric, haematologic, immunological, allergic, infectious, obstetric, psychiatric, renal or pulmonary disorders. The present CC gediatric, psychiatric, renal or pulmonary disorders. The present crimentibody of the creation of a sequence is that of a peptide which may be used during the creation of a creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of a composition of the creation of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CH1 deleted mimetibody; osteopathic; cardiovascular-Gen; dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen; gynaecological-Gen; hepatotropic; haemostatic; immunomodulator; antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CH1 deleted mimetibody polypeptide and nucleic acid, useful for diagnosing, preventing or treating cardiovascular, dermatologic, endocrine, gastrointestinal, gynecologic, infectious, neurologic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nutritional disorders.
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Kutoloski KA;
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19-SEP-2002; 2002US-0412144P.
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                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    mimetibody of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                       14;
w
                                                                                 1 CADGETLREWISEC 14
                                                                                                                                                                                                               Similarity
CADGPTLREWISFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 512; 123pp; English.
                                                                                                                                                                       Conservative
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                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                           0
                                                                                                                                                                                                                    Score 85;
Pred. No.
                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                             DB 8;
                                                                                                                                                                                                                                                             Length 18;
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                          The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mum. compound (especially if modified, see features table) can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bon marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haematology; thrombocytopenia; TPO; TR; proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW09458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW09458 standard;
                                                                                                                                                                                                     Thrombopoletin receptor-binding/activating peptide(s) and pep mimetic(s) - useful in treatment of haematological disorders, thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9640189-A1
                                                                                                                                                                       Claim 18; Page 89; 106pp;
                                                                                                                                                                                                   thrombocytopenia resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                  Barrett RW,
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                                                                                                                                                                                                                                                                                                                                GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                         95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US008998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selected from hydroxy, lower alkoxy, and -NR3R4, where R3 and R4 are independently selected from hydrogen and lower alkyl, and where the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide forming a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                      Schatz PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Preferably N-terminus is selected from:
NRC(0)R; -NRC(0)OR; -NRS(0)2R; -NHC(0)NHR; succ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Preferably C-terminus is -C(O)R2 where R2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H2OC(O)NR-; phosphonate; -CH2S(C
-NHC(O)NH; where R is hydrogen
ower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding
                                                                                                                                                                                                                                                                                                    Cwirla SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemotherapy;
                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                     rla SE, Duffin DJ,
Wagstrom CR, Wrig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               radiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                     Wrighton
                                                                                                                                                                                                                                                                                        Gates
ton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or lower alkyl
                                                                                                                                                                                                                                                                                                     3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from:
                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                     Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; -C(O)NR6
and R6 is
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Sequence

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RESULT 30
AAU25822
ID AAU25

AAU25822 standard; peptide; 19

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AAW33025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                           Matches
                                                     Query Match
Best Local Similarity
                                                                                                                     The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                            Peptides and peptide mimetics which bind to thrombopoietin receptor - useful in treatmedisorders, esp. thrombocytopenia resulting
                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin receptor; haematological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW33025 standard;
                                                                                       Sequence 19
                                                                                                                                                                                                                                      Claim 19; Page 89; 106pp;
                                                                                                                                                                                                                                                                                                            WPI; 1997-052226/05
                                                                                                                                                                                                                                                                                                                                  Mattheakis
                                                                                                                                                                                                                                                                                                                                              Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9640750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                               lines
                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CADGPTLREWISFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CADGPTLREWISEC
              CADGPTLREWISFC
CADGPTLREWISFC
                                                                                                                                                                                                                                                                                                                                  ۲,
                                                                                                                                                                                                                                                                                                                                 Barret RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    llarity 100
Conservative
                                                                                        B
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                    GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                        95US-00478128
95US-00485301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US009623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor activation; cell
                                                                                                                                                                                                                                                                                                                                  Cwirla SE, Duffi
PJ, Wagstrom CR,
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding
                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
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Pred. No.
                                                      Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
                                                                                                                                                                                                                                                                                                                                              Duffin DJ,
                                                                                                                                                                                                                                                            bind to and activate the treatment of haematological sulting from chemotherapy, etc.
                                                     9
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                                                     DB 2; ; ; 9.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .6e-07;
                                                                                                                                                                                                                                                                                                                                 DJ, Gates CM, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 19
                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                             Indels
                                                                  19
                                                                                                                                                                                                                                                                                                                                               Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                             Gaps
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RESULT 31
AAW09467
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                                                                                                                                                                                                        Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that control of activating thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPD) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological materials. They may also be used for in purified or natural biological materials. They may also be used for in
                                                                                                      Query Match
Best Local :
                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
                                                                                                                                                                                                                                                                                                                                                                                                         Activating thrombopoietin receptors in cells, thrombocytopenia and hematological disorders, with peptides and peptide mimetics attached to
                                                                                                                                                             situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dower WJ, Barrett
Balasubramanian P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6251864-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU25822
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO
                                              w
                                                                                                       Similarity
                                              CADGPTLREWISFC
                                                                     CADGPTLREWISFC 14
                                                                                                                                                                                                                                                                                                                                                                                      Col 67-68; 128pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-00516704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GROUP LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00478128.
95US-00485301.
96WO-US009623.
96US-00699027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RW, Cwirla S
Wagstrom CR,
                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cwirla SE,
                                                                                            0
                                                                                                       Score 85;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TPO-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E, Gates
Hendren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activator peptide
                                                                                                       9.6e-07;
                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RW,
                                                                                                                                                                                                                                                                                                                                                                                                            used to treat comprises contacting co hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deprince RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schatz PJ;
                                                                                                                  Length 19;
                                                                                             0
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                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          cells
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RESULT 32
AAW35399
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                                                                                                                                                                                                                                 Query Match
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                 The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                   Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin receptor binding compound cyclic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW09467 standard; protein; 13
                                 AAW35399
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 30; Page 91; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-051883/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                Local
                                                                                                                                                                                              l Similarity
13; Conserv
                                                                                                                                                            N
                                                                                                                                                            ADGPTLREWISFC 14
                             standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barrett RW, Cw
LC, Schatz PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transfusion; chemotherapy;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00472371.
95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= OTHER /label= OTHER /label= "S-carboxymethyl-cysteine alpha-carboxamide; forming a linkage onto the Ala at position one with delta C of this residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "The Ala is linked with the
                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                   89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cwirla SE,
                                   13
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                                                                                                                                                                                                                  Score 7
Pred.
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                                     ₿
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                  76;
. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duffin DJ,
m CR, Wrig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          radiation
                                                                                                                                                                                                                  DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n DJ, Gates
Wrighton NC;
                                                                                                                                                                                                                                   Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson SS;
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                                                                                                                                                                                                   Gaps
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RESULT 33
AAW35417
ID AAW35
XX
XX
AC AAW35
XX
DT 11-M
XX
Thron
XX
Thron
KW haeme
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                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                          The present peptide, which binds the thrombopoietin receptor (TR), (used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin receptor; binding peptide; treatment; agon. haematological disorder; thrombocytopaenia; themotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dower WJ, Barret RW,
Mattheakis LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 63; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombopoietin receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1998
Thrombogoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy;
                                                                                                                  AAW35417 standard; peptide; 13
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9640750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                 l Similarity
13; Conserv
                                                                                                                                                                                  -
                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLAXO
                                                                                                                                                                                                     ADGPTLREWISFC 14
                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                  ADGPTLREWISFC 13
                                                                                                                                                                                                                                                                                      ξ
                                                                                                                                                                                                                                   89.4%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GROUP LID
                                      receptor binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00478128.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US009623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "NH2-cytosine linked via sulphoxidised thiol group
to Ala1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cwirla SE, Du
PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "COCH2-alanine linked via
                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                   Score 76; DB ;; Pred. No. 1.9 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duffin DJ, Gate
                                                                                                                                                                                                                                                DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment; agonist;
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phton NC;
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AC AAW33
AC AAW33
AC Thron
Thron
XX Thron
KW Thron
KW haema
KW radia
KW radia
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
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                                                              Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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07-JUN-1995;
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Cross-links
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Page 73; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dower WJ,
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 Modified-site
                                      Synthetic
                                                                                                                                                          11-MAR-1998
                                                                                                                                                                                   AAW33033;
                                                                                                                                                                                                           AAW33033 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                           thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                             investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                               Thrombopoietin
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                                                                                                                                                                                                                                                                                                                              l Similarity
13; Conserv
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s LC, Schatz
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95US-00485301.
                                                                                                                                receptor binding peptide.
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peptide"
13
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Schatz PJ, Wagst
Location/Qualifiers
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                          Length 13;
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RESULT 35
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AAW35423
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AC AAW35
AC Thron
DT 11-MA
DT Thron
XX Thron
KW Thron
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microw. It can be used treat disorders which are susceptible to treatment with a thrombopoiet agonist, preferably haematological disorders and thrombocycopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate th mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
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                                                                                                                                                       Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
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                                                                                                                                        signal transduction; receptor activation;
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              WO9640750-A1
                                                  Modified-site
                                                                            Modified-site
                                                                                                                 Synthetic
                                                                                                                                                                                                         Thrombopoietin receptor binding peptide.
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LC, Schatz
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95US-00485301.
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13
                                                                                        Location/Qualifiers
                                        note=
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100.0%; Pred. No.
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PJ, Wagstr
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                                                                "Br-Ala"
                                        "NH2-Cys
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1.9e-05;
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hton NC;
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thrombopoietin
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RESULT 36
AAW35406
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AC AAW35
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Best Local S
Matches 13
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                                                                                                                                                                                                                                                                          Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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07-JUN-1995;
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                             07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                               Synthetic
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                                                                       07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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; LC, Sc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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95US-00485301.
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                             95US-00478128
95US-00485301
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                                                                                                                                                           /note= "NH2-cytosine linked via thiol
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PJ, Wagstrom CR, Wrighton NC;
                                                                                                                                                                                         "CO-CH(Ph)-alanine linked via CH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 76;
Pred. No.
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(GLAX) GLAXO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
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Peptides and peptide mimetics which bind
                                               WPI; 1997-052226/05
                                                                                                                                                                                                                    07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                          07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-links
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                                                                                             Barret
LC, Sc
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LC, Schatz
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95US-00485301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor activation;
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PJ, Wagstrom
                                                                                             Cwirla SE, Du
PJ, Wagstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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                                                                                          Duffin DJ, Gate om CR, Wrighton
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  and activate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pietin receptor (TR)
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                                                                Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombopoietin receptor - useful in treatment of haematological
                                           Example
                                                                                                                                     Mattheakis
                                                                                                                                               Dower WJ,
                                                                                                                                                                                           07-JUN-1995;
07-JUN-1995;
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                                          6; Page 63;
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LC, Schatz
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                                                                                                                                                                                           95US-00478128
95US-00485301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor binding peptide.
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13
                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
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                                          106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which binds the thrombopoietin
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                                                                                                                                     Cwirla SE, Duffin PJ, Wagstrom CR,
                                                                                                                                                                                                                                                                                                "NH2-cytosine linked via thiol group to
                                                                                                                                                                                                                                                                                                                       "COCH2-alanine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 76;
Pred. No.
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                                                                                                                                     DJ, Gate
Wrighton
                                                                                                                                                                                                                                                                                                                                                                                                                            treatment; agonist;
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                                                                                                                                      Gates C
hton NC;
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used to treat disorders which are susceptible to thrombopoietin agonist, preferably haematological

which binds the thrombopoietin receptor (TR), ers which are susceptible to treatment with a st, preferably haematological disorders and

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The present peptide, which bin used to treat disorders which

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RESULT 39
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Best Local S
Matches 13
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; Chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; tissue homogenate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
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                                                                                                                                                                                                                                                                                                                                         Activating thrombopoietin receptors in cells, thrombocytopenia and hematological disorders, with peptides and peptide mimetics attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Balasubramanian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dower WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human thrombopoietin receptor (TPO-R) activator peptide #183.
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                                                                                                                                                                                                                                                                                                     Disclosure;
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o hydrophilic
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07-JUN-1995;
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15-AUG-1996;
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Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO
                                                                                                                                                                                                                                                                                                                                                                                                     Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting with peptides and peptide mimetics attached to hydrophilic polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
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                            thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemetherapy, radiation therapy marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction receptor activation, or to maintain the proliferation and growth
                                                                                                                                                                                                                                                                                              Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
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                                                                                                                                 The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably hasmatological disorders and
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     thrombopoietin dependent cell lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         etin receptor; binding peptide; treatment; agonist; jical disorder; thrombocytopaenia; chemotherapy; therapy; bone marrow transfusion; diagnosis; ansduction; receptor activation; cell culture.
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                                                                                                                                                                                                                                              Page 63; 106pp;
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LC, Schatz
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95US-00485301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cwirla SE, Du
PJ, Wagstrom
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Pred. No.
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                                                                                                     chemotherapy, radiation therapy or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wrighton
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                                                                                                                                                                                                                                                                                                chemotherapy, etc
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RESULT 4:
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Matches
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                                  The present peptide, which binds the thrombopoietin receptor (TR), cused to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombopoietin agonist, preferably haematological disorders and thrombopoitopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
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                                                                                                                                                                                                                                                                                       07-JUN-1995;
07-JUN-1995;
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                        thrombopoietin
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                                                                                                                               Page 63; 106pp; English.
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LC, Schatz
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                "NH2-Cys"
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                           cell lines
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2e-05;
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Query Match Best Local :

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RESULT 44
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-052226/05
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Mattheakis
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Modified-site
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                                                                                                           ADGPTLREWISEC 14
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LC, Schatz
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                                                                                                                                                                                                                                                                                                                                                                                    or to maintain the proliferation dent cell lines
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PJ, Wagstrom CR,
                                                                                                                                                                                                                      0
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Pred. No.
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2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
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                                                                                                            Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 139; 128pp; English.
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07-JUN-1995;
07-JUN-1996;
15-AUG-1996;
                                                                                                                                                                                                                                                                                             cransplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Activating thrombopoietin receptors in cells, thrombocytopenia and hematological disorders, with peptides and peptide mimetics attached to
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HIV-1 retropepsin calcium-stimulated androgen-regulated HIV-1 retropepsin pol polyprotein -DNA-directed RNA p S-layer protein -ribosomal protein HIV-1 retropepsin

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glucose-6-phosphat glucose-6-phosphat conserved hypothet

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ALIGNMENTS

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C;Species: Solanum tuberosum (potato)
C;Date: 03-Mar-1994 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S53489; S34189
R,Sonnewald, U: Basner, A.; Greve, B.; Steup, M.
Plant Mol. Biol. 27, 567-576, 1995
A,Fittle: A second L-type isozyme of potato glucan phosphorylase: cloning, antisense inhi A;Fittle: A second L-type isozyme of potato glucan phosphorylase: S53489; MUID:95201249; PMID:7894019
A;Accession: S53489
A,Accession: S53489
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S34189
A; Molecule |
A; Residues:
                                                                                                                                                        Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - Pacific electric ray (;Species: Torpedo californica (Pacific electric ray) C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2 C;Accession: S00503; S28885; S29880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P53535; EMBL:X73684; NID:g313348; PIDN:CAA52036.1; PID:g3133 (C;Superfamily: glucan phosphorylase C;Kepwords: glycosyltransferase; phosphoprotein; pyridoxal phosphate C;Keywords: glycosyltransferase; phosphoprotein; pyridoxal phosphate F;820/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                    A; Title: Primary structure of the alpha-subunit of Torpedo californica (Na(+)+K(+)) ATPas A; Reference number: S00503; MUID:85296307; PMID:2993905
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A; Residues: 1-974 <SO2>
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A;Residues: 1-108 <SCH's
A;Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.30
A;Experimental source: BAC clone B24B19; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z25022
A; Accession: T49731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change
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C;Species: Solanum tuberosum (potato)
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                                                                                                             R;Kawakami, K.; Noguchi, (
Nature 316, 733-736, 1985
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Matches 7
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Best Local
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1-1022 <KAW1>
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7; Conserve
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7; Conserv
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58.3%;
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Pred. No.
                                                                                                                                     M.; Takahashi, H.; Ohta,
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R;Ohta, T.; Nagano, K.; Yoshida, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986
A;Title: The active site structure of Na(+)/K(+)-transporting
A;Reference number: S29880; MUID:86177549; PMID:3008150
A;Accession: S29880
                      A;Molecule type: mRNA
A;Residues: 199-942 <CHE>
A;Cross-references: GB:J03007
A;Shull, M.M.; Pugh, D.G.; Lingrel,
Genomics 6, 451-460, 1990
A;Title: The human Na, K-ATPase alpl
                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 168-189;213-214,'X',216-244 <SHU>
R;Residues: 168-189;213-214,'X',216-244 <SHU>
R;Chehab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blostein, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7901-7905, 1987
A;Title: Human placental Na+,K+-ATPase alpha subunit: cDNA cloning, tissue expression, A;Reference number: A39910; MUID:88068506; PMID:2891135
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-1023 <KRW>
A;Residues: 1-1023 <KRW>
A;Cross-references: UNIPROT:P05023; EMBL:X04297; NID:g28926; PIDN:CAA27840.1; PID:g28927
R;Shull, M.M.; Lingrel, J.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
A;Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit.
A;Reference number: A94158; MUID:87231946; PMID:3035563
A;Accession: A27795
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C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24414; A27795; A39910; I60116; S09171
C;Accession: A24414; A27795; A39910; I60116; S09171
R;Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K.
J. Biochem. 100, 389-397, 1986
A;Tille: Primary structure of the alpha-subunit of human Na,K-ATPase deduced A;Tille: Primary structure of the alpha-subunit of human Na,K-ATPase deduced A;Reference number: A24414; MUID:87057096; PMID:2430951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - human N;Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-A chain
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A;Residues: 386-402;502-512;671-689;887-906 <OHT>
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
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A; Residues: 228-240; 431-438; 535-550; 671-690; 1011-1022 < KAW2>
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Best Local (
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e human Na, K-ATPase alpha 1 gene: characterization
number: I60116; MUID:90228961; PMID:1970326
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in: intracellular #status predicted <IW72>
in: transmembrane #status predicted <IW3>
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in: intracellular #status predicted <IW3>
in: ATPase nucleotide-binding domain homology <A
in: transmembrane #status predicted <IW5>
in: transmembrane #status predicted <IW5>
in: transmembrane #status predicted <IW7>
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70.0%;
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RESULT 5
T47701
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A;Experimental source: cultivar Columbia; BAC clo-
C;Genetics:
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C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
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A; Residues: 1-61 < RES>
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A; Status: translation
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T09084
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A;Molecule type: DNA
A;Residues: 1-245 <BEN>
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phosphatidylinositol 3-kinase - Chlamydomonas
C;Species: Chlamydomonas reinhardtii
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C; Superfamily: c
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A; Introns: 4/1;
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F;291-313/Domain: transmembrane #status predicted <INT2>
F;291-313/Domain: transmembrane #status predicted <INT2>
F;320-348/Domain: transmembrane #status predicted <INT3>
F;349-786/Domain: intracellular #status predicted <INT3>
F;349-783/Domain: ATPase nucleotide-binding domain homology
F;879-810/Domain: transmembrane #status predicted <INT3>
F;849-874/Domain: transmembrane #status predicted <INT3>
F;879-952/Domain: intracellular #status predicted <INT6>
F;875-952/Domain: intracellular #status predicted <INT6>
F;875-978/Domain: transmembrane #status predicted <INT6>
F;875-978/Domain: intracellular #status predicted <INT6>
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F;875-978/Domain: transmembrane #status predicted
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                                           R;Sverdlov, E.D.; Monastyrskaya, ov, N.N.; Ovchinnikov, Y.A. Dokl. Biochem. 297, 426-431, 198
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R;Molendijk, A.J.; Irvine, R.F.
Plant Mol. Biol. 37, 53-66, 1998
A;Title: Inositide signalling in Chlamydomonas: Characterization
A;Reference number: Z16411; MUID:98281574; PMID:9620264
A;Accession: T09084
                                                                                              C;Species: Homo Sapiens (man)
C;Species: Homo Sapiens (man)
C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: S00801; S004019; Ā27397; S02275
R;Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Melkov, dyanov, N.N.; Sverdlov, E.D.
TEBS Lett. 233, 87-94, 1988
A;Title: Family of human Na,K-ATPase genes. Structure of the gene for the catalyth A;Reference number: S00801; MUID:88255304; PMID:2838329
A;Reference snoan
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A;Residues: 1-1010 <TRA2>
A;Residues: 1-1010 <TRA2>
A;Cross-references: UNIPROT:P24798; GB:M59960; NID:g212407; PIDN:AAA48982.1; PID:g212400;
A;Cross-references: UNIPROT:P24798; GB:M59960; NID:g212407; PIDN:AAA48982.1; PID:g212400;
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain potassium transport; sodium traffy-references: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium traffy-references: ATP, S74-770/Domain: ATPase nucleotide-binding domain homology ATN>
F;574-770/Binding site: carbohydrate (Asn) (covalant) #status predicted
F;363/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;495/Binding site: ATP (Lys) #status predicted
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Am. J. Physiol. 259, C619-C630, 1990
A;Title: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms
A;Reference number: A37227; MUID:91023019; PMID:2171348
A;Accession: B37227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - chicken C;Species: Gallus gallus (chicken) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004 C;Accession: B37227; I50395
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A; Experimental source: strain cw-15
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A; Residues: 1-490 < MOL>
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A; Molecule type: DNA
A; Residues: 1-1013 < OVC>
A; Cross references: UNIPROT: P13637;
                                                                                                                                                                                                                                                                                                                     Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - human
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of human Na(+), K(+)-ATPase

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Structure

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426-431, 1987

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EMBL:M37456 S.; Broude,

N.B.;

Ushkarev,

Y.A.; Melkov, A.M.;

Smir

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A;Residues: 1, EIH, 3-1013 <SVE1>
A;Cross-references: EMBL:X12910; NID:g28963
A;Cross-references: EMBL:X12910; NID:g28963
A;Note: the authors translated the codon TTC for residue 283 as Ser and TCT for re A;Note: this paper is a translation of the Russian paper published in Dokl. Akad. R;Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Allikmets, Fina, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchnikov, Y.A.
TEBS Lett. 217, 275-278, 1937
A;Reference number: A27397; MUID:87247232; PMID:3036582
A;Accession: A27397; MUID:87247232; PMID:3036582
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A;Residues: 1-1013 <SHU>
A;Residues: 1-1013 <SHU>
A;Residues: 1-1013 <SHU>
A;Residues: 1-1013 <SHU>
A;Residues: 1-1013 <SHU>
A;Cross-references: UNIPROT:P06687; EMBL:M14513; NID:g203030; PIDN:AAA40777.1; PID:g2031
A;Note: in the authors' translation 405-Ser is shown after residue 409 and, consequent1:
R;Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.; I
J. Biochem: 102, 43-58, 1987
J. Biochem: 102, 43-58, 1987
A;Title: Primary structures of two types of alpha-subunit of rat brain Na(+),K(+)-ATPas:
A;Reference number: S00460; MUID:88032933; PMID:2822682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 30-Jun-1988 #sequence revision 23-Apr-1993 #text_change 09-Jul-2004 C;Accession: C24639; S00514; B27180; A60470 R;Shull, G.E.; Greeb, J.; Lingrel, J.B. Biochemistry 25, 8125-8132, 1986 A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpl A;Reference number: A90512; MUID:87128908; PMID:3028470 A;Accession: C24639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - rat
N;Alternate names: Na+/K+-transporting ATPase alpha(III) chain
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:865-942/Domain: intracellular #status predicted <INT4>
F:943-968/Domain: transmembrane #status predicted <TM7>
F:969-1013/Domain: extracellular #status predicted <EXT7>
F:969-1013/Domain: extracellular #status predicted <EXT7>
F:366/Active site: Asp (aspartylphosphate intermediate) #
F:498/Binding site: ATP (Lys) #status predicted
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A:Introns: 2/3; 31/3; 51/3; 119/3; 157/3; 202/3; 242/1; 331/3; 398/1; 435/2; 479/3; 544/
C:Superfamily: Na+/K--transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; heterodimer; hydrolase; int transport; phosphoprotein; potassium transp
g:86-110/Domain: transmembrane #status predicted <TM1>
g:120-139/Domain: transmembrane #status predicted <TM2>
g:140-280/Domain: intracellular #status predicted <TM3>
g:281-303/Domain: transmembrane #status predicted <TM3>
g:310-386/Domain: transmembrane #status predicted <TM3>
g:310-386/Domain: transmembrane #status predicted <TM3>
g:33-776/Domain: transmembrane #status predicted <TM3>
g:37-773/Domain: transmembrane #status predicted <TM5>
g:77-800/Domain: transmembrane #status predicted <TM5>
g:77-800/Domain: transmembrane #status predicted <TM5>
g:33-864/Domain: transmembrane #status predicted <TM5>
g:33-864/Domain: transmembrane #status predicted <TM5>
g:33-864/Domain: transmembrane #status predicted <TM5>
A;Cross-references: EMBL:X05883; NID:g55769; PIDN:CAA29307.1; PID:g55770 R;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Gii
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A;Residues: 243-434 <SVE2>
A;Cross-references: GB:M27570
                                                                                 A; Molecule type: mRNA
A; Residues: 1-907, 'C',
                                                                                                                                                                      A; Accession: S00514
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                                                                                     1-907, 'C', 909-1013 <HAR>
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64;
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        R.; Nadal-Ginard,
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                                          F;371/Active site: Asp (aspartylphosphate intermediate)
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A; Kolecule type: mRNA
A; Kolecule type: mRNA
A; Rolecules: 3-1017 <TA2>
A; Residues: 3-1017 <TA2>
C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nuclections: ATP; glycoprotein; hydrolase; phosphoprotein
C; Keywords: ATP; glycoprotein; hydrolase; phosphoprotein
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F; 581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
F; 581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
F; 581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
F; 581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
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F; 581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
F; 581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
F; 581-777/Domain: ATPase 
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A;Rosidues: 1-1017 <TAKS
A;Residues: 1-1017 <TAKS
A;Cross-references: UNIPROT:P24797; GB:M59959; NID:g212405; PIDN:AAA48981.1; PID:g212406
A;Cross-references: UNIPROT:P24797; GB:M59959; NID:g212405; PIDN:AAA48981.1; PID:g212406
R;Takeyasu, K.; Lemas, V.; Fambrough, D.M.
Am. J. Physiol. 259, C619-C630, 1990
A;Title: Stability of Na(+)-K(+)-A970
A;Title: Stability of Na(+)-K(+)-A970
A;Reference number: A37227; MUID:91023019; PMID:2171348
A;Accession: A37227
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A;Residues: 1,'NL',4-103,'R',105-113,'E',115-127,'G',129-148,'Q',150-151,'T',153-165,'D'
A;Residues: 1,'NL',4-103,'R',105-113,'E',115-127,'G',129-148,'Q',150-151,'T',153-165,'D'
A;Residues: L'NL',4-103,'R',1019-1503,'BID:,205633,'BIDN:,AAAA1672.1; PID:g205634
A;Note: the authors translated the codon CAG for residue 149 as Glu, GGC for residue 194
R;Hsu, Y.M.; Guidotti, G.
B;Cohemistry 28, 569-573, 1989
A;Title: Rat brain has the alpha3 form of the (Na+,K+)ATPase.
A;Reference number: A60470; MUID:89223049; PMID:2540801
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F;310-38/Domain: transmembrane #status predicted <TM4>
F;310-38/Domain: intracellular #status predicted <TM4>
F;339-776/Domain: ATPase nucleotide-binding domain homology
F;577-773/Domain: transmembrane #status predicted <TM5>
F;777-800/Domain: transmembrane #status predicted <TM6>
F;805-942/Domain: intracellular #status predicted <TM74>
F;865-942/Domain: intracellular #status predicted <TM74>
F;943-968/Domain: transmembrane #status predicted <TM74>
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A; Accession: I50394
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Am. J. Physiol. 259, 619-630, 1991
A;Title: Stability of the Na+,K+-ATPase alpha-subunit isoforms
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C;Species: Gallus gallus (chicken)
C;Date: 16-Sep_1992 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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A;Residues: 117-132;586-595,'X',597-601
C;Comment: The alpha-3 form appears to b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A60470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics
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Title: Three differentially expressed Na,
Reference number: A92749; MUID:88033255;
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PMID:2822726
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64;
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predicted

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A;Molecule type: DNA
A;Residues: 211-249 <SH2>
A;Residues: 211-249 <SH2>
A;Residues: 211-249 <SH2>
A;Residues: 211-249 <SH2>
A;Cross-references: GB:M16795; NID:g179196; PIDN:AAA51799.1; PID:g553194
R;Sverdlov, E.D; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Allikmets, R.L.; Markeryov, Y.A.; Allikmets, R.L.; Molecular, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchnikov, Y.A.
FEBS Lett. 217, 275-278, 1937
A;Title: The family of human Na+,K+ATPase genes. No less than five genes and/or pseudog A;Heference number: A27397; MUID:87247232; PMID:3036582
A;Accession: D27397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;94-118/Domain: transmembrane #status predicted <TM1>
F;128-147/Domain: transmembrane #status predicted <TM2>
F;128-284/Domain: intracellular #status predicted <TM2>
F;289-311/Domain: transmembrane #status predicted <TM3>
F;318-346/Domain: transmembrane #status predicted <TM4>
F;318-346/Domain: intracellular #status predicted <TM4>
F;347-783/Domain: intracellular #status predicted <TM5>
F;584-780/Domain: ATPase nucleotide-binding domain homology
F;784-807/Domain: transmembrane #status predicted <TM5>
F;846-871/Domain: transmembrane #status predicted <TM6>
F;846-871/Domain: transmembrane #status predicted <TM6>
F;846-871/Domain: transmembrane #status predicted <TM6>
F;846-871/Domain: transmembrane #status predicted <TM6>
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F;846-871/Domain: transmembrane #status predicted <TM6>
F;846-871/Domain: transmembrane #status predicted <TM6-8

F;846-871/Domain: transmembrane #status predicted <TM6-8

F;846-871/Domain: transmembrane #status predicted <TM6-8

F;846-871/Domain: transmembrane #status predicted <TM6-8

F;846-871/Domain: transmembrane #status predicted <TM6-8

F;846-871/Domain: transmembrane #status predicted <TM6-8

F;846-871/Domain: transmembrane #status predicted <TM6-8

F;846-871/Domain: transmembrane #status predicted <TM6-8

F;846-871/Domain: transmembrane #status predicted <TM6-8

F;846-871
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C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C; Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp F; 6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>
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Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
A;Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit A;Reference number: A94158; MUID:87231946; PMID:3035563
A;Accession: B27795
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N;Alternate names: Na+/K+-exchanging ATPase alpha chain-4; sodium/potassium transporting
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A; Residues: 251-442 < SVE>
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A;Residues: 1-1020 <SHU>
A;Residues: 1-1020 <SHU>
A;Cross-references: UNIPROT:P50993; GB:J05096; NID:g179164; PIDN:AAA51797.1;
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J. B.Gol. Chem. 264, 17532-17543, 1989
A;Title: Characterization of the human Na,K-ATPase alpha2 gene and identification A;Reference number: A34474; MUID:90008924; PMID:2477373
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;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004;
;Accession: A34474; B27795; D27397
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;374/Active site: Asp (aspartylphosphate intermediate) #status
;505/Binding site: ATP (Lys) #status predicted
;714,718,723/Active site: Asp, Asp, Lys #status predicted
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Best Local
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91
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Pred. No.
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Pred. No.
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F;248-288/DOMMAIN: AUGUSTANANA #STATUS predicted <TW3>
F;289-311/Domain: transmembrane #Status predicted <TW4>
F;318-346/Domain: transmembrane #Status predicted <TW4>
F;347-783/Domain: intracellular #Status predicted <INT3>
F;347-80/Domain: ATPass nucleotide binding domain homology
F;584-780/Domain: transmembrane #Status predicted <TW5>
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C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Superfamily: Na+/K+-transporting ATPase alpha chain; phosphoprotein; potassium transports; keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transports; phosphoprotein; potassium transporting ATPase alpha-2 chain #status predicted <MAT>
F;6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Shull, G.E.; Schwartz, A.; Lingrel, J.B.

Nature 316, 691-695, 1985

A;Title: Amino-acid sequence of the catalytic subunit of the (Na(+)+K(+)) ATPase deduced A;Reference number: A01074; MUID:85296299; PMID:2993903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep N;Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPa C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 09-Jul-2004 C;Accession: A01074; A35426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Molecular cloning of three distinct A;Reference number: A90512; MUID:87128908; PW A;Accession: B24639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: Na+/K+-transporting ATPase alpha-plus chain C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004 C;Accession: B24639
                                                                                                                                                                                                                    R;Hinz, H.R.; Kirley, T.L.

J. Biol. Chem. 265, 10260-10265, 1990

A;Title: Lysine 480 is an essential re
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F;374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;505/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               r;872-949/Domain: intracellular #status predicted <INT4>
F;950-975/Domain: transmembrane #status predicted <TM7>
F;950-975/Domain: transmembrane #status predicted <TM7>
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F;128-147/Domain: transmembrane #status predicted <TM2
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A; Residues: 1-1020 <SHU>
                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1021 <SHU>
A; Cross-referes: UNIPROT: P04074; GB: X02813; NID: g1205;
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C;Comment: This is the catalytic component of the active enzyme, which catalyzes the reates the electrochemical gradient of sodium and potassium, providing the energy for
                                                                   A; Molecule type: protein A; Residues: 475-492 <HIN>
                                                                                                                            A; Status: preliminary
                                                                                                                                                              A;Accession: A35426
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                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A01074
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                                                                                                                                                                                                   ssential residue in the putative MUID:90285144; PMID:2162343
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PMID:3028470
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C;Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin c (Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; hydrolase; phosphoprotein; potassium transport; sodium transport; transfer; 6-1021/Product: Na+/K+-transporting ATPase alpha chain #status predicted <MAT> F;94-115/Domain: transmembrane #status predicted <TM1> F;128-144/Domain: transmembrane #status predicted <TM2> F;289-311/Domain: transmembrane #status predicted <TM3> F;318-346/Domain: transmembrane #status predicted <TM4> F;318-346/Domain: transmembrane #status predicted <TM4> F;318-346/Domain: transmembrane #status predicted <TM5> F;385-981/Domain: transmembrane #status predicted <TM6> F;785-980/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM5> F;951-976/Domain: transmembrane #status predicted <TM5> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: transmembrane #status predicted <TM6> F;951-976/Domain: t
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C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transpre, 6-1021/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <NAT>
F;6-93/Domain: intracellular #status predicted <NT1>
F;94-118/Domain: transmembrane #status predicted <TM1>
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A;Residues: 1-1021 <KAN>
A;Cross-references: UNIPROT:P18907; EMBL:X16773; NID:g1010; PIDN:CAA34716.1; PID:g87102
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A;Title: Structure of the alpha(1) subunit of horse Na,K-ATPase (A;Reference number: S04630; MUID:89290042; PMID:2544461
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Na+/K+-exchanging ATPase
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                                                                         RESULT 15
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A; Accession: S04630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;374/Active site: Asp (aspartylphosphate intermediate) #status predicted;506/Binding site: ATP (Lys) #status predicted;715,719,724/Active site: Asp, Asp, Lys #status predicted
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   3.6.3.9) alpha chain -
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Pred. No.
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                                          A; Contents: annotation; membrane topology C; Superfamily: Na+/K+-transporting ATPase
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w;Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chain; Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B24862; I46572; A35504; S00011; S00502; S02569; S29762
R;Ovchinnikov, Y.A.; Modyanov, N.N.; Broude, N.E.; Petrukhin, K.E.; Grishin, A.V.; Arzam FEBS Lett. 201, 237-245, 1986
A;Title: Pig kidney Na+,K+-ATPase. Primary structure and spatial organization.
A;Accession: B24862
A;Molecule ***Comparization**
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A; Molecule type: MRNA
A; Rolecules: 1-1021 <TAKS
A; Residues: 1-1021 <TAKS
A; Residues: 1-1021 <TAKS
A; Cross-references: UNIPROT: P09572; GB: J03230; NID: g211219; PIDN: AAA48607.1; PID: g211220
C; Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C; Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein
F; 585-781/Domain: ATPase nucleotide-binding domain homology ATNN
F; 213, 481/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F; 506/Binding site: ATP (Lys) #status predicted
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A;Title: Amino acid sequence of the 17-kilodalton fragment of the cytoplasmic region of A;Reference number: 146572
A;Accession: 146572
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A;Residues: 469-617 <0VCl>
A;Cross-references: GB:M32512; NID:g164385; PIDN:AAA31004.1; PID:g164386
A;Cross-references: GB:M32512; NID:g164385; PIDN:AAA31004.1; PID:g164386
R;Karlish, S.J.D.; Goldshleger, R.; Stein, W.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 4566-4570, 1990
A;Title: A 19-kDa C-terminal tryptic f6-4570, 1990
A;Title: A 19-kDa C-terminal tryptic f8-4570, 1990
A;Reference number: A35504; MUID:90280416; PMID:2162048
A;Accession: A35504
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A;Title: Ouabain-sensitive (Na(+) + K(+))-ATPase activity expressed A;Reference number: A28199; MUID:88153759; PMID:2831227
A;Accession: A28199
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C;Date: 21-Sep-1988 #sequence_revision 21-Sep-1988 #text_change 09-Jul-2004
C;Accession: A28199
A;Contents: annotation; membrane topology R;Oontents: annotation; membrane topology R;Ovchinnikov, Y.A.; Luneva, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Arzamazova, N.M. FEBS Lett. 227, 230-234, 1988
A;Title: Topology of Na, K-ATPase: identification of the extra- and intracellular hydrogation of the extra- and intracellular hydrogation of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of the extra- and intracellular hydrogatic topology of Na, K-ATPase: identification of Na, K-ATPase: identifi
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A;Residues: 836-845, 'R',847-851 <KAR>
A;Residues: 836-845, 'R',847-851 <KAR>
R;Ovchinnikov, Y.A., Tazamazova, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Aldanova, N. FEBS Lett. 217, 269-274, 1987
A;Title: Detailed structural analysis of exposed domains of membrane-bound Na+,K+-ATPaseA;Reference number: 500011; MUID:87247231; PMID:3036581
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A; Residues: 1-1021 < OVC2>
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J. Biol. Chem. :
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rting ATPase alpha chain; ATPase nucleotide-binding domain hydrolase; ion transport; phosphoprotein; potassium transp

hydrop

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Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain [validated] - rat N;Alternate names: Na+/K+-transporting ATPase alpha chain, kidney-type N;Contains: Na+/K+-transporting ATPase alpha-S chain C;Species: Rattus norvegicus (Norway rat) C;Date: 18-Aug-2000 #sequence revision 18-Aug-2000 #text_change 09-Jul-2004 C;Accession: A24639; S00460; A27180; S11020; A25171; S29877; S10758 R;Shull, G.E.; Greeb, J.; Lingrel, J.B. Biochemistry 25, 8125-8132, 1986 Biochemistry 25, 8125-8132, 1986 A;Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit A;Reference number: A90512; MUID:87128908; PMID:3028470
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A;Residues: 1-1022 <CUT>
A;Residues: 1-1022 <CUT>
A;COBS-references: UNIPROT:Q92030; EMBL:X76108; NID:g509405; PIDN:CAA53714.1; PID:g5094
A;Cross-references: UNIPROT:Q92030; EMBL:X76108; NID:g509405; PIDN:CAA53714.1; PID:g5094
A;Cross-references: UNIPROT:Q92030; EMBL:X76108; NID:g509405; PIDN:CAA53714.1; PID:g5094
C;Superfamily: Na-/K+-transporting ATPase alpha chain; potassium transport; transmemb C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; transmemb F;586-782/Domain: ATPase nucleotide-binding domain homology <ATN-F;582/Binding site: carbohydrate (Asn) (covalent) #status predicted F;375/Active site: Asp (aspartylphosphate intermediate) #status predicted F;507/Binding site: ATP (Lys) #status predicted
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A;Accession: S49127
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                                      A;Molecule type: mRNA
A;Residues: 1-1023 <S
                                                                                                  A; Accession: A24639
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;1148-288/Domain: intracellular #status predicted <TM2>
;289-311/Domain: transmembrane #status predicted <TM3>
;289-311/Domain: transmembrane #status predicted <TM3>
;347-784/Domain: intracellular #status predicted <TM4>
;347-784/Domain: intracellular #status predicted <TM3>
;585-781/Domain: transmembrane #status predicted <TM5>
;785-808/Domain: transmembrane #status predicted <TM6>
;847-872/Domain: transmembrane #status predicted <TM6>
;873-950/Domain: transmembrane #status predicted <TM7>
;951-976/Domain: transmembrane #status predicted <TM7>
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374/Active site: Asp (aspartylphosphate intermediate) #status predicted
506/Binding site: ATP (Lys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
Cross-references: UNIPROT: P06685; EMBL: M14511; NID: g203026; PIDN: AAA40775.1; PID: g2030
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6; Conserve
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Pred. No.
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R;Schneider, J.W.; Mercer, R.W.; Caplan, M.; Emanuel, J.R.; Sweadner, K Proc. Natl. Acad. Sci. U.S.A. 82, 6357-6361, 1985
A;Title: Molecular cloning of rat brain Na,K-ATPase alpha-subunit cDNA. A;Reference number: A25171; MUID:85298352; PMID:2994074
A;Accession: A25171
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A;Title: Three differentially expressed Na,K-ATPase alpha subunit isoforms: A;Reference number: A92749; MUID:88033255; PMID:2822726
A;Accession: A27180
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A;Molecule type: mRNA
A;Residues: 1-1023 <HAR>
A;Residues: 1-1023 <HAR>
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
A;Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
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A;Cross-references: EMBL:X05882; NID:g55771; PID:g55772; PID:g55772; PID:g55772
A;Cross-references: EMBL:X05882; PID:g55772;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 6-19 <LYT>
A;Residues: K.; Hosoi, K.; Kodama, A.; Ueha, T.
B;Ckrihara, K.; Hosoi, K.; Kodama, A.; Ueha, T.
Biochim. Biophys. Acta 1039, 234-240, 1990
A;Title: A new electrophoretic variant of alpha subunit of Na(+)/K(+)-ATPase from the A;Reference number: S10758; MUID:90304196; PMID:2163680
A;Accession: S10758
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A;Tille: Primary structures of two types of alpha-subunit of A;Reference number: S00460; MUID:88032933; PMID:2822682
                                                                                                                                                                                                                                                                                                                                                                                                                                              F;130-149/Domain: transmembrane #status predicted <TM2>
F;150-290/Domain: intracellular #status predicted <1MT2>
F;291-131/Domain: transmembrane #status predicted <TM3>
F;291-31/Domain: transmembrane #status predicted <TM4>
F;320-348/Domain: intracellular #status predicted <TM4>
F;349-786/Domain: ATPase nucleotide-binding domain homology
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Biochim. Biophys. Acta 1049, 286-292, 1990
A;Title: Cloning and analysis of the 5'-flanking region of
A;Reference number: S11020; MUID:90344872; PMID:2166579
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A;Residues: 1-67,'PV',70-174,'E',176-187,'V',189-334,'V',336-1023 <HER>
A;Cross-references: EMBL_M28647; NID:g205831; PIDN:AAA41671.1; PID:g205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transf.;6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 6,'X',8-10,'X',12-16 <KUR>
A;Experimental source: submandibular gland
A;Note: designated alpha-S form; thought to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 132, 764-769, 1985
A;Title: The catalytic subunits of the (Na(+), K(+))-ATPase alpha and alpha(+) isozymes
A;Reference number: S29877; MUID:86050667; PMID:2998384
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A; Residues: 1-41 < YAG>
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                                                     F;376/Active site: Asp (aspartylphosphate intermediate)
F;508/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                          F;953-978/Domain: transmembrane
                                                                                                                                                                                                                                                                               F;875-952/Domain: intracellular
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A;Residues: 489-533 <SCH>
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                                                                                                                                                                    cransmembrane #status predicted <TM7>
extracellular #status predicted <EXT>
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#status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to arise from alpha-1 chain by post-translation
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F;376/Active site: Asp (aspartylphosphate intermediate) #status predicted F;508/Binding site: ATP (Lys) #status predicted F;717,721,726/Active site: Asp, Asp, Lys #status predicted
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F;150-290/Domain: intracellular #status predicted <INT2>
F;251-313/Domain: transmembrane #status predicted <TM3>
F;291-313/Domain: transmembrane #status predicted <TM4>
F;349-786/Domain: intracellular #status predicted <INT3>
F;349-786/Domain: ATPase nucleotide-binding domain homology F;587-783/Domain: transmembrane #status predicted <INT5>
F;787-810/Domain: transmembrane #status predicted <TM6>
F;849-874/Domain: intracellular #status predicted <INT4>
F;953-978/Domain: transmembrane #status predicted <INT7>
F;953-978/Domain: transmembrane #status predicted <INT7>
A;Residues: 1-1025 <VER>
A;Residues: 1-1025 <VER>
A;Cross-references: UNIPROT:Q92123; GB:U10108; NID:g499225; PIDN:AAA19022.1; PID:g499226 C;Comment: The alpha chain is the catalytic chain.
                                                                                                                                             A;Title: Primary sequence of Xenopus laevis Na(+)-K(+)-ATPase A;Reference number: A60444; MUID:89285429; PMID:2544104 A;Accession: A60444
                                                                                                                                                                                                                                                                                                                          Na+/K+-exchanging ATPase (EC 3.6.39) alpha chain precursor - African clawe N;Alternate names: sodium pump alpha chain C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
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A;Note: sequence extracted from NCBI backbone (NCBIF:111876)
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Superfamily: heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp F;6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
F;6-95/Domain: intracellular #status predicted <INTI>
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A;Cross-references: UNIPROT:P30714; EMBL:Z11798; NID:g62491; PIDN:CAA77842.1; A;Experimental source: urinary bladder cell line TBM 18-23
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J. Biol. Chem. 267, 16895-16903, 1992
A;Title: Primary sequence and functional expression of a novel ouabain-resistant Na,K-ATA;Reference number: A43451; MUID:92380991; PMID:1380956
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A; Accession: A43451
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                                                                                   A; Molecule type: mRNA
                                                                                                                        A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                       ;Accession: A60444;
;Verrey, F.; Kairouz, P.; Schaerer, E
m. J. Physiol. 256, F1034-F1043, 1989
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Pred. No.
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RESULT 22
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F;217,485/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;378/Active site: Asp (aspartylphosphate intermediate) #status predicted
A; Notice type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1038 < LEB>
A; Cross-references: UNIPROT: P13607;
A; Cross-references: Trom Fig. 9 is
                                                                                                                                                                                                                                             Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - fruit fly (Drosophila melanogaster) N;Alternate names: sodium pump alpha chain C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 30-Unn-1993 #sequence revision 30-Unn-1993 #text_change 09-Jul-2004 C;Accession: S03632; S07049
                                                                                                                                      R, Lebovitz, R.M.; Takeyasu, K.; Fambrough, D.M. EMBO J. 8, 193-202, 1989
A, Title: Molecular characterization and expression of the A; Reference number: S03632; MUID:89231618; PMID:2540956
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A;Title: Sodium and potassium ATPase of the teleost fish Catostomus commersoni. Sequence A;Reference number: S14740; MUID:91282983; PMID:1711856
                                                                                                          A; Reference number: S03632;
A; Accession: S03632
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A;Residues i 1027 <5CH>
A;Cross-references: UNIPROT:P25489; EMBL:X58629; NID:g62641; PIDN:CAA41483.1; PID:g62642
A;Cross-references: UNIPROT:P25489; EMBL:X58629; NID:g62641; PIDN:CAA41483.1; PID:g62642
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Superfamily: Na+/K+-transporting ATPase alpha chain; potassium transport; sodium t
C;Superfamily: NTP; hydrolase; ion transport; phosphopyrotein; potassium transport; sodium t
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
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transmembrane #status predicted <TM6>
intracellular #status predicted <IM74>
transmembrane #status predicted <IM74>
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transmembrane #status predicted <TM4>
intracellular #status predicted <INT3>
Allease nucleotide-binding domain homology
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#status predicted <INT2>
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EMBL:X14476 inconsistent

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from Fig.

8 in having 89-Asp

Ehr1

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A;Cross-references: EMBL:X17471
A;Note: the authors translated the codon
C;Genetics:
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C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; heterodimer; hydrolase; ion transport: phosphoprotein. potantium trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 258, 203-207, 1989
A;Title: Amplification of the phosphorylation site - ATP-binding site cDNA fragment A;Reference number: S07049; MUID:90092469; PMID:2557235
A;Accession: S07049
                                                                                                                                                                                                                                                                                                    F;111-130/Domain:
F;131-271/Domain:
F;272-296/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-1004 <MAC>
A;Residues: 1-1004 <MAC>
A;Residues: 1-1004 <MAC>
A;Residues: 1-1004 <MAC>
A;Residues: 1-1004 <MC>
A;Residues: 1-1004 <MC>
A;Residues: 1-1004 <MC>
A;Residues: 1-1004 <MC>
A;Residues: 1-1004 <MC
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transport; 1-1004 /Froduct: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>
E;2-1004 /Froduct: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Macias, M.T.; Palmero, I.; Sastre, L.
Gene 105, 197-204, 1991
A;Title: Cloning of a cDNA encoding an Artemia franciscana Na/K ATPase alpha-subunit.
A;Reference number: JH0470; MUID:92039032; PMID:1657719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain (clone pArATNa136) - brine shrimp
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F;364-801/Domain: intracellular #status predicted <INT3>
F;602-798/Domain: ATPase nucleotide-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S07049
A;Molecule type: mRNA
A;Residues: 397-521 <VAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: JH0470
                                                 ;111-130/Domain: transmembrane #status predicted <TM2>
;131-271/Domain: intracellular #status predicted <TM7>
;272-296/Domain: transmembrane #status predicted <TM3>
;272-296/Domain: transmembrane #status predicted <TM3>
;301-329/Domain: intracellular #status predicted <TM3>
;301-767/Domain: intracellular #status predicted <TM5>
;568-764/Domain: ATPase nucleotide-binding domain homology <ATN>
;768-791/Domain: transmembrane #status predicted <TM5>
;830-855/Domain: transmembrane #status predicted <TM6>
;856-936/Domain: intracellular #status predicted <TM7>
;937-955/Domain: transmembrane #status predicted <TM7>
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;956-1004/Domain: extracellular #status predicted <EXT>;357/Active site: Asp (aspartylphosphate intermediate)
                                                                                                                                                                                                                                                                                                                                                                                                            ;76-97/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Date: 30-Jun-1992 #sequence_revision; Accession: JH0470; S24196
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864-889/Domain: transmembrane #status predicted <TM6>
890-966/Domain: intracellular #status predicted <INT4>
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:Cross-references: FlyBase:FBgn0002921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Artemia franciscana (brine shrimp)
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Best Local
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146-165/Domain: transmembrane
166-305/Domain: intracellular
306-328/Domain: transmembrane
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#status predicted <TM2>
#status predicted <TMT2>
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status predicted <TM4>
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A; Gene: MTH943
A; Start codon: (
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein MTH943 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Dec-2002
C;Accession: D6928
C;Accession: D6928
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.
R;Smith, D.R.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Batteriol. 179, 7135-7155, 1997
J. Batteriol. 179, 7135-7155, 1997
J. Batteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
F86876
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                                                                                                                                                                                                                                                                                                                         A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A;Reference number: A69000; MUID:98037514; PMID:9371463 A;Accession: D69226
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                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-522 <MTH>
A;Cross-references: GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AAB85441.1; PID:g26220
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-312 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: F86876
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;Experimental source: strain IL1403
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Best Local (
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                                   ADGPTLREWI 11
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ADGVTVKEWI
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                                                                                               Score 42; DB 2;
Pred. No. 50;
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RESULT 26 S62941

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RESULT
T12091
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A;Accession: AI1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Bercl.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P53966; EMBL:Z71305; NID:g1301864; PID:g1301865; MIPS:YNLO29
A;Experimental source: strain S288C
R;Duesterhoeft, A.; Floett, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, April 1996
starch phosphorylase
                                                                                                                                                                                                                                        A; Gene: IIII C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision
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R;Andre, B.; Iraqui Houssaini, I.; Urrestarazu, L.A.; Vissers, submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YNL029c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N2755
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr.1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q92DB8; GB:AL592022; A;Experimental source: strain Clip11262
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A; Residues: 1-725 <GLA>
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A;Experimental source: strain S288C
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A; Residues: 1-522 < DUE >
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A; Accession: S62941
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H, cytosolic isoform
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C;Species: mitochondrion Paramecium tetraurelia (C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 # R;Pritchard, A.E.; Seilhamer, J.J.; Mahalingam, R.; Nucleic Acids Res. 18, 173-180, 1990 A;Title: Nucleotide sequence of the mitochondrial ge A;Reference number: S07725; MUID:90174913; PMID:2308 A;Accession: S07755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Buchner, P.; Borisjuk, L.; Wobus, U.
Planta 199, 64-73, 1996
A;Title: Glucan phosphorylases in Vicia faba L.: cloning,
A;Reference number: Z17412; MUID:96236831; PMID:8680306
A;Accession: T12091
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                R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: catalyzes the formation of glucose 1-phosphate from C;Superfamily: glucan phosphorylase C;Keywords: glycosyltransferase; phosphoproteir C;Keywords: glycosyltransferase; phosphoproteir E;688/Binding site: pyridoxal phosphate (Lys) (covalent) #status pi
                                                                                                                                    hypothetical protein Rv0079 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70849
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C;Keywords: mitochondrion
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A; Residues: 1-189 < PRI>
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A; Residues: 1-842 < BUC>
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  R.; Sulston, J.E.; Taylor, K.; ng the biology of Mycobacterium
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ce: strain Vicia
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osphate (Lys) (covalent) #status pre
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Pred. No. 27;
1; Mismatches
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PMID:2308823
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A;Cross-references: C;Genetics:
C;Gene: At2g42400
A;Map position: 2
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A;Accession: H70849
A;Status: preliminary; nucleic acid sequence not shown;
A;Molecule type: DNA
A;Residues: 1-273 <COL>
A;Cross-references: UNIPROT:053624; GB:AL021428; GB:AL12
A;Eross-referental source: strain H37Rv
C;Genetics:
                                                           A; Note: starch phosphorylase C; Function:
                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-955 <LIN>
A;Cross-references: UNIPROT:P27598; EMBL:M64362; NII
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A;Description: catalyzes the formation of glu-
C;Superfamily: glucan phosphorylase
C;Keywords: chloroplast; glycosyltransferase;
                                                                                                                                                                                                                                               A;Reference number: Z17224
A;Accession: T10947
                                                                                                                                                                                                                                                                                        R;Lin, C.T.; Yeh, K.W.; Lee, P.D.; Su, J.C. submitted to the EMBL Data Library, July 1991
A;Description: Primary structure of sweet potato starch phosphorylase deduced
                                                                                                                                                                                                                                                                                                                                                                   starch phosphorylase (EC 2.4.1.1) precursor - sweet potato C;Species: Ipomoea batatas (sweet potato) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-473 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein At2942400 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84853
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C;Superfamily: Mycobacterium tuberculosis hypothetical protein
                                                                                                                                             A; Experimental source: cv.
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Best Local :
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                                                                                                                                           UNIPROT: P27598; EMBL: M64362; NID: g168275; ce: cv. Tainong 57; tuberous root
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Pred. No.
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Pred. No.
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                                        glucose 1-phosphate
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    hexosyltransferase; phosphoprotein;
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E.; Umayam, L.; Tallon, L
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      611
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starch phosphorylase (EC 2.4.1.1) precursor - potato N,Alternate names: alpha-glucan phosphorylase (;Species: Solanum tuberosum (potato) C;Date: 04-Dec-1986 #sequence revision 30-Sep-1990 #text_change C;Accession: JU0130; A00574; PQ0139; S15531; S12033 R;Nakano, K.; Mori, H.; Fukui, T.
                                                                                                                   C;Comment: Phosphorylase, an important allosteric enzyme in carbohydrate metabolism, gulatory mechanisms and in their natural substrates. However, all known phosphorylass (;Superfamily: glucan phosphorylase) etc.;Superfamily: glucan phosphorylase c;Keywords: allosteric regulation; carbohydrate metabolism; glycosyltransferase; hex c;Keywords: transit peptide (amyloplast) #status predicted <TNP>
F;51-506/Product: phosphorylase #status experimental <MATP
F;51-966/Product: phosphorylase #status experimental <MATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cube - ... Fukui, T. R; Nakano, K.; Fukui, T. R; Nakano, K.; Fukui, T. J. Biol. Chem. 261, 8230-8236, 1986
J. Biol. Chem. 261, 8230-8236, 1986
A; Title: The complete amino acid sequence of potato alpha-glucan
A; Title: The complete A92591; MUID:86250715; PMID:3722153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1-43/Domain: transit peptide (chloroplast) #status predicted <frace, F;44-955/Product: starch phosphorylase #status predicted WAT>
F;801/Binding site:
pyridoxal phosphate (Lys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                    Mol. Gen. Genet. 224, 33-37, A; Title: Occurrence of a cop A; Reference number: S12033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library,
A;Reference number: S15531
A;Accession: S15531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type:
A; Residues: 51-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Molecular cloning of cDNA encoding potato amyloplast alpha-glucan phosphorylas: A;Reference number: A91915; MUID:90110071; PMID:2481677
                                                                                 F;51-966/Product: pnospnory.asc noccess F;812/Binding site: pyridoxal phosphate
                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 416-595 < CAM>
A; Cross-references: EMBL: X52385
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-158,'D',160-966 <BR2>
A;Cross-references: EMBL:XS2385; NID:g21578; PIDN:CAA36612.1; PID:g21579
R;Camirand, A.; St-Pierre, B.; Marineau, C.; Brisson, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-130 <BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Title: Maturation and subcellular compartmentation of A, Reference number: PQ0139; MUID:92404721; PMID:2535551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:P04045; GB:D00520; NID:g3702676; PIDN:BAA00407.1; PID:g2179 R;Nakano, K.; Fukui, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues:
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                                                                                                                                                                                                                                                                                                                                                     A;Accession: S12033
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                            Local Similarity
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  Conservative
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33; MUID:91117174; PMID:1703627
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58.3%;
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Pred.
۲;
                          Score 41; DB 1;
Pred. No. 1.3e+02;
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     4.
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A;Genome: nuclear
C;Superfamily: glu
C;Keywords: chlorop
F;1-61/Domain: trai
F;62-1000/Product:
F;846/Binding site
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C;Function:
A;Description:
C;Superfamily:
C;Keywords: carl
F;817/Binding s:
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                                                                   RESULT :
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R;BuChner, P; Borisjuk, L.; Wobus, U.

R;BuChner, P; Borisjuk, L.; Wobus, U.

submitted to the EMBL Data Library, August 1994

R;Description: alpha-1,4 glucan phosphorylases in Vicia faba L.: cDNA-Characterization

A;Reference number: S47243
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S-layer protein
C;Species: Bacil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-1000 <BUC>
A;Cross-references: EMBL:236880
A;Cross-references: Etrain Vicia faba var. minor; cultivar
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A;Experimental source: U.S. hybrid
C;Genetics:
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L; Mismatches
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C;Species: Homo sapi
C;Date: 20-Feb-1995
C;Accession: S21826
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T-cell receptor beta chain V region homolog -
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man) revision 20-Feb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: A70301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 13-Aug-1999
C;Accession: A70301
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A70301
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C;Function:
A;Pathway: butirosin biosynthesis
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A;Title: Biosynthesis of butirosin in Bacillus circulans
A;Reference number: Z18808; MUID:94374689; PMID:7522196
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 A; Introns: 134/3; C; Superfamily: ir F; 56-133/Domain:
                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-152 <GEO>
                                                                                                                                                                 R;George Jr., J.F.; So
submitted to the EMBL
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C; Superfamily:
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A,Molecule type: DNA
A,Residues: 1-98 <AQF>
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A; Residues: 1-1616 < AUB>
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                                                 C;Genetics:
                                                                A;Cross-references: EMBL:X56142; NID:g37500; PIDN:CAA39607.1; PID:g388518
                                                                                                                                                A; Reference number:
                                                                                                                                                                                                                                                                                  RESULT 38
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                                                                                                                                                                   Data
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region; immunoglobulin homology
homology <IMM>
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N;Alternate names: II-2; T-cell growth factor (TCGF)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A93550; A54490; Ā94064; I48597; A01850; I84713
R;Fuse, A.; Fujita, T.; Yasumitsu, H.; Kashima, N.; Hasegawa, K.; Taniguchi, Nucleic Acids Res. 12, 9323-9331, 1984
A;Title: Organization and structure of the mouse interleukin-2 gene.
A;Reference number: A93550; MUID:85087940; PMID:6240025
A;Accession: A93550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:K02292; NID:g198330; PIDN:AAA39289.1; PID:g309404 R;Kashima, N.; Nishi-Takaoka, C.; Fujita, T.; Taki, S.; Yamada, G.; Hamus Mature 313, 402-404, 1985 Partitle: Unique structure of murine interleukin-2 as deduced from cloned A;Reference number: I48597; MUID:85111148; PMID:2578624 A;Accession: I48597
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R;Yokota, T.; Arai, N.; Lee, F.; Rennick, D.; Mosmann, T.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 82, 68-72, 1985
A;Title: Use of a cDNA expression vector for isolation of mouse interleukin 2 cDNA clone A;Reference number: A94064; MUID:85113172; PMID:3918306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Degrave, W.; Simons, G.; Devos, R.; Plaetinck, G.; Ren Mol. Biol. Rep. 11, 57-61, 1986
A;Title: Cloning and structure of a mouse interleukin-2 A;Reference number: A54490; MUID:86118396; PMID:3003564
A;Accession: A54490
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C; Superfamily: interleukin-2
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A; Residues: 1-169 < YOK>
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A; Residues: 1-169 < DEG>
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A; Residues: 1-169 < FUS>
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                                            RESULT 40
S37289
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interleukin-2 precursor - mouse
C;Species: Mus musculus (house mouse)
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                             92-140/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                  ;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; 1.-20/Domain: signal sequence #status predicted <SIG>;21-169/product: interleukin-2 #status predicted <MAT>;23/Binding site: carbohydrate (Thr) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
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                                                                                                                                                                                                                           Matches
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50.0%;
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Pred. No.
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Pred. No.
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       Best Local
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-169 < KUR>
A; Cross-references: UNIPROT:(992W14; GB:AL591985; PIDN:CAC48933.1; PID:g15140418; GSPDB: A; Cross-references: UNIPROT:(992W14; GB:AL591985; PIDN:CAC48933.1; PID:g15140418; GSPDB: A; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; F18her, R.F.
L; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure hebault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Matesanz, F.; Alcina, A.; Pellicer, A.
Biochim. Biophys. Acta 1132, 335-336, 1992
A;Title: A new cDNA sequence for the murine interleukin-2 gene.
A;Reference number: S27205; MUID:93041941; PMID:1420317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: cytokine; glycoprotein; growth factor; lymphokine; T-cell F;1-20/Domain: signal sequence #status predicted <SIG> F;21-63/Product: interleukin-2 #status predicted <MAT>
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R;Todd, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid C;Species: Sinorhizobium meliloti (C;Species: Sinorhizobium meliloti (C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
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C;Superfamily: interleukin-2
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A; Residues: 1-50 <GHO>
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A; Residues: 1-63 < MATE>
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C;Accession: S37289; S27205; S36162; S24936
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                                                              A;Gene: SMb20554
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Pred. No. 36;
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Cordell, H.J.;
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Hearne, C.M.; Cornall,
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Similarity

47.1%; 53.8%;

Score 40; Pred. No.

DB

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Length 169;

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RESULT 44
B69096
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J. Bacteriol. 183, 4823-4838, 2001
A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97072
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S46354
R;Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.; EMBO J. 13, 2935-2947, 1994
A;Title: Mosaic genome structure of simian immunodeficiency virus from West African gree A;Reference number: S46335; MUID:94298785; PMID:8026477
A;Accession: S46354
corrinoid/iron-sulfur protein, small subunit - Methanobacterium thermoautotrophicum C_iSpecies: Methanobacterium thermoautotrophicum
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C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97072
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C;Superfamily: Mg-dependent DNase, TatD type
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A; Residues: 1-252 < KUR>
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A;Experimental source: isolate SABD37; sabaeus monkey
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;Superfamily: pol polyprotein
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6; Conserv
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Pred. No. 52;
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Search completed: September Job time: 11.6763 secs

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A; Fitle: Isolation of a Miller-Dieker lissencephaly gene containing A; Reference number: $36113; MUID:93361119; PMID:8355785
A; Accession: $36113
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1409 < RAS>
C; Genetics:
C; Genetics:
C; Genetics: TI-10
C; Superfamily: WD repeat homology < WD1>
F; 103-116/Domain: WD repeat homology < WD1>
F; 145-178/Domain: WD repeat homology < WD1>
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C;Accession: B69096
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
J. Bacteriol. 179, 7135-7155, 1997
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S36113
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C;Superfamily:
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A;Accession: B69096
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R;Reiner, O.; Carrozzo, R.; Shen, Y.; Wehnert,
Nature 364, 717-721, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIS-1 protein - human
C;Species: Homo sapiens (man)
C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
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A; Residues: 1-389 < MTH>
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nes 7; Conserv
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355
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nain: WD repeat homology <WD2>
nain: WD repeat homology <WD2>
nain: WD repeat homology <WD3>
nain: WD repeat homology <WD4>
nain: WD repeat homology <WD4>
nain: WD repeat homology <WD5>
nain: WD repeat homology <WD6>
CADDKTLRVW
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                                                                        CADGPTLREW 10
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STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
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Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL; BX294144; CAD74759.1; -.
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STRAIN=1;
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HSSP; P77407; 1PQY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodopirellula baltica.
                                                 GO; GO:0008152; P:metabolism; IEA
                                                                                                                                                                                                                                                 Phyllobacteriaceae;
                                                                                  DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                    NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000194; ATPase_a/bcentre.
InterPro; IPR003169; GYP.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UPROSITE; PS50829; GYF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Planctomycetaceae; Pirellula.
                                    interPro;
                                                                                                  Mesorhizobium loti."
                                                                                                            Complete genome structure
                                                                                                                                                                                                                                                                                                                                                                                                                           175
                    Pro; IPR003673; CAIB_BAI
PF02515; COA_transf_3;
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8; Conser
           proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADGPTLREWIS 12
                                                                                                                                                                                                                                                 Proteobacteria; Alphaproteobacteria; Rhizobiales;
teriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                         loti (Mesorhizobium loti).
                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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AA;
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 42226 MW;
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18,
24,
                                     BAIF.
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Pred. No. 0.94
3; Mismatches
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 64643EBEC8F25518 CRC64;
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475F670F02C78E9B CRC64;
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                                                                                                             symbiotic bacterium
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RESULT 4
Q7QC63
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Q8KJF9
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Matches 9
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Q7QC63;
01-MAR-2004
         EMBL;
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Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J. Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J. Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossb Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson "Comparative sequence analysis of the symbiosis island of Mesorhizobium loti strain R7A.";

M. Bacteriol. 184:3086-3095(2002).
                             Neoptera; Endopterygota; Diptera;
NCBI TaxID=180454;
                                                                                                                              Name=agCG53078; ORFNames=ENSANGG00000018866;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                GO; GO:0008152; P:metabolism; IEA.
InterPro; IPRO03673; CAIB BAIF.
Pfam; PF02515; COA transf 3; 1.
SEQUENCE 389 AA; 42703 MW; 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=R7A;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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01-OCT-2002 (TrEMBLrel. 22, Last seque
01-UN-2003 (TrEMBLrel. 24, Last annot
PUTATIVE RACEMASE/DEHYDRATASE PROTEIN.
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01-OCT-2002
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HSSP; P77407; 1PQY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21999272; PubMed=12003951;
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                                                                           STRAIN=PEST;
                                                                                      SEQUENCE FROM N.A.
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GO:0005524; F:ATP binding;
          preliminary data.
U; AAAB01008859; E
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42.9%;
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Pred. No. 3.
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Pred. No. 3
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IEA.
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Culicoidea; Ano
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onson C.W.;
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Matches 8; Conserv
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InterPro; IPR001719; Prot Kinase.
InterPro; IPR000719; Prot Kinase.
InterPro; IPR000726; S_methyl_trans.
Pfam; PF00069; Pkinase; 1.
Pfam; PF02574; S-methyl_trans; 1.
ProDom; PD000001; Prot Kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
SEQUENCE 1123 AA; 120006 MW; D3CC001D8D4882AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         888
                                                                                                                        "Complete genome sequence and comparative analy microorganism Streptcomyces avermitilis."; Nat. Biotechnol. 2:526-531(2003).

EMBL; AP005042; BAC72938.1; -.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:000355; P:regulation of transcription, InterPro; IPR009471; HTH_ICLR.

InterPro; IPR099058; Wing_hix_DNA_bnd.

Pfam; PF01614; IclR; 1.
                                                                                                                                                                                                                                                                                                                                                      STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
Wigenome sequence of an industrial microorganism Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces avermitilis. Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=SAV5226;
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01-MAR-2004
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01-JUN-2003
                                                                                                 Complete proteome. SEQUENCE 283 AA;
                                                                                                                                                                                                                                        Ikeda H., Ishikawa J., Hanamoto
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                               avermitilis: deducing the ability of metabolites.";
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                                                                                                                                                                                                                                                                  MEDLINE=22608306; PubMed=12692562;
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 CAEGPTTPAVHEWVDF 167
                      CADGPT---LREWISF 13
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                   Acad. Sci. U.S.A. 98:12215-12220(2001).
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75.0%;
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Pred. No.
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                                                                                                   F63B1705578EEE67 CRC64;
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Q9RKM5;
Q1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
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EMBL; AL939118; CAB56383.1; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity
GO; GO:0006355; P:regulation of transcription,
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Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS50937; HTH_MERR; 2
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preliminary data.
EMBL; AAAB01008944; F
                                                                                                                                                                                      ENSANGP00000020769 (Frac
Name=ENSANGG00000018280)
                                                                                                                                                                                                                 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; DNA-binding.
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InterPro; IPR009061; Putativ_DNA_bind
Pfam; PF00376; MerR; 1.
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                         Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ da
-i- CAUTION; The sequence shown here is derived
EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Ho
Neoptera; Endopterygota; Diptera;
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                                                                                                                             NCBI_TaxID=180454;
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RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA ROYA., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex I.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
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InterPro: IER003726; S methyl_trans.
Pfam; PF02574; S-methyl_trans; 1.
NON TER 1.
SEQÜENCE 347 AA; 38585 MW; 66FP58A1000CDA4F CRC64;
                                                                                   Q8C4M6;
          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:Cl30070D15 product:unclassifiable, full insert
sequence
                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 1
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                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Head;

MEDLINB=20530913; PubMedc1107886; DOI=10.1101/gr.152600;

MEDLINB=20530913; PubMedc1107886; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yoneda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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Nature 420:563-573(2002).
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length CDNA cloning.";
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=20499774; PubMed=11042159; DOI=10.1101/gr.145100;
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303:19-44(1999).
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52.9%;
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   Score 45;
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                                      Length 173;
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Matches 9
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                                                                                             MEDLINE-21681879; PubMed=11823852; DOI=10.1038/415497a; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
PROBABLE TRANSCRIPTION REGULATOR PROTEIN.
Name=RS04642; OrderedLocusNames=RSc1360;
Ralstonia solanacearum (Pseudomonas solanacearum).
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STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707; DOI=10.1038/nbc923;
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Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=RPA4277;
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05-JUL-2004
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EMBL; AL646064; CAD15062.1; HSSP; Q9WXC7; 1IXC. GO; GO:0003700; F:transcript
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=GMI1000;
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EMBL; BX572606; CAE29718.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkholderiaceae;
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InterPro; IPR000357; HEAT.
Pfam; PF02985; HEAT; 2.
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GO:0003700; F:transcription
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llarity 50.0%;
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Q9P858;
01-OCT-2000
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Pfam; PF03466; LysR_substrate; 1.
PROSITE; PS50931; HTH_LYSR; 1.
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Q6QHD2;
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Pleosporales; Phaeosphaeriaceae;
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             Submitted (FEB-2004) to the EMBL; AY541676; AAS48543.1;
                                                 SEQUENCE FROM N.I.
Villarreal L.Y.,
D'elboux A.N.;
                                                                                                                                                                                                      P32 (Fragment)
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                                                                                                                                                 Viruses; dsDNA viruses,
Alphaherpesvirinae; Ilt
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Pred. No. 36;
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                                                                           Doretto L.J.,
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05-JUL-2004 (TrEMBLrel.:
05-JUL-2004 (TrEMBLrel.:
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Hypothetical protein SCO2976.
ORFNames=SCE50.04c;
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Perreira C.A., Ferreira A.J.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ
EMBL; AY598339; AAT09767.1; -
InterPro; IPR003363; Herpes_gG.
InterPro; IPR003163; Herpes_gG.
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Viruses; dsDNA viruses, no RN7
Alphaherpesvirinae; Iltovirus.
RCBI_TaxID=10386;
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Seeger
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173 AA;
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178 AA;
Saunders D.,
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Hopwood D.A.;
"Complete genome sequence of the maccelicolor A3(2)";
Nature 417:141-147(2002).
EMBL; AL939114; CAB87326.1;
Complete proteome; Hypothetical particular proteome; Hypothetical particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particular particu
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EMBL; U2883; AEC55098.1; -.
InterPro; IPR003363; Herpes gG.
InterPro; IPR007110; Ig-like.
Pfam; PP02400; Herpes gG; 1.
SEQUENCE 292 AA; 31696 MW;
SEQUENCE FROM N.A.
MEDLINE=94075939; PubMed=8212855; DOI=10.1016/0168-1702(93)90054-Q;
Kongsuwan K., Johnson M.A., Prideaux C.T., Sheppard M.;
Kongsuwan K., an infectious laryngotracheitis virus gene encod
"Identification of an infectious laryngotracheitis virus gene encod
an immunogenic protein with a predicted M(r) of 32 kilodaltons.";
                                                                                                                                                                              Viruses; dsDNA viruses, Alphaherpesvirinae; Ilt. NCBI_TaxID=10386;
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Gallid herpesvirus 1.
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Gallid herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Best Local
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PHS2_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Desiree; TISSUE=Leaf;
MEDLINE=95201249; PubMed=7894019;
Sonnewald U., Basner A., Greve B., Steup M.;
Sonnewald U., Basner A., Greve B., Steup M.;
"A second t-type isozyme of potato glucan phosphorylase: cloning, antisense inhibition and expression analysis.";
Plant Mol. Biol. 27:567-576 (1995).
-i- FUNCTION: Phosphorylase is an important allosteric enzyme in carbohydrate metabolism. Enzymes from different sources differ their regulatory mechanisms and in their natural substrates.
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; S66009, AAB28457.1; -.

InterPro; IPR003363; Herpes gG.

InterPro; IPR007110; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                Allosteric enzyme; Amyloplast; Carbohydrate Glycosyltransferase; Multigene family; Pyrid Transferase; Transit peptide.
                                                                                                                                                                                                                                                                          EMBL; X73684; CAA520;
PIR; S53489; S34189.
HSSP; P06738; 1YGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4113;
                                                                                                                                                                            InterPro; IPR000811; Glyco_trans_35.
Pfam; Pr00343; Phosphorylase; 1.
PIRSE; PIRSF000460; Pprylas Glgp; 1.
PROSITE; PS00102; PHOSPHORYLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-OCT-2094 (Rel. 45, Last annotation update)
Alpha-1,4 glucan phosphorylase, L-2 isozyme, chloroplast precursor (EC 2.4.1.1) (Starch phosphorylase L-2).
     BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
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7; Conserv
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     820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               all known phosphorylases share catalytic
                                                      82
                                                                                                                                                                                                                                                                                                                               CAA52036.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes_gG; 1.
AA; 32325 MW;
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                                                    81
974
     820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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Pred. No.
  Chloroplast
Alpha-1,4 gli
isozyme.
Pyridoxal ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           737E428E3CBA4215 CRC64;
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     phosphate
                                                    glucan
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ucan phosphorylase,
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     (By similarity)
                                                                                                                             phosphate;
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                                                                                                                                                                                                                     RESULT
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Ha Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Ha Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
Hantraye F., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Hantraye F., Koszul R., Catas S., Ozier-Kalogeropoulos O.,
Hantraye F., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Pellenz S., Potier S., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T., Genome and M. C., Strander M., Thierry A.,
Thierry A.,
Thierry A., Wicker P., Soudet J.L.,
Thierry A., Wicker P., Soudet J.L.,
Thierry A., Wicker P., Soudet J.L.,
Thierry M., Wincker P., Soudet J.L.,
Thierry A., Wincker P., Wincker P., Wincker P., Wincker P., 
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches
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Best Local (
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Q8AY57;
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6BI26;
Name=ATP1A2;
Fundulus heteroclitus (Killifish) (Mummichog).
Fundulus heteroclitus (Cordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ
EMBL; CR382139; CAG90631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales;
NCBI_TaxID=284592;
                                                                                Sodium/potassium
                                                                                                01-MAR-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CBS767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Debaryomyces hansenii CBS767.
Bukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORFNames=DEHA0G14795g;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 430:35-44(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                               LREWFSFC
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997 AA; 112803
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                                                                                                                                                                                                                                                                                                                                                        51.8%;
ilarity 87.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation updat
CA6145|IPF1869 Candida albicans IPF186
                                                                           (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 26, Last annotation updat
spium ATPase alpha subunit isoform 2.
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                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                      14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110700 MW;
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MW;
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Pred. No. 1.2e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             Score 44;
Pred. No.
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                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                           core 44; DB 2; I red. No. 1.3e+02; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5EF8A23C237463D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           3C05D6EAFF05875C CRC64;
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                                                                              tation update) isoform 2.
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IPF1869.
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                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weissenbach J.,
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Best Local S
Matches
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R GO; GO:0005890; C:sodium:potassium-exchanging ATPase complex; ISS.
R GO; GO:0005891; F:sodium:potassium-exchanging ATPase activity; ISS.
R GO; GO:0005891; F:ATP hydrolysis coupled proton transport; ISS.
R GO; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.
R GO; GO:0030641; P:hydrogen ion homeostasis; ISS.
R GO; GO:0006813; P:potassium ion transport; ISS.
R GO; GO:0006814; P:sodium ion transport; ISS.
R InterPro; IPR006069; Cation_ATPase_C.
InterPro; IPR006069; Cation_ATPase_C.
InterPro; IPR006069; Cation_ATPase_C.
InterPro; IPR006069; Cation_ATPase_reg.
InterPro; IPR005834; Debal like hydro.
R InterPro; IPR005835; Debal like hydro.
R InterPro; IPR005836; E1-E2_ATPase_reg.
InterPro; IPR005836; Cation_ATPase_L.
R Ffam; PF00690; Cation_ATPase_C; I.
Pfam; PF00690; Cation_ATPase_C; I.
R Pfam; PF00690; Cation_ATPase_N; 1.
Pfam; PF00122; E1-E2_ATPase_N; 1.
R Pfam; PF00122; E1-E2_ATPase_N; 1.
R Pfam; PF00122; Mydroflase; I.
R Pfam; PF00121; Mydroflase; I.
R PRINTS; PR001116; CATATPASE.
R PRINTS; PR00121; MAKATPASE.
R PRINTS; PR00121; MAKATPASE.
PubMed=14610032;
Richards J.G., Semple J.W., Bystriansky J.S., Scillahards J.G., Semple J.W., Bystriansky J.S., Scillahards J.G., Arpase alpha-isoform switching in gi. "Na(+)/K(+)-Arpase alpha-isoform switching in gi."
(Oncorhynchus mykiss) during salinity transfer."
J. Exp. Biol. 206:4475-4486(2003).
EMBL; AY319388; AAQ82787.1; -.
EMBL; AY319388; AAQ82787.1; -.
EMSL; AY319388; AAQ82787.1; -.
EMSL; GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6VYM7;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Na/K ATPase alpha subunit isoform 3.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii, Meopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRRAMS; TIGRO1106; ATPASE P-LYDE; ATPASE E P-LYDE; ATPASE EL E2; UNKNU SEQUENCE 1008 AA; 111293 MW; EA3/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Cyprinodontiformes; Fundulidae; Fundulus.
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                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6VYM7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.30); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNKNOWN 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EA3A7CED8E33E037 CRC64;
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smatches 3;
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                                                                                                                                                         transfer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
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                                                                                                                                                                                     Schulte P., gills of r
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ATPase activity; ISS
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                                                                                                                                                                                            rainbow
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AT1A TORCA
P05025;
13-AUG-1987
13-AUG-1987
                                                                                                                                                                                                                                                         Nature 316:733-736(1985)
           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=85296307; PubMed=2993905; Kawakami K., Noguchi S., Noda M., Takahas
                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; (
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea;
Torpediniformes; Torpedinoidei; Torpedinidae; Torped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sodium/potassium-transporting ATPase alpha chain precursor (EC 3.6.3.9) (Sodium pump alpha chain) (Na+/K+ ATPase alpha chain).
Torpedo californica (Pacific electric ray).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TORCA
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PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN
SEQUENCE 1011 AA; 111140 MW; 06D12F
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                                                                                                                                                                                                                                                                                       Numa S.; "Primary structure of the alpha-subunit from cDNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                          Torpediniformes;
NCBI_TaxID=7787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO01119; CATATPASE.
PRINTS; PR00121; NAKATPASE.
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                                                                                                                                                                                                                                                                                                                                   Nojima H.,
                                                                                                    gamma.
SUBCELLULAR LOCATION:
SIMILARITY: Belongs to
                                                                                                                                                 providing the energy for active transport of CATALYTIC ACTIVITY: ATP + H(2)O + Na(+)(In) phosphate + Na(+)(Out) + K(+)(In). SUBUNIT: Composed of three subunits: alpha
                                                                                                                                                                                                           FUNCTION: This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions,
                                                                                      SIMILARITY: Belongs to the ATPases). Subfamily IIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
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                                                                                                                                                                                                                                                                                                                                    K., Hirose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
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70.0%;
                                                                                                      Integral mem
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                   Takahashi H
Inayama S.,
                                                                                                                                                                                                                                                                                                                                    Inayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06D12FA68A23456C CRC64;
                                                                                                      membrane prot
ion transport
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ic cation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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InterPro; IPR006068; Cation_ATPASE_C.
InterPro; IPR006068; Cation_ATPASE_C.
InterPro; IPR004014; Cation_ATPASE_N.
InterPro; IPR005334; Dehal Tike_hydro.
InterPro; IPR005394; Dehal Tike_hydro.
InterPro; IPR008250; E1-E2_ATPASE_reg.
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Pfam; PF00639; Cation_ATPASE_C; I.
Pfam; PF00122; E1-E2_ATPASE_N; 1.
Pfam; PF00126; E1-E2_ATPASE_N; 1.
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Cytoplasmic (Potential).
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     25-JAN-2005 (Rel. 46, Last annotation update) Sodium/potassium-transporting ATPase alpha-1 ch (EC 3.6.3.9) (Sodium pump 1) (Na+/K+ ATPase 1). Name=ATP1A1;
TISSUE=Placenta;
MEDLINE=88068506; PubMed=2891135;
Chehab F.F., Kan Y.W., Law M.L., Hartz J., Kao
"Human placental Na+,K+-ATPase alpha subunit: c
"Human placental Na+,K+-ATPase alpha chromosomal l
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Mammalia; Eutheria;
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Petrukhin K.E.,
                                                    SEQUENCE OF 198
TISSUE=Placenta
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155:179-184(1995).
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RA Strausberg R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D.,
RA Altschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bolkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Maraa M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT proc Natl Asad Schi U.S. A 00.16001-16001/7002)
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MEDILINE=87057096; PubMed=2430951;

Kawakami K., Ohta T., Nojima H., Nagano
"Primary structure of the alpha-subunit
from cDNA sequence.";
                                                                                                                                                                                                                                                                                        SEQUENCE OF 253-341 AND 420-444 FROM N.A.
SEQUENCE OF 253-341 AND 420-444 FROM N.A.
MEDLINE=87247232; PubMed=3036582; DOI=10.1016/0014-5793(87)80677-4;
MEDLINE=8 R12.4 R548493 G.S.; Broude N.E., Ushkaryov Y.A.,
Allikmets R.L., Melkov A.M., Smirnov Y.V., Malyshev I.V.,
Dulubova I.E., Petrukhin K.E., Gryshin A.V., Kiyatkin N.I.,
Kostina M.B., Sverdlov V.E., Modyanov N.N., Ovchinnikov Y.A.;
"The family of human Na+,K+-ATPase genes. No less than five genes
and/or pseudogenes related to the alpha-subunit.";
FEBS Lett. 217:275-278(1987).
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TISSUE=Brain, Cervix, and Skin;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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MEDLINE=95237606; PubMed=7536695; DOI=10.1016/0378-1119(94)00812-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Amino acid sequence of the 17-kilodalton fra region of the alpha-subunit of NA+,K+-ATPase. pokl. Biochem. 288:270-272(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .A., Monastyrskaya G.S., Arsenyan
., Grishin A.V., Arzamazova N.M.,
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o F.T., Blostein R.; cDNA cloning, tissue localization.";
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Severtsova
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Shull M.M., Lingrel J.B.;
"Multiple genes encode the human Na+,K+-ATPase catalytic subunit.";
"Multiple genes encode the human Na+,K+-ATPase catalytic subunit.";
"Multiple genes encode the human Na+,K+-ATPase catalytic subunit.";
"Multiple genes encode the human Na+,K+-ATPase catalytic subunit.";
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"The human Na, K-ATPase alpha 1 gene: characterization of the 5'-
flanking region and identification of a restriction fragment lengt
polymorphism.";
                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
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Genome Biol. 5:RESEARCH008.1-RESEARCH008.16 (2004).

-I-FUNCTION: This is the catalytic component of the active enzyme, which catalytes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions, providing the energy for active transport of various nutrients.

-I-CATALYTIC ACTIVITY: ATP + H(2)0 + Na(+)(In) + K(+)(Out) = ADP +
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Zhang J.-S., Yan
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               L; U16798; AACS0131.1; -.
L; BC003077; AAH03077.1; -.
L; BC003397; AAH0307.1; -.
L; BC003399; AAH50355.1; -.
L; X047297; CAA273940.1; -.
L; X03757; CAA27390.1; -.
L; M27579; AAA35573.1; -.
L; M27579; AAA35574.2; -.
L; M27579; AAA35574.2; -.
L; M27579; AAA35574.1; -.
L; M30301; AAA51803.1; -.
L; M30301; AAA51801.1; JOINED.
L; M16793; AAD56252.1; -.
L; M16794; AAD56252.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SIMILARITY: Belongs to the cation transport ATPases family (P-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate + Na(+) (Out) + K(+) (In). SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATPases). Subfamily IIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                             D00099; BAA00061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note=May be produced at ver codon in the mRNA, leading
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Note=May be produced at very low levels due to a premature stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P05023-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6:451-460(1990).
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A24414
                                                                                                                                                                                                                                                                                                                                                                                                                                                license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tyr-10 modulates
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Matches 7
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InterPro; IPR00609; Cation_ATPase_C.
InterPro; IPR006089; Cation_ATPase_C.
InterPro; IPR004014; Cation_ATPase_N.
InterPro; IPR005834; Dehal_Tike_hydro.
InterPro; IPR005834; Dehal_Tike_hydro.
InterPro; IPR005836; E1-E2_ATPase_reg.
InterPro; IPR005775; Na/K_ATPase_alph.
Pfam; PF00689; Cation_ATPase_C; I.
Pfam; PF00689; Cation_ATPase_N; 1.
Pfam; PF00690; Cation_ATPase_1.
Pfam; PF00690; Cation_ATPase_1.
Pfam; PF00702; Hydrolase; 1.
Pfam; PF00712; E1-E2_ATPase; 1.
                                                                                                                   Q7ZYK8
Q7ZYK8;
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TRANSMEM
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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GO; GO:0005890; C:sodium/potassium-exchanging ATPase complex; I.
GO; GO:0005391; F:sodium/potassium-exchanging ATPase activity;
GO; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.
GO; GO:0010641; P:hydrogen ion homeostasis; ISS.
GO; GO:0006813; P:potassium ion transport; ISS.
GO; GO:0006814; P:sodium ion transport; ISS.
GO; GO:0006814; P:sodium ion transport; ISS.
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Genew; HGNC:799; ATP1A1.
H-InvDB; HIX0000926; -.
MIM; 182310; -.
                                                                              01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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TIGRPAMS; TIGRO1494; ATPASE_P-type; 5.
PROSITE; PS00154; ATPASE_E1_E2; 1.
Alternative splicing; ATP-binding; Hydrolase; Magnesium;
                                                                Atpla3-prov protein.
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PRINTS; PR00121; NAKATPASE.
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                                                                                            Last sequence update)
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Cytoplasmic (Potential)
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                                          Craniata; Vertebrata; Euteleostomi;
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KILein S., Strausberg R.;

KILein S., Strausberg R.;

KILein S., Strausberg R.;

KMBIL; BC043743; AAH43743.1; -.

KMBIL; BC043743; AAH43743.1; -.

RMBIL; BC043743; AAH43743.1; -.

RGO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016562; F.ATP binding; IEA.

GO; GO:0005562; F.ATPase activity; coupled to transmembrane m. ..

RGO; GO:0016562; F.ATPase activity; IEA.

GO; GO:0016787; F:hydrolase activity, acting on acid anhydrid. ..

RGO; GO:001677; F:monovalent inorganic cation transporter act. ..

RGO; GO:001577; F:monovalent inorganic cation transporter act. ..

RGO; GO:001577; F:monovalent inorganic cation transport; IEA.

GO; GO:001577; F:monovalent inorganic cation transport; IEA.

RGO; GO:001577; F:monovalent inorganic cation transport; IEA.

RGO; GO:001577; ATPase E1-E2.

RGO; GO:001577; ATPase C.

RINterPro; IPR0050669; Cation ATPase C.

RINterPro; IPR0050669; Cation ATPase reg.

RINterPro; IPR008250; E1-E2 ATPase reg.

RINterPro; IPR008250; E1-E2 ATPase alph.

RGO; GO:00122; E1-E2 ATPase [1]

RFAm; PF00690; Cation ATPase [1]

RFAm; PF00690; Cation ATPase [1]

RFAM; PF00690; Cation ATPase [1]

RRANTS; PR00112; E1-E2 ATPase; 1.

RRANTS; PR00119; CATATPASE; 1.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Millalon D.K., Muzny D.M., Green B.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kornes G. T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,

Kornes G. T. Malek U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                 Query Match
Best Local
Matches
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TIGRAMS; TIGRO1494; ATPASE P-type; 4.
PROSITE; PS00154; ATPASE E1_E2; UNKNOWN 1.
SEQUENCE 1025 AA; 112954 MW; FA0C021193F5288E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00122; E1-E2 ATPase
Pfam; PF00702; Hydrolase; 1
PRINTS; PR00119; CATATPASE
PRINTS; PR00121; NAKATPASE
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Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifto
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86
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                                                                                                                                                                 Similarity
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0; Mismatches
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DR HSSP; P6685; 1MO7.

DR RGD; 61952; Atpla4.

DR GO; GO:0005391; F:sodium/potassium-exchanging ATPase complex; ISS.

GO; GO:0005391; P:ATP hydrolysis coupled proton transport; ISS.

DR GO; GO:0005391; P:ATP hydrolysis coupled proton transport; ISS.

DR GO; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.

DR GO; GO:0030641; P:hydrogen ion homeostasis; ISS.

DR GO; GO:0030813; P:sperm motility; ISS.

DR GO; GO:0030317; P:sperm motility; ISS.

DR GO; GO:0030317; P:sperm motility; ISS.

DR GO; GO:0030317; P:sperm motility; ISS.

DR InterPro; IPR006069; Cation_ATPase C.

InterPro; IPR006069; Cation_ATPase C.

DR InterPro; IPR006069; Cation_ATPase C.

DR InterPro; IPR005834; Dehal_Tike_hydro.

DR InterPro; IPR005834; Dehal_Tike_hydro.

DR InterPro; IPR005834; Dehal_Tike_hydro.

DR InterPro; IPR0058375; NaK,ATPase alph.

Pfam; PF00689; Cation_ATPase C; I.

Pfam; PF00689; Cation_ATPase N; 1.

Pfam; PF00689; Cation_ATPase N; 1.

Pfam; PF0012; Hydrolase; 1.

DR Pfam; PF0012; Hydrolase; 1.

DR PRINTS; PR00112; CATATPASE.

DR PRINTS; PR00112; NAKATPASE.

DR PRINTS; PR00112; NAKATPASE.

DR PRINTS; PR00114; ATPase PI-CX-K; 1.

DR PRINTS; PR00114; ATPase PI-CX-K; 1.

DR PROSITE; PS00154; ATPASE EI-E2; 1.

DR PROSITE; PS00154; ATPASE EI-E2; 1.

DR PROSITE; PS00154; ATPASE EI-E2; 1.

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Q64541;
16-OCT-2001
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STRAIN-Sprague-Dawley; TISSUE=Testis;
MEDLINE=95108076; PubMed=7809153;
Shamzaj O.I., Lingrel J.B.;
The putative fourth Na+, K(+)-ATPase alpha-subunit gene
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05-JUL-2004 (Rel. 44, Last annotation update)
Sodium/potassium-transporting ATPase alpha-4
(Sodium pump 4) (Na+/K+ ATPase 4).
Name=Atpla4; Synonyms=Atpla12;
Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the cation transport ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions,
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Sciurognathi; Muridae; Murinae; Rattus.
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Gene 251:81-90(2000).
EMBL; AF235504; AAF86384.1; -.
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No.
                                                                                                                                                                                                                                                                                                                      DOI=10.1016/S0378-1119(00)00171-2;
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RESULT 28
Q9N0Z5
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Q9NEX6
ID Q9
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Best Local S
Matches 8
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                                                                                                                                                                                                                              Q9N0Z5
Q9N0Z5;
01-OCT-2000
01-MAR-2004
01-MAR-2004
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Q9NEX6;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein Trems.
Hendrickx J., Fransen P.;
submitted (SEP-2003) to the
EMBL; AF235025; AAF60311.2;
GO; GO:0016020; C:membrane;
GO; GO:0015662; F:ATPase act
                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Na/K ATPase alpha 2 subunit (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Oryctolagus.
                                                                                              MEDLINE=21600302; PubMed=11738066; DOI=10.1016/S0008-6363(01)00412-6; Fransen P., Hendrickx J., Brutsaert D.L., Sys S.U.; Piatribution and role of Na(+)/X(+) ATPase in endocardial endothelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein Y105E8A.21. ORFNames=Y105E8A.21;
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
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                                                                                                                                               SEQUENCE FROM
                                                                                     Cardiovasc. Res.
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57.1%;
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                                     EMBL/GenBank/DDBJ
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Pred. No. 1.5e
2; Mismatches
                IEA
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Best Local S
Matches 6
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Best Local S
Matches 6
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016820; F:hydrolase activity, acting on a GO; GO:0016820; F:hydrolase activity, acting on a GO; GO:0005391; F:sodium:potassium-exchanging ATI GO; GO:0006812; P:cation transport; IEA.
InterPro; IPR006099; Cation ATPase.
InterPro; IPR008250; Cation ATPase N.
InterPro; IPR008250; E1-E2_ATPase reg.
Pfam; PF00629; Cation ATPase; 1.
Pfam; PF00122; E1-E2_ATPase; 1.
PRINTS; PR00121; NAKATPASE.
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Q8HYW6;
01-MAR-2003
                                                          Q866A9;
01-JUN-2003
01-JUN-2003
01-MAR-2004
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InterPro; IPR004014; Cation ATPase N.
Pfam; PF00690; Cation ATPase_N; 1.
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TISSUE-Adrenal medulla;
Benavides A.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                  Alphal subunit of equine Na/K Equus caballus (Horse).
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    Eukaryota;
                                                                                                                                           Q866A9
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase.
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171
171 AA;
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127 AA;
    Metazoa; Chordata; Craniata;
                                                          (TrEMBLrel. 24, (TrEMBLrel. 24, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                         Conservative
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Cetartiodactyla;
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Last sequence update)

Last annotation updat

//K ATPase (Fragment).
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Pred. No.
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actyla; Ruminantia; Pec
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    Vertebrata;
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Pecora; Bovidae;
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    Euteleostomi;
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activity; IEA.
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GO; GO:0016620; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0015662; F:ATPase activity, coupl
GO; GO:0016820; F:hydrolase activity, ac
GO; GO:0006812; P:cation transport; IEA.
Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaki M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
                                                                                                                                                                                                                                                            Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P., Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=F1I16_30; Synonyms=At3g55620;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (APR
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Lemcke K., Mayer K.F
Submitted (MAR-2000)
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          Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
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Q9VK55;
01-MAY-2000
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Park S., Wan K., Yu C., Rubin G.M., Celniker S.;

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ da

EMBL; BT011561; AAS15697.1; -

INTERPRO, IPRO00345; CYTCCHROME C; UNKNOWN 1.

PROSTITE; PS00190; CYTOCHROME C; UNKNOWN 1.

SEQUENCE 407 AA; 46390 MW; BFAC2D74079EE009
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HSSP; Q12522; 1G62.
GO: GO:0003743; Fitranslation initiation factor
GO; GO:0006413; Pitranslational initiation; IEA.
                                                                                                                                                                  01-MAY-2000
01-MAR-2004
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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SMART; SM00654; eIF6;
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHaon D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Spier E., Sjeden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.",

RY The genome sequence of Drosophila melanogaster.",
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                                                             MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S. Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman E Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                        Stapleton M.,
Lewis S.E.;
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                                                                                                                                                                                                                                                                                          Ashburner M., Celniker S.E.;
"The transposable elements of the a genomics perspective.";
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                  Drosophila melanogaster
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Q37839;
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[5]
SEQUENCE FROM
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004270;
01-JUL-1997
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ThterPro: IPR000345; Cytc heme BS.
PROSITE; PS00190; CYTCCHROME C; UNKNOWN 1.
SEQUENCE 407 AA; 46420 MW; BFAC2105079EE508 CRC64;
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Name=ORF469;
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NCBI_TaxID=10732;
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Takahashi H., Shirai M.;
"The sre gene (ORF469) encodes a site-specific
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"A gene essential for the site-specific excision of
prophage genome from the chromosome of a lysogen.";
J. Gen. Appl. Microbiol. 41:53-61(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for integration of the R4 phage genome.",
J. Bacteriol. 178:3374-3376(1996).
EMBL; D38173; BAA07372.1;
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Best Local
SEQUENCE FROM N.A.

STRAIN=(57BL/6J; TISSUE=Eyeball;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Gr
"Analysis of the mouse transcriptome bas
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
[4]
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Q8BIG9;
01-MAR-2003
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched
library, clone:E130306F09 product:NA,K-ATPASE ALPHA 1 ISOFORM (EC
3.6.1.37) homolog.
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Bukaryota; Viridiplantae; Chlorophyta; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/63; TISSUE=Eyeball;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-le
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"Inositide signalling in Chlamydomonas:
phosphatidylinositol 3-kinase gene.";
Plant Mol. Biol. 37:53-66(1998).
                                                                                                                                                                                            Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Eyeball;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
[1]
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                                                                                                             Nature 409:685-690(2001).
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GO:0016301; F:kinase activity; IEA.
GO:0016303; F:phosphatidylinositol
cerpro; IPR008973; C2 CalB.
cerpro; IPR002420; PI3K_C2.
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Rodentia;
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Pred.
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Sciurognathi; Muridae;
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                                                                                                                                                  DOI=10.1038/35055500;
                                                                                                                                                                                                                                  DOI=10.1016/S0076-6879(99)03004-9;
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                                         annotation
                                                    Team;
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RA Fukuda S., Furuno M., Haragaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Okazaki Y.,
RA Saito R., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RI Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

RA GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015024; F:ATP binding; IEA.
GO; GO:001562; F:hydrolase activity, IEA.
GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. ..; IE.
GO; GO:0016812; P:cation transport; IEA.
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Best Local S
Matches 6
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GO; GO:0015524; F:ATP binding; IEA.
GO; GO:0015622; F:ATPase activity, coupled to t
GO; GO:0015620; F:hydrolase activity, acting or
GO; GO:0016820; F:hydrolase activity, acting or
GO; GO:0016812; P:cation transport; IEA.
InterPro; IPR005.757; ATPase E1-E2.
InterPro; IPR006069; Cation_ATPase.
InterPro; IPR00614; Cation_ATPase_N.
InterPro; IPR008250; E1-E2_ATPase_N.
InterPro; IPR008250; E1-E2_ATPase_N.
Pfam; PF00122; E1-E2_ATPase_N; 1.
Pfam; PF00122; E1-E2_ATPase; 1.
Q80UZ8;
Q80UZ8;
01-JUN-2003
01-JUN-2003
01-MAR-2004
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PROSITE; P
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STRAIN-C57BL/6J; TISSUE=Eyeball;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUE=Eyeball;
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STRAIN=C57BL/6J; TISSUE=Eyeball;
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PS00154; ATPASE_E1_E2; UNKNOWN_1.
509 AA; 55779 MW; 132C342CA9000E97
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MGD; MGD; MGD; AED1a2.

MGD; GO:0005990; C:sodium:potassium-exchanging ATPase complex; ISS.

MGO; GO:0005931; F:sodium:potassium-exchanging ATPase activity; ISS.

MGO; GO:0005391; F:ATP hydrolysis coupled proton transport; ISS.

MGO; GO:001591; P:ATP hydrolysis coupled proton transport; ISS.

MGO; GO:0001504; P:hydrogen ion homeostasis; ISS.

MGO; GO:0006134; P:hodium ion transport; ISS.

MGO; GO:0006814; P:sodium ion tr
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

Bosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Altschul S.F., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Altalalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Altalaley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Korzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Karywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                              PROSITE;
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TIGREAMS; TIGRO1494; ATPASE_E1_E2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2002) to the EMBL; BC041774; AAH41774.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CZECH II; TISSUE=Mammary tumor; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Mammalia; Eutheria;
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Name=Atpla2;
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Rodentia;
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XX MEDLINE-Z2388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
XX MEDLINE-Z2388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
XX Altausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
XX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altaches S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
XX Altaches S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XX Altaches S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XX Altaches S., Worley C., Shevchenko Y., Bouffard G.G.,
XX Altaches B., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,
XX Altaches B., Worley G., Shevchenko Y., Bouffard G.G.,
XX Blakes B.Y. W., Touchman J.W., Green B.D., Dickson M.C.,
XX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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Q91YY9;
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Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
""" Acad. Sci. U.S.A. 99
                                                                                                                                                                                                                                                                                                 PRINTS; PR00119; CATATPASE.
PRINTS; PR00121; NAKATPASE.
TIGREAMS; TIGR01106; ATPASE-IIC_X-K; 1.
TIGREAMS; TIGR01494; ATPASE_E1_E2; UNKNOWN_1.
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Pfam; PF00689; Cation_ATPase_N; 1.
Pfam; PF00689; Cation_ATPase_N; 1.
Pfam; PF00702; Hydrolase; 1.
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STRAIN=Czech II; TISSUE=Mammary
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01-MAR-2004 (TrEMBLrel.
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STRAIN=Czech II; T
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                                                                                                              Conservative
                                                                                                                                                                                                                                                                               protein.
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                                                                                                                                         Score 43; DB 2;
Pred. No. 1.8e+0
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                                                                                                                 Mismatches
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ATPase activity; ISS
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DR HSSP; P06685; 1MO8.

DR HSSP; P06685; 1MO8.

DR GO; GO:0005890; C:sodium:potassium-exchanging ATPase complex; ISS.

DR GO; GO:0005391; F:sodium:potassium-exchanging ATPase activity; ISS.

DR GO; GO:0005391; F:sodium:potassium-exchanging ATPase activity; ISS.

DR GO; GO:0005391; P:ATP hydrolysis coupled proton transport; ISS.

DR GO; GO:0006813; P:potassium ion transport; ISS.

DR GO; GO:0006813; P:potassium ion transport; ISS.

DR GO; GO:0006814; P:sodium ion transport; ISS.

DR GO; GO:0006814; P:sodium ion transport; ISS.

DR GO; GO:0006817; P:sperm motility; ISS.

DR GO; GO:0006817; P:sperm motility; ISS.

DR InterPro; IPR006068; Cation_ATPase_C.

InterPro; IPR006068; Cation_ATPase_reg.

InterPro; IPR008250; E1-E2_ATPase alph.

DR Pfam; PF00689; Cation_ATPase_N; 1.

DR Pfam; PF00690; Cation_ATPase_N; 1.

DR Pfam; PF00122; E1-E2_ATPase; 1.

DR Pfam; PF00702; Hydrolase; 1.

DR Pfam; PF00702; Hydrolase; 1.
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01-OCT-2003
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Electrophorus electricus (Electric eel).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Electrophoridae; Electrophorus.
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Q98SL3; PRELIMINARY;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR, 2004 (TrEMBLrel. 26,
                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Electric organ;
MEDLINE=98068871; PubMed=9405797;
Kaya S., Yokoyama A., Imagawa T.,
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Mammalia; Eutheria;
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; TIGRO1494; ATPASE_P-type; 3.
PS00154; ATPASE_EI_E2; UNKNOWN 1.
PS00154; ATPASE_EI_E2; UNKNOWN 1.
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                                       eel electroplax Na+,K(+)-ATPase
. Sci. 834:129-131(1997).
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SIMILARITY: Belongs to t ATPases). Subfamily IIC.

the cation transport ATPases family (P-type

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InterPro; IPR006069; Cation_ATPASE.
InterPro; IPR006069; Cation_ATPASE.
InterPro; IPR006068; Cation_ATPASE_C.
InterPro; IPR006068; Cation_ATPASE_N.
InterPro; IPR005834; Dehal_Tike_hydro.
InterPro; IPR005836; E1-E2_ATPASE_reg.
InterPro; IPR005850; E1-E2_ATPASE_alph.
Pfam; PP00609; Cation_ATPASE_C; I.
Pfam; PP00609; Cation_ATPASE_N; 1.
Pfam; PP007012; E1-E2_ATPASE_N; 1.
Pfam; PP007012; E1-E2_ATPASE.
PRINTS; PR00119; CATATPASE.
PRINTS; PR00119; CATATPASE.
PRINTS; PR00121; NAKATPASE.
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H8SP; P06685; 1M07.
GO; GO:0016021; C:integral to
GO; GO:0005524; F:ATP binding
GO; GO:0015662; F:ATPase acti
GO; GO:00156787; F:hydrolase a
GO; GO:0016820; F:hydrolase a
GO; GO:0015977; F:monovalent
GO; GO:0001577; P:monovalent
GO; GO:0001577; P:monovalent
GO; GO:00101577; P:monovalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3. (Sodium pump 3) (Na+/K+ ATPase 3) (Alpha(III)).
Name=ATP1A3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.1
TISSUE=Electric of
Kaya S., Yokoyama
                                                 SEQUENCE FROM N.A.

MEDILINB=91023019; PubMed=2171348;

MEDILINB=91023019; PubMed=2171348;

Takeyasu K., Lemas V., Fambrough D.M.;

Takeyasu K., Lemas V., Fambrough D.M.;

"Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.";

Am. J. Physiol. 259:C619-C630(1990).

-!- FUNCTION: This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions, providing the energy for active transport of various nutrients.

-!- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+)(In) + K(+)(Out) = ADP + phosphate + Na(+)(Out) + K(+)(In).

-!- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO1106; ATPASE-IIC_X-K; 1.
TIGREAMS; TIGRO1494; ATPASE_P-type; 4.
PROSITE; PS00154; ATPASE_E1 E2; UKNOWN 1.
SEQUENCE 1009 AA; 110950 MW; F37C78TLA4487577 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
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GO:0016820; F:hydrolase activity, acting of GO:0015077; F:monovalent inorganic cation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0016021; C:integral to membrane; GO:0005524; F:ATP binding; IEA. GO:0015662; F:ATPase activity, coup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0008152; P:metabolism; IEA.
GO:0015672; P:monovalent inorganic
gamma.
SUBCELLULAR LOCATION: Integral membrane protein
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Yokoyama A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB pred. No. 1.9e
1; Mismatches
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Pfam; PF00690; Cation ATPase N; 1
Pfam; PF00122; E1-E2 ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
PRINTS; PR00121; NAKATPASE.
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GO; GO:0005391; F:sodium/potassium-exchanging ATPase activity; ISS.
GO; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.
GO; GO:0030641; P:hydrogen ion homeostas; ISS.
GO; GO:0006813; P:potassium ion transport; ISS.
GO; GO:0006814; P:sodium ion transport; ISS.
GO; GO:0006817; P:sperm motility; ISS.
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DOMAIN
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DOMAIN
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InterPro; IPR006069; Cation ATPase C.
InterPro; IPR006068; Cation ATPase C.
InterPro; IPR004014; Cation ATPase N.
InterPro; IPR008250; E1-E2 ATPase reg.
InterPro; IPR0082775; Na/K_ATPase_alph.
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GO:0030317; P:sperm motility; ISS.
erPro; IPR001757; ATPase_E1-E2.
  Similarity 6; Conserv
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Score 43; DB Pred. No. 1.9e
1; Mismatches
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Magnesium (By simila:
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Binding of phosphoinositide-3
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R InterPro; IPR006068; Cation_ATPase C.
R InterPro; IPR004014; Cation_ATPase N.
R InterPro; IPR004014; Cation_ATPase N.
R InterPro; IPR00823; Dehal_like_hydro.
R InterPro; IPR008250; E1-E2_ATPase_reg.
R InterPro; IPR008250; E1-E2_ATPase_alph.
R Pfam; PF00699; Cation_ATPase_N; 1.
R Pfam; PF00699; Cation_ATPase_N; 1.
R Pfam; PF00122; E1-E2_ATPase; 1.
R Pfam; PF00122; E1-E2_ATPase; 1.
R Pfam; PF00122; E1-E2_ATPase; 1.
R Pfam; PF00122; Hydrolase; 1.
R Pfam; PF00121; NAKATPASE.
R PRINTS; PR00121; NAKATPASE.
R PRINTS; PR00121; NAKATPASE.
R PRINTS; PR00121; NAKATPASE.
R PIGRPAMs; TIGR01949; ATPase P-type; 5.
R TIGRPAMs; TIGR01949; ATPASE_E1-E2; 1.
R TIGRPAMs; TIGR0195; ATPASE_E1-E2; 1.
R PROSITE; PS00154; ATPASE_E1-E2; 1.
R PROSITE; PS00154; ATPASE_E1-E2; 1.
R PROSITE; PS00154; ATPASE_E1-E2; 1.
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R PROSITE; PS00154; ATPASE_E1-E2; 1.
R PROSITE; PS00154; ATPASE_E1-E2; 1.
R PROSITE; PS00154; ATPAS
Phosphorylation;
DOMAIN 1
TRANSMEM 75
DOMAIN 96
TRANSMEM 119
DOMAIN 140
TRANSMEM 276
DOMAIN 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (Stor send an email to license@isb-sib.ch).
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InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR006069; Cation_ATPase
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SUBCELLULAR LOCATION:
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Best Local S
Matches 6
                             EMBL; AY313387; AAQ82786.1; C.

GO; GO:00015021; C:integral to membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000562; F:ATPase activity; coupled to t
GO; GO:0016820; F:ATPase activity; IEA.
GO; GO:00168787; F:hydrolase activity; acting
GO; GO:0016787; F:hydrolase activity, acting
GO; GO:0016970; F:momovalent inorganic cation t
GO; GO:0015077; F:momovalent inorganic cation t
GO; GO:0015672; P:menovalent inorganic cation t
GO; GO:0015672; P:momovalent inorganic cation t
InterPro; IPR006757; ATPase_E1-E2.
InterPro; IPR006069; Cation_ATPase_C.
InterPro; IPR006069; Cation_ATPase_N.
InterPro; IPR006184; Cation_ATPase_N.
InterPro; IPR005834; Dehal like hydro.
InterPro; IPR005834; Dehal like hydro.
InterPro; IPR005775; Na/K_ATPase_alph.
InterPro; IPR005775; Na/K_ATPase_alph.
InterPro; IPR0050504; RNA rec_mot.
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Q6VYM8;
05-JUL-2004
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DOMAIN
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Na/K ATPase alpha subunit isoform 2.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
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DOMAIN
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Richards J.G., Semple J.W., Bystriansky J.S., Sch
"Na(+)/K(+)-ATPase alpha-isoform switching in gil
(Oncorhynchus mykiss) during salinity transfer.";
J. Exp. Biol. 206:4475-4486(2003).
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NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Onco
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            00504; RNA_rec_mot.
Cation_ATPase_C; 1
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Pred. No. 1.9e
1; Mismatches
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Magnesium (By similarity).
MW; 9FEDB07C7547F0D1 CRC64
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Phosphoserine (by PKA) (By sin Binding of phosphoinositide-3 similarity).
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Cytoplasmic
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Cytoplasmic
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RX MEDLINE-22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins N.J., Usdin T.B., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Williamo N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K., Challe S., Garcia A.M., Gibbs R.A.,
RA Richards S., Wadan A., Young A.C., Sheychenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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PROSITE; P
PROSITE; P
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P13637; Q16735; Q969K5;
Q1-JAN-1990 (Rel. 13, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Sodium/potassium-transporting ATPase alpha-3 ch
(Sodium pump 3) (Na+/K+ ATPase 3) (Alpha(III)).
Name=ATP1A3;
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A1A3_I
                                                                                                                                                                                                                                                                                                                                                                                    Sverdlov E.D., Monastyrskaya G.S., Broude N.E., Ushkarev Y.A., Melkov A.M., Smirnov Y.V., Malyshev I.V., Allikmets R.L., Kostina M.B., Dulubova I.E., Kiyatkin N.I., Grishin A.V., Modyanov N.N., Ovchinnikov Y.A., Modyanov N.N., Ovchinnikov Y.A., "Family of human Na(+),K(+)-ATPase genes. Structure of the genisoform alpha-III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catalytic subunit (alpha III-form) and structural features of the protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDILINE=8825304, PubMed=2838329; DOI=10.1016/0014-5793(88)81

Ovchinnikov Y.A., Monastyrskaya G.S., Broude N.E., Ushkaryov Melkov A.M., Smirnov Y.V., Malyshev I.V., Allikmets R.L., Kostina M.B., Dulubova I.E., Kiyatkin N.I., Grishin A.V., Modyanov N.N., Sverdlov E.D.;

Modyanov N.N., Sverdlov E.D.;

Modyanov N.N., Sverdlov E.D.;
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Mammalia; Eutheria;
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Lett. 233:87-94(1988)
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PS00154; ATPASE E1 E2; UNKNOWN
PS00030; RRM RNF 1; UNKNOWN 1.
1012 AA; I11220 MW; FF93D6;
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Hydrolase; 1.
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB
Pred. No. 1.9e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOI=10.1016/0014-5793(88)81361-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its relationship
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AAA51798.1; AAA51798.1;

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MEDLINE-8724723; PubMed-3036582; DOI=10.1016/0014-5793(87)80677-4;
A Sverdlov E.D., Monastyrskaya G.S., Broude N.E., Ushkaryov Y.A.,
A Allikmets R.L., Melkov A.M., Smirnov Y.V., Malyshev I.V.,
A Allikmets R.L., Melkov A.M., Smirnov Y.V., Kiyatkin N.I.,
A Loubova I.E., Petrukhin K.E., Gryshin A.V., Kiyatkin N.I.,
A Kostina M.B., Sverdlov V.E., Modyanov N.N., Ovchinnikov Y.A.;
A Kostina M.B., Sverdlov V.E., Modyanov N.N., Ovchinnikov Y.A.;
A Kostina M.B., Sverdlov V.E., Modyanov N.N., Ovchinnikov Y.A.;
T FEBS Lett. 217:275-278(1987).
C -!- FUNCTION. This is the cattalytic component of the active enzyme,
which catalyzes the hydrolysis of AIP coupled with the exchange of
sodium and potassium ions across the plasma membrane. This action
c creates the electrochemical gradient of sodium and potassium ions,
providing the energy for active transport of various nutrients.
- CATALYTIC ACTIVITY: AIP + H(2)O + M(+)(In) + K(+)(Out) = ADP +
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EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 120-387; 494-538 AND 545-1013 FROM N.A. SEQUENCE OF 120-387; 494-538 AND 545-1013 FROM N.A. OVChINNIKOV Y.A., McDARSTYSKAYA G.S., Broude N.E., A Ushkaryov Y.A., Melkov A.M., Smirnov Y.V., Malyshev Dulubova I.E., Petrukhin K.E., Gryshin A.V., Sverdlov Kiyatkin N.I., Kostina M.B., Modyanov N.N., Sverdlov "The family of human Na+,K+-ArPase genes. A partial sequence related to the alpha-subunit."; FEBS Lett. 213:73-80(1987).
                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schnerch
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SUBCELLULAR LOCATION: Integral
SIMILARITY: Belongs to the cati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                         ATPases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate + Na(+)(Out) + K(+)(In). SUBUNIT: Composed of three subunits: alpha
M37457
M37436
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M37441
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Subfamily
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AAA51798.1;
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Malyshev I.V.,
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GO; GC:0006810; P:transport; TAS:
InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR006069; Cation_ATPase.
InterPro; IPR006069; Cation_ATPase.
InterPro; IPR006089; Cation_ATPase.
InterPro; IPR006081; Cation_ATPase C.
InterPro; IPR0080834; Dehal Ilke_hydro.
InterPro; IPR008350; II-E2_ATPase_N;
InterPro; IPR0085775; Na/K_ATPase_alph.
Pfam; PP00699; Cation_ATPase_C; I.
Pfam; PP00699; Cation_ATPase_N; 1.
Pfam; PP00122; E1-E2_ATPase; 1.
Pfam; PP00122; E1-E2_ATPase; 1.
Pfam; PP00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
PRINTS; PR00119; CATATPASE.
TIGRPAMS; TIGR01106; ATPase_P-type; 5.
PRINTS; PR00116; ATPase_P-type; 5.
PROSITE; PS00154; ATPASE E:
ATP-binding; Hydrolase; May Phosphorylation; Sodium/poi DOMAIN 78 98 121 TRANSMEM 122 142 DOMAIN 143 278 TRANSMEM 279 298 DOMAIN 299 310 TRANSMEM 299 310 TRANSMEM 299 310 TRANSMEM 299 310 TRANSMEM 299 310 TRANSMEM 299 310 TRANSMEM 311 328 DOMAIN 329 762 TRANSMEM 763 782 DOMAIN 329 762 TRANSMEM 763 782 DOMAIN 329 762
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HSSP; P06685; 1MO7.
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(c) 18250; -.

(c) 1805890; C:sodium/potassium-exchanging ATPase complex; I GO:0005890; P:sodium/potassium-exchanging ATPase activity; GO:0005391; P:sodium/potassium-exchanging ATPase activity; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.

(c) 10030641; P:hydrogen ion homeostasis; ISS.

(c) 10030611; P:potassium ion transport; ISS.

(c) 10030611; P:sodium ion transport; ISS.

(c) 10030611; P:sperm motility; ISS.

(c) 10030610; P:transport; ISS.
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M37456; AAA51798.1; JOII

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M32777; AAA58380.1; JOII

M37577; AAA58380.1; JOII
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                                                                                                                                                                                                                                                                                                                         Magnesium; Metal-binding; Multigene
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RESULT 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., McEwan R.J., Malek J.A., Gunaratne P.H., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman M.R., Mannara M.A., Touchman M.R
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Q6PIC6;
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                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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(COTT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Sodium/potassium-transporting ATPase alpha-3 chain
(Na+/K+ ATPase 3) (Alpha(III)).
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Mammalia; Eutheria;
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SIMINATIC ACTIVITY: ATP + H(2)O + Na(+)(In)
phosphate + Na(+)(Out) + K(+)(In).
SUBUNIT: Composed of three subunits: alpha
                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: This is the catalytic component of the activation which catalyzes the hydrolysis of ATP coupled with the sodium and potassium ions across the plasma membrane. creates the electrochemical gradient of sodium and poproviding the energy for active transport of various interval.
                                                                                                                                                                                                                      gamma (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the cation transport ATPA
ATPases). Subfamily IIC.
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                   BC034645;
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an email to license@isb-sib.
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Rodentia;
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Search completed: September 1, Job time: 54.0719 secs
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Best Local Similarity
Matches 6; Conserv
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Phosphorylation; Sodium/p
DOMAIN 199 121
TRANSMEM 99 121
TRANSMEM 142 142
DOMAIN 279 298
DOMAIN 279 310
TRANSMEM 311 328
DOMAIN 329 762
TRANSMEM 763 782
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4-asparty,phosphate intermediate (By similarity).

Phosphoserine (by PKA) (By similarity).

Binding of phosphoinositide-3 kinase (By similarity).

Magnesium (By similarity).

Magnesium (By similarity).

Magnesium (By similarity).
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Pred. No. 1.9e+02;
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07-JUN-1995;
07-JUN-1995;
                             receptor
affinity
                                                                                                                                Claim 18; Page 89; 106pp; English.
                                                                                                                                                                                   thrombocytopenia resulting
                                                                                                                                                                                                           Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
                                                                                                                                                                                                                                                                                                                                                                      Dower WJ,
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07-JUN-1995;
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                                                                             present sequence is
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(TR). It has a molecular weight of < 8000 Da, and a to TR as expressed by an IC50 of no more than about (especially if modified, see features table) can be
                                                                                                                                                                                                                                                                                                                                         Barrett RW,
LC, Schatz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombocytopenia; TPO; TR; proliferation;
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95US-00473604.
95US-00476168.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Preferably N-terminus is selected from: -NRR1; NRC(O)R; -NRC(O)OR; -NRS(O)ZR; -NHC(O)NIE; succinimide; benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and RI are independently selected from hydrogen and lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Preferably linkages are selected from: -
CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C
; -NHC(O)NH; where R is hydrogen or lower alkyl and
lower alkyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Preferably C-terminus is -C(0)R2 where R2 is
selected from hydroxy, lower alkoxy, and -NR3R4, whe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            PJ,
                                                                             a compound which binds to thrombopoietin (TPO)
                                                                                                                                                                                                                                                                                                                                                                      Cwirla SE,
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AAB17285
                                                                                                                                                                                                                                                                                                                                            Wagstrom
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                                                                                                                                                                                chemotherapy, etc
                                                                                                                                                                                                                                                                                                                                            Duffin DJ, Gat
m CR, Wrighton
                                                                                                                                                                                                                                                                                                                                            Gates CM, iton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adq16710 Immunoglo
Aab17285 TPO-mimet
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                                100
                                                  binding
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RESULT 2
AAW09468
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Best Local
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or hamarow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                     The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It is part of a dimer linked by the omega amino acid to the omega amino acid in the sequence in AAW19534. The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemocherapy, radiation therapy or bon marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp
                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW09468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                     thrombocytopenia resulting
                                                                                                                                                                                                                        WPI; 1997-051883/05
                                                                                                                                                                                                                                                              Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone marrow transfusion; chemotherapy; radiation therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haematology; thrombocytopenia; TPO; TR; proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-SEP-1997
                                                                                                                                                                                                                                                                                      (GLAX ) GLAXO
                                                                                                                                           30; Page 91; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; protein; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEGPTLROWLAARA 14
                                                                                                                                                                                                                                               Barrett RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                      GROUP LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor binding compound peptide (part
                                                                                                                                                                                                                                                                                                              95US-00484090.
95US-00485301.
                                                                                                                                                                                                                                                                                                                                        95US-00476168.
95US-00478128.
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95US-00476168.
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                                                                                                                                                                                                                                                Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                ρJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Linked to the
                                                                                                                                                                                                                                                              Cwirla SE,
                                                                                                                                           English.
                                                                                                                                                                      from
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                                                                                                                                                                                                                                               rla SE, Duffin DJ,
Wagstrom CR, Wrig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73;
Pred. No.
                                                                                                                                                                     chemotherapy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 omega Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4e-05;
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                                                                                                                                                                                                                                               n DJ, Gates CM,
Wrighton NC;
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                                                                                                                                                                                                                                                              Johnson
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Sequence 14

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RESULT 4
AAW33034
ID AAW3
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Best Local S
Matches 14
                                                                                                                        Query Match
Best Local S
Matches 14
                                                                                                                                                                                                               The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transflusions. It can also be used disgnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin receptor; binding peptide; treatment; agon haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                   Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
07-JUN-1995;
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                                                                                                                                                                            Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dower WJ,
Mattheakis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                           Claim 19; Page 89; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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Similarity 100.0%;
14; Conservative (
                                                                                                                                    Similarity
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                                                                                            IEGPTLRQWLAARA 14
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LC, Schatz PJ, Wagstrom
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00478128.
95US-00485301.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide; 14 AA
                                                                                                                                   100.0%;
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                                                                                                                                    Score 73; DB 2;
Pred. No. 1.4e-05;
                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duffin DJ, Gates CM, om CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment; agonist;
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                                                                                                                         Indels
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AAW33034 standard; peptide; 14 AA

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RESULT 5
AAW36774
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SEXEXEXE
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                        resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                                                                                                                                                                                                       The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a Ta binding affinity as expressed by an IC50 of no more than about 100 microw. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signal transduction; receptor activation; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis;
                                                                                                                                                                                                                                                  Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW33034;
           Thrombopoietin receptor binding peptide
                                    11-MAR-1998
                                                                                   AAW36774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mattheakis LC,
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                                                                                                                                                                                                                                                                                                                                                                                                                   30; Page 91; 106pp;
                                                                                                                                                                                                   14;
                                                                                                                                                   u
                                                                                                                                                                                                              Similarity
                                                                                      standard;
                                                                                                                                                   IEGPTLROWLARRA 14
                                                                                                                                                                      IEGPTLROWLAARA 14
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                                                                                                                                                                                                 Conservative
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                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor binding peptide
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95US-00485301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "terminal carboxy group linked to epsilon amino
group of Lys16 in AAW33035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                     peptide;
                                                                                                                                                                                                   100.0%; (
100.0%; 1
htive 0;
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PJ, Wagstrom CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding peptide; treatment; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                      14
                                                                                                                                                                                                              Score 73;
Pred. No.
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duffin DJ,
                                                                                                                                                                                                                1.4e-05;
                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gates
                                                                                                                                                                                                                           Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                              chemotherapy, etc.
                                                                                                                                                                                                     Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
             WO9946283-A1
                                                                            HIV; cancer; diabetes; incontinence; hypertension; amnesia; Alzheimer's disease; fever; depression; sex hormone regulation; eating disorder; schizophrenia; osteoporosis; insomnia;
                                                                                                                   pharmacologically active peptide conjugate; enzymatic cleavage; pain;
                                                                                                                                               AF 12505 as
                                                                                                                                                                                                                            ADI24843 standard;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present peptide, which binds the thrombopoietin receptor (TR), used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; Page 77; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-052226/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dower WJ, Barret
Mattheakis LC, So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
07-JUN-1995;
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Modified-site
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                                                                                                                                                                         15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                             μ
                                                                 nervous system
                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                             IEGPTLROWLAARA
                                                                                                                                                                                                                                                                                                                        IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Ŗ,
                                                                                                                                              active moiety for pharmacologically active peptide
                                                                                                                                                                         (first entry)
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95US-00485301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RW.
                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                                                                                                             100.0%;
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PJ, Wagstrom CR,
                                                                                                                                                                                                                                                                                              14
                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                 Score 73; DB 2; 1
Pred. No. 1.4e-05;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duffin DJ, Gates Com CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gates CM,
                                                                                                                                                                                                                                                                                                                                                                          Length 14;
                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone
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RESULT 7
AAY96515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC halogen, hydroxy, amino, cyano, nitro, sulfono, and carboxy, or R1 and R CC ycolohexyl or cycloheptyl ring, e.g. 2,4-diaminobutanoic acid and 2,3-CC diaminopropanoic acid; the ratio between the half-life of the peptide CC conjugate and the half-life of the corresponding active peptide sequence, X, when treated with carboxypeptidase A or leucine aminopeptidase in CC A, when treated with carboxypeptidase A or leucine aminopeptidase in CC or in serum or plasma is at least about 2 (preferably at least about 10), CC or when the pharmacologically active peptide X is not orally absorbed, or a salt, with the proviso that the CC pharmacologically active peptide conjugate is not selected from sequences (ADI24837)-(ADI24841). The peptide conjugates can be used for treating CC e.g. pain, HIV, cancer, depression, sex hormone regulation, eating CC e.g. pain, HIV, cancer, depression, sex hormone regulation, eating CC expression schizophrenia, osteoporosis or insommia. They can also be used CC peptides are less susceptible to degradation by proteases compared to the corresponding free pharmacologically active peptide as the X part of the crepresents a pharmacologically active peptide as the X part of the corresponding free pharmacologically active peptide as the X part of the corresponding free pharmacologically active peptide as the X part of the corresponding free pharmacologically active peptide as the X part of the corresponding free pharmacologically active peptide as the X part of the corresponding the converse of the invention.
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Matches :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel pharmacologically active peptide conjugate having a reduced tendency towards enzymatic cleavage comprises X and Z, where: (a) X is a pharmacologically active peptide sequence; and (b) Z is a stabilising peptide sequence of 4-20 amino acid units covalently bound to X, where each amino acid unit in the stabilizing peptide sequence, Z being selected from Ala, Leu, Ser, Thr. Tyr. Asn, Gln, Asp, Glu, Lys, Arg, His, Met, Orn, and amino acid units of formula - MH-C(R1)(R2)-C(=0)-(1), where: R1 and R2 are H, 1-6C alkyl, phenyl, and phenyl-methyl, where 1-6C-alkyl is optionally substituted with 1-3 substituted with 1-3 substituted with 1-3 substituted with 1-3 substituted with 1-3 substituted with 1-3 substituted with 1-3 substituted from 1-6C-alkyl, 2-6C-alkyl, and phenyl-methyl are optionally substituted with 1-3 substituted with 1-3 substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted with 1-3 substituted with 1-3 substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted with 1-3 substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted with 1-3 substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted with 1-3 substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted with 1-3 substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted with 1-3 substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted with 1-3 substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted with 1-3 substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted selected from 1-6C-alkyl, 2-6C-alkenyl, and phenyl-methyl are optionally substituted selected from 1-6C-alkyl, 2-6C-alkenyl
                                                                                    Thrombopoietin mimetic
                                                                                                                                                04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                            AAY96515;
                                                                                                                                                                                                                                                                 AAY96515 standard; peptide; 14 AA
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                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                    peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treating,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73; DB 2;
Pred. No. 1.4e-05;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Thrombopoietin; mimetic; TMP; TPO; anti-human immunodeficiency virus;

platelet; megakaryocyte; production; anti-HIV; anti-anemic; dermatological;

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RESULT 8
AAB16962
ID AAB1
XX
AC AAB1
XC
AC
DT 31-(
XX
DE TPO-
XX
KW Annw
KW inmw
KW inmh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc mimetic peptide (TMP) dimer joined by a linker [TMP] = (1.1) mTMP 2], is cc new. TMP1 and TMP2 are amino acid sequences varying from at least 10 to cc 14 residues in length comprising x_2x_10, x_2x_11, x_2x_12, x_2-c CC x_13, x_2x_14, x_1x_10, x_1x_11, x_1-x_12, x_1-x_12, x_2-c CC x_13, x_2-x_14, x_1-x_12, x_1-x_12, x_1-x_13, and x_1-c CC x_14, x_1-x_10, x_1-x_11, x_1-x_12, x_1-x_13, and x_1-c CC x_14, x_1-x_10, x_1-x_11, x_1-x_12, x_1-x_13, and x_1-c CC x_19 = W, y or F; x_10 = L, I, v, h, F, M, or K; x_1 = B, I, v, L, F, CC S, T, K, H, or B; \overline{X}_1^2 = A, I, v, L, F, G, S, or \overline{Q}; x_11 = A, I, v, L, F, CC x_10 = M, x_10 = L, I, v, h, F, M, or K; x_11 = A, I, v, L, F, CC x_10 = M, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 = L, x_10 
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
                                               Modified peptide; therapeutic agent; autoimmune disease; cytostatic; antia
                                                                                                                   TPO-mimetic
                                                                                                                                                            31-OCT-2000
                                                                                                                                                                                                                                               AAB16962 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compound which
                                                                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         und which binds
peptide (TMP) d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feige U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 60; 91pp; English
                                                                                                                                                                                                                                                                                                                                                          Ŗ,
                                                                                                                 peptide TMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                            (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "subunits in the dimer are covalently bonded at each carboxy terminus through peptide linkage with NH2-(CH2)4-CH(CONH2)-NH-CO-(CH2)2-NH2"
                                                                                                                                                                                                                                             peptide;
                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to an mpl
                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                   IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73;
Pred. No.
                                                                                                                   NO:13
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor
                                                                      fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ptor comprising a thrombopoietin
a linker (TMP_1-(L_1)_nTMP_2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                          FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 14;
                                                                          domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                        cancer
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 14
                             haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nove1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 19; Page 189; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2
                                                                                           Peptide mimetic; human; thrombopoietin receptor;
                                                                                                                           Human thrombopoietin receptor (TPO-R) activator peptide
                                                                                                                                                            17-DEC-2001
                                                                                                                                                                                                                        AAU25827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      composition of matter comprising an Fc domain and pharmacologically e peptides, useful for treating cancer and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMGEN
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                 IEGPTLROWLAARA
                                                                                                                                                                                                                                                                                                                      IEGPTLROWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
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                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                    100
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Pred. No. 1.4
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                                                                                                TPO-R; TPO;
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                                                                                                cytokine;
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in vitro

expansion;

megakaryocyte;

Dimer gene;

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                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC cells with effective amounts of peptides and peptide mimetics attached to CC hydrophilic polymers. The methods are used to treat thrombocytopenia such CC as that due to chemotherapy, radiation therapy or bone-marrow CC transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders CC including thrombocytopenia and prevent haematological disorders cas unique tools for understanding the biological role of thrombopietin CC (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living CC cells and fixed cells, in biological fluids, in tissue homogenates, and CC in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed compounds or in conjunction with additional cytokines
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07-JUN-1995;
07-JUN-1996;
               haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                              Human thrombopoietin receptor (TPO-R) activator peptide #190
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of activating thrombopoietin receptors in cells comprise contacting
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                                                                             Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine
                                                                                                                                                17-DEC-2001
                                                                                                                                                                                                              AAU26004 standard;
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 expansion; megakaryocyte;
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Wanian P,
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96WO-US009623.
96US-00699027.
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                                                                                                                                                                                                              peptide;
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Pred. No. 1.4e-05;
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Matches
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07-JUN-1996;
15-AUG-1996;
Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                         TPO mimetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mces AAU25815-AAU26049 represent peptides and peptide mimetics that to and activate the human thrombopoietin receptor (TPO-R). Methods
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                                                                                         peptide SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.4e-05;
Mismatches 0;
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Hendren
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RESULT 12
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Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel vehicle-peptide more diseases, inflammatory and autoimmune diseases, sleep of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
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Pred. No. 1.4e-05;
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BXXXE

AAE18011;

07-MAY-2002

(first entry)

AAE18011 RESULT 13

AAE18011 standard; peptide;

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                                                                                                                                                                                                                                                                        CC mimetic such as an erythropoletin (RPO) or thrombopoletin (RPO) mimetic, ct that is flanked with proline at its carboxy terminus. (I) has can tianaemic, haemostatic and nephrotropic activities, and can be used as can tianaemic, haemostatic and nephrotropic activities, and can be used as can activate the control of proliferation, differentiation and maturation of can stimulator of proliferation, differentiation and maturation of content activities, where (I) is useful corresponding proliferation, differentiation or growth of corresponding to corresponding to corresponding to content activity of the corresponding to content activity of the corresponding to content activity of the corresponding to content activity of the corresponding to content activity of the corresponding to content activity of the corresponding to content activity of the corresponding to content activity of the corresponding to content activity of the corresponding to content activity of the content activity of the content activity of the content activity of the content activity of the content activity of content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity of the content activity 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A novel
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04-MAY-2001; 2001US-0288889P
29-MAY-2001; 2001US-0294068P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementarity determining regrou; .....complementarity determining regrou; .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 6; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-566610/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bowdish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2001; 2001WO-US047656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombopoetin mimetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determining region are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200246238-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin (TPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALEX-)
                                                                                                                                                                                                                                                        exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogen molecule comprising a region in which amino acid s corresponding to at least a portion of the complementary ning region are replaced or fused with an erythropoietin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KS,
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                                                                                                                            Similarity
IEGPTLROWLAARA 14
                                                                                                                                                                                                         14
                                                                                                 100.0%; Score 73; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                      ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barbas-Frederickson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region; immunoglobin;
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Renshaw
                                                                                                                              1.4e-05;
                                                                                                                                                         Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IJ
                                                                                                            Indels
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RESULT 14
ABG71747
ID ABG71
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KW compl
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                      and a composition for targetting an adenoviral vector. A system comprising a cell having a non-native cell-surface receptor, and a virus having a non-native ligand which binds the non-native cell-surface receptor of the cell is useful for propagating a virus and also for assaying gene function. The system is also useful for isolating a nucleic acid encoding a product comprising a desired property. Further the system is useful for identifying functionally related coding sequences. Adenoviral vector comprising a non-native nucleic acid encoding a therapeutic agent such as anti-tumour agent, preferably tumour necrosis factor and a second non-native nucleic acid encoding an agent that facilitates imaging and a targetting agent is useful for treating an animal. The therapeutic agent can be used to treat cancer of the brain, lung, ovary, breast and prostate. The present sequence is human non-native ligand attached to an adenoviral vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; anti------ovary; breast; prostate.
Agonist; immunoglobulin; Ig; variable domain; heavy chain; light chain; complementarity determining region; CDR; antigenic; thrombopoietin; TPO thrombopoietin receptor; MPL; cytotoxic T-lymphocyte; CTL; epitope;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2000; 2000US-0208451P.
02-AUG-2000; 2000US-00631191.
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                                                                                                                                                                     ABG71747 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to adenoviral coat proteins comprising various non-
native ligands. The invention provides a method of controlled gene
expression utilising selectively replication competence and also a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-147620/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200192549-A2
                                                                    TPO receptor,
                                                                                                      20-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 45; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenoviral coat protein which permits production of adenoviral vectors that bind and infect host cells not naturally infected by adenovirus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; adenoviral coat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-tumour agent; tumour necrosis factor; cancer; brain; lung;
                                                                                                                                                                                                                                                                                  IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                         IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   various non-native ligands.
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                      (first
                                                                 MPL,
                                                                    agonist peptide, AF12505.
                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                       Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-native ligand; cell-surface receptor;
                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                           1.4e-05;
                                                                                                                                                                                                                                                                                                                                                          DB 5;
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                                                                                                                                                                                                                                                                                                                                                          Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brough DE;
                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                           Gaps
                     TPO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a variant of an immunoglobulin (Ig) variable care heavy or light chain domain that comprises at least one complementarity consists that complementarity controls are consisted as a consistion of the CDR. The CDR calso has added or substituted to it, at least one binding sequence which is heterologous to the CDR and is an antigenic, agonistic sequence from a combination of the CDR, and it is an antigenic, agonistic sequence consists and the CDR, and it is an antigenic. The antigenic sequence consists agonistic sequence and combination of each. The variant or thrombopoietin coll sequence, a T-helper cell sequence, a B-helper cell sequence, a B-helper cell sequence, a B-helper cell sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells sequence, a B-helper cells particularly platelet progenitor cells. The variants are also consisted for treating or preventing haematopoietic or immune disorders cells, particularly platelet progenitor cells. The variants are also consisted for the creating or preventing haematopoietic or immune disorders consisted progenitions comprising the synthebodies can be used for the mobilisation, amplification and ex vivo expansion of stem cells and committed precursor cells for autologous and allogeneic transplantation cells and committed precursor cells for autologous and allogeneic transplantation cells for sensence presented is the TDO recentor (MDI) accorder in reported. AFT366
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New thrombopoietin synthebodies, useful for stimulating proliferation, growth, or differentiation of hematopoietic cells, for treating or preventing hematopoietic or immune disorders, e.g. thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; diagnostic; haemostatic; immunomodulator; anticoagulant
                                                                                                                                                                          ABR62907 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 62; Page 71; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soltis DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2001; 2001US-0281183P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-2002; 2002WO-US010301.
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                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                      IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           presented is the TPO receptor (MPL) agonist peptide, AF12505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burch RM,
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 73; DB 6;
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 14;
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Thrombopoietin; mimetic; thrombocytopaenia; antibody targeting

Thrombopoietin mimetic peptide AF12505.

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RESULT 16
ADC33697
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of thrombopoietin (TPO) mimetic peptide AF12505, which mimics the activity of recombinant TPO. The invention provides antibody targeting compounds that are used to reprogram the specificity of an antibody. The antibody targeting compound is linked to the combining site of the antibody, such that the modified antibody takes on the binding specificity of the targeting agent. In an example from the invention, a TPO receptor targeting antibody agent. In an example from the proportion of the targeting antibody accompound was prepared by covalently linking peptide AB12505 to aldolase monoclonal antibody 38C2. The TPO receptor targeting antibody compound can be used to treat thrombocytopaenia resulting from chemotherapy and bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody targeting compound useful e.g. for diagnostic immunoassays treating microbial diseases comprises targeting or biological agent covalently linked to combining site of the antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-2001; 2001US-0344614P
19-SEP-2002; 2002US-0412455P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                           18-SEP-2003
                                                                                                                                    WO2003076596-A2
                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                             18-DEC-2003
                                                                                                                                                                                                                                                                                                                  ADC33697 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Page 62; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-636673/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2002; 2002WO-US033991.
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 Green
                                                                                                                                                                                         cytostatic;
                                                                                                                                                                                                      chimeric retrovirus envelope protein;
                                                                                                                                                                                                                                Erythropoietin receptor/erythropoietin consensus peptide SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCRI ) SCRIPPS RES INST.
                                                    08-MAR-2002; 2002US-0362655P
                                                                                07-MAR-2003; 2003WO-US007323
                           (UYMA-) UNIV MASSACHUSETTS
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 Gollan TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rader C,
                                                                                                                                                                                         gene therapy; cancer.
                                                                                                                                                                                                                                                             (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73; DB 7;
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                        ecotropic envelope protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 14
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C(I) comprising an ecotropic envelope protein and a heterologous short constraint and cancer constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the constraints of the present sequence represents an of the constraints of the present invention.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a chimeric retrovirus envelope protein (I) comprising an ecotropic envelope protein and a hararologue protein
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                                                                                                                                                                                                                                                                                                                                                                                                       Haemostatic; antianaemic; immunosuppressive; platelet;
transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN59652 standard; peptide; 14 AA
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                                   Min H,
                                                                                                               11-OCT-2001;
10-OCT-2002;
                                                                                                                                                                       11-OCT-2002; 2002WO-US032552.
                                                                                                                                                                                                             17-APR-2003.
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                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                           Lupoid
                                                                                                                                                                                                                                                                                                                                             autoimmune haemolytic anaemia; Hughe's syndrome
                                                                                                                                                                                                                                                                                                                                                                 thrombocytopaenia; aplastic anaemia; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                   TMP; c-mpl receptor; platelet precursor; megakaryocyte
                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombopoietin mimetic peptide (TMP), seq id 1.
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2002US-00269806.
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                                                                                                                                                                                                                                                                                                                                                                     thrombocytopaenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC binds to the c-mpl (mpl) receptor, and which stimulates the production of platelets to the c-mpl (mpl) receptor, and which stimulates the production of disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The CC and a pharmaceutical composition comprising (II) and a carrier. The CC platelets in a patient. The TMP of the invention is useful for treating CC conditions involving a megakaryocyte and/or platelet deficiency, e.g. CC disease conditions involving thrombocytopaenia such as aplastic anaemia, CC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia, autoimmune thrombocytopaenia, and for invention is useful for component of the viability or storage life of platelets and/or megakaryocytes and its derived cells. The compounds demonstrate an cC improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior chromobopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of compounds also exhibit compounds also exhibit superior therapeutic properties, such as improved plasma half-life, compounds also exhibit superior therapeutic properties, such as improved plasma half-life, compounds also exhibit such as a trivity and in vivo circulation time. The current sequence compounds also exhibit such as improved plasma half-life, compounds also exhibit such as a trivity and in vivo circulation time. The current sequence
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                                                                                                                             Garnier L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a thrombopoietin agonist peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-2004
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                                                                                                                                                                                                                                                                 14-AUG-2002; 2002EP-00292043
                                                                                                                                                                                                                                                                                                                                                                                                      11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004020639-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion protein; C4bp; alpha chain; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                   12-AUG-2003; 2003WO-EP008928
                                                                                                                                                                                                   (AVID-) AVIDIS
                                                                  2004-239202/22.
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                                                                                                                             Hill F,
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Pred. No. 1.4e-05;
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Obtaining a recombinant fusion protein, useful for treating lupus

Thrombopoietin another method

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                                                                                                                                                                                                                                                                   Increasing hematopoietic stem cell production in subject, usefureducing the incidence of delayed primary engraftment, comprises administering a Thrombopoietin mimetic compound e.g., a peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises providing a prokaryotic host cell carrying a nucleic acid encoding the recombinant protein operably linked to a promoter func
                                                                                            The invention cell production
                                                                                                                                                                                  Disclosure; Fig 2; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-283153/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaushansky K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-2002;
18-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stem cell therapy; HSC; transplantation; engraftment; mimetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the prokaryotic
invention relates to a method (M1) for increasing haematopoietic production in a subject which involves administering a production (TPO) mimetic compound to the subject. Also included inher method (M2) of providing haematopoietic stem cells to a subject hinvolves administering a TPO mimetic compound to a subject to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haematopoietic stem cell; thrombopoietin; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-DIMENSIONAL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-0411700P.
2002US-0411779P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macdonald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73; DB 8;
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                       useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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ADQ16584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin; complementarity determining region; CDR; peptide mimetic;
erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14
New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced with EPO mimetic
                                                                                                                                                                                                                                                                                                                  02-DEC-2002; 2002US-00307724
                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-2003; 2003WO-US036894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004050017-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agonist TPO mimetic peptide SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ16584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ16584 standard; peptide; 14 AA
                                                                                                              WPI; 2004-460973/43
                                                                                                                                                                                                                                                    (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IEGPTLROWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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A
                                                                                                                                                                                 Frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 8;
Pred. No. 1.4e-05;
                                                                                                                                                                             Renshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  얁
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RESULT 21
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia.
                                                Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising a region where amino acid residues corresponding to at portion of a two complementarity determining regions (CDRs) are re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or a TPO mimetic, useful for treating thrombocytopenia
                                                                                                                                                                                            07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                  Cross-links
                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW35416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW35416 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a TPO mimetic peptide.
                        Example 9; Page 73; 106pp; English.
                                                                                                     WPI; 1997-052226/05.
                                                                                                                                          Dower WJ,
                                                                                                                                                                                                                                   07-JUN-1996;
                                                                                                                                                                                                                                                             19-DEC-1996.
                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel immunoglobulin molecule or
                                                                                                                              Mattheakis
                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                       WO9640750-A1
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8
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                                                                                                                            Barret RW,
LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO 1; 107pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor binding peptide.
                                                                                                                                                                                            95US-00478128.
95US-00485301.
                                                                                                                                                                                                                                  96WO-US009623
                                                                                                                                                                                                                                                                                                                            /note= "linked via disulfide bond to Cysl of identical
peptide"
15
                                                                                                                                                                                                                                                                                                                 /note= "NH2-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 73; Di
100.0%; Pred. No. 1.
tive 0; Mismatches
                                                                                                                            Cwirla SE, Duffin PJ, Wagstrom CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                              DJ, Gates CM,
Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                             Johnson
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to at least a
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The present peptide, which binds the thrombopoietin receptor (TR), can

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ARBSULT 22
AAW366776
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ID AAW36778
AC AAW3678
AC AAW3678
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AC AAW3678
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AC Thron
KW haema
KW radia
KW radia
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Cross
FT Cross
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FT Modif
FT WO964
AXX O7-JU
PR 07-JU
PR
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Best Local S
Matches 14
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                      The present peptide, which binds the thrombopoietin receptor (TR), cused to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombopotetin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of
                                                                                                                                                                                                                                                                                                                     Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW36776 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                            disorders, esp. thrombocytopenia resulting from chemotherapy, etc
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-052226/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dower WJ, Barret RW,
Mattheakis LC, Schat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9640750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     radiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLAX ) GLAXO
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                                                                                                                                                                                                                                          Page 77; 106pp;
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                                                                                                                                                                                                                                             English.
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Pred. No.
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                   The invention relates to peptide compounds composed of two peptide chains CC attached to each of the amino groups of a single Lys in the amide form. CC The compounds are of formula (Pepi) (Pep2)K(NH2), where Pepi is of CC formula: X1-1-E-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9-X10; and pep2 is of CC formula: X1-1-E-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9-X10; X1 = H or acyl; X2 CC = Gly or Sar (sarcosine); X3 = Arg, Ala, Nle (norleucine) or N-CC acetyllysine; X4 = Gln or Glu; X5 = Trp, L-1-naphthylalanine or Phe; X6 = CC Ala, 5-aminopentanoic acid or 2-aminobutyric acid; X7 = Ala, CC diphenylalanine, or is absent; X8 = Arg, P- amino-phenylalanine, N-CC diphenylalanine, or is absent; X9, X9' = Ala, beta Ala, N-methyl-alanine, CC are capable of binding to, and activating, the thrombopoietin (TPO) CC are capable of binding to, and activating, the thrombopoietin (TPO) CC are capable of Dro. They may be used as competitive binders in assays CC to screen for new TPO receptor agonists. They may be used as reagents for may may be used as competitive binders in assays CC actoric mby receptors in living capits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor - may be used in treating haematolog methods for screening for new thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide compound(s) which can bind and activate thrombopoietin receptor - may be used in treating haematological disorders and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombopoietin receptor; haematological disorder; screening; assay; megakaryocyte; blood disorder; thrombocytopaenia; TPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Wagstrom CR,
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Pred. No. 1.5e-05;
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                                                                                                                                                                                                  The present invention discloses an active peptide which promotes thrombocyte generation. The active peptide can be synthesised by a polypeptide solid-phase synthesis method, and has the monomer sequenc IEGPTLRQWILARAC and the amidated peptide chain structure of IEGPTLRQWILARAC-NH2. Its activity is increased by 20 times for its monomer, or by 10 times for the amidated peptide chain compared with monomer, or by 100 times for its dimer compared with its monomer
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-terminal cysteine of a similar peptide"
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                                                                                                                                                                       CC bind to and activate the human thrombopoietin receptor (TPO)R). Methods colls with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow contacting the composition polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow contractions and to prevent thrombocytopenia in patients at risk. The concluding thrombocytopenia and platelet disorders. They are used in vitro cas unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO creeptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and conjunctified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed compositions alone or in conjunction with additional cytokines
                                                              Query Match
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07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
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                                                                                                                         Sequence 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrett RW, Cwirl
anian P, Wagstrom
                                                                                                                                AA;
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95US-00485301.
96WO-US009623.
96US-00699027.
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100.0%; {
tive 0;
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   Score 73; DB
Pred. No. 1.5
0; Mismatches
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                                                                    DB 4;
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Deprince R
                                                              Length 15
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RESULT 26
AAU25831
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                                                                                                                                                            Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods CC of activating thrombopoietin receptors in cells comprise contacting the CC ells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such CC as that due to chemotherapy, radiation therapy or bone-marrow CC transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC including thrombocytopenia and platelet disorders. They are used in vitro CC receptor. The peptides can be used to detect TPO receptors on living CC receptor. The peptides can be used to detect TPO receptors on living CC ells and fixed cells, in biological fluids, in tissue homogenates, and CC in purified or natural biological materials. They may also be used for in Situ staining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed committed committed or in conjunction with additional cytokines
                                                      Query Match
Best Local S
Matches 14
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07-JUN-1995;
07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemostatic; thrombocytopenia; chemotherapy; radiation therapy; RLISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human thrombopoietin receptor (TPO-R) activator peptide #17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU25831 standard; peptide; 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-2001
                                                                                                                                 Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Col 69-70; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2000; 2000US-00516704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yin Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide mimetic; human; thrombopoietin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Balasubramanian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vitro expansion;
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                                                                          Similarity
Barrett RW, Cwirla SE, Gates CM,
nnian P, Wagstrom CR, Hendren RW,
                                                                                                                                 Å.
                                                        Conservative
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95US-00485301.
96WO-US009623.
96US-00699027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              megakaryocyte; Headpiece Dimer gene; lacI gene
                                                                        100.0%;
                                                        <u>.</u>
                                                                        Score 73;
Pred. No.
                                                          Mismatches
                                                                        DB 4; I
1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deprince RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schatz PJ;
                                                                                          Length 15;
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                                                          Gaps
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Conservative

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Mismatches

Indels

0;

Gaps

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CC replaced or fused with biologically active peptides e.g. a peptide comimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic, that is flanked with proline at its carboxy terminus. (I) has carboxy terminus. (I) has contained to the proliferation, differentiation and maturation of can be used as a stimulator of proliferation, differentiation or growth of containing proliferation, differentiation or growth of contents of the promegakaryocytes or megakaryocytes, which results in increased platelet contents of CDR is replaced with an EPO mimetic, or which has one or control of CDR is replaced with an EPO mimetic, is useful for increasing the production of red blood cells, where (I) is contacted with has made or their progenitors. (I) is useful for diagnostics or therapeutics, in cell populations caused by disease, contacted with hasmatopoietic stem cells or their progenitors. (I) is useful for diagnostics or contacted with hasmatopoietic stem cells or treatments related to the suppression of hasmatopoiesis. (ABO73288 to ABO73377 and ABP51695 to ABD51696 represent sequences used in
Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunoglobin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP51670 standard; peptide; 15
                                                                    Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 19; Page 6; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-566610/60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2001;
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04-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an immunoglobin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (I) comprising a region where amino acid residues corresponding
least a portion of the complementary determining region (CDR) as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALEX-)
                                                                                                         exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALEXION PHARM INC
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2001US-0288889P.
2001US-0294068P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TPO)
                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agonist mimetic
                  Score 73; DB 5;
Pred. No. 1.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Renshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                     Length 15;
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RESULT 28
ABR62908
RESULT 29
ADM72485
ID ADM72
XX
AC ADM72
XX
AC ADM72
DX 17-JU
XX
DX TPO n
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                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                          The present sequence is that of thrombopoietin (TPO) mimetic peptide AF12505, modified to include an N-terminal Cys residue. AF12505 mimics the activity of recombinant TPO. The invention provides antibody targeting compounds that are used to reprogram the specificity of an antibody. The antibody targeting compound is linked to the combining site of the antibody, such that the modified antibody takes on the binding specificity of the targeting agent. In an example from the invention, a TPO receptor targeting antibody compound was prepared by covalently linking Cys-modified peptide AB12505 to aldolase monoclonal antibody antibody compound can be used to treat thrombocytopaenia resulting from chemotherapy and bone marrow transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR62908 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody targeting compound useful e.g. for diagnostic immunoassays and treating microbial diseases comprises targeting or biological agent covalently linked to combining site of the antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin; mimetic; thrombocytopaenia; antibody targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin mimetic peptide AF12505
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                                                                                                                                                                                                                                                                                    Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-2001; 2001US-0344614P
19-SEP-2002; 2002US-0412455P
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                TPO mimetic
                                            17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page 62; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-636673/60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-2003
                                                                                                ADM72485 standard; peptide; 15 AA.
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                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                   IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rader C,
              peptide fragment
                                                                                                                                                                                                                             Conservative
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                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sinha SC,
                                                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                                                                         Score 73; DB 7;
Pred. No. 1.5e-05;
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                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lerner R;
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                                                                                                                                                                                                                                                        Length 15;
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                                                                                                                                                                                                                               Gaps
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Increasing hematopoietic stem cell production in subject, useful in reducing the incidence of delayed primary engraftment, comprises administering a Thrombopoietin mimetic compound e.g., a peptide to
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18-SEP-2002; 2002US-0411779P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO;
                                                                                                     WPI; 2004-283153/26.
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                                                                                                                                                   Kaushansky K,
                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004026332-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                (THRE-) 3-DIMENSIONAL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematopoietic stem cell; thrombopoietin; haemostatic; cell therapy; HSC; transplantation; engraftment; mimetic.
                                                                                                                                                     Macdonald BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= bAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "beta-alanine"
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Disclosure; Fig 2; 32pp; English.

CC The invention relates to a method (M1) for increasing haematopoietic stem cell production in a subject which involves administering a CC another method (M2) of providing haematopoietic stem cells to a subject canother method (M2) of providing haematopoietic stem cells to a subject compound to the subject to compound to a subject to compound to involves administering a TPO mimetic compound to a subject to compound to a subject to compound to a subject to compound to a subject to compound to a subject to compound to a subject to compound to a subject to compound to a subject to circulation, and transplanting the harvested stem cells into the subject. Involves administering a compound to the subject, involves administering a compound to the subject, involves administering a compound to the subject, involves administering a compound to the subject, involves administering a compound to the subject, involves administering a compound to the subject, involves administering a compound to the subject, involves administering a compound to the subject, involves administering a compound to the subject and/or more of the stem cells in compounds are disclosed as peptides, including cyclic or modified compounds are disclosed as peptides, including cyclic or modified compounds are disclosed as peptides, including cyclic or modified compounds. In a subject e.g., human. (M3) is useful for reducing the incidence of secondary engraftment following reinfusion of stem cells for reducing the incidence of platelet production and reducing the incidence of secondary failure of platelet production and reducing the incidence of secondary failure of platelet production and reducing the number of stem cells in a subject. (M1) is also useful for increasing the number of stem cells in a subject. On the transplantation to proceed in patients who would not otherwise be considered as candidates because of unacceptably high risk of failed engraftment, reduces the increasing the number of haematopotetic stem cells (H3Cs) available for transplant

Matches Query Match Best Local

14;

Conservative

0,

Mismatches

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Gaps

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1.5e-05;

Length 15; Indels

Similarity

100.0%; Score 73; DB 8; 100.0%; Pred. No. 1.5e-05

Sequence 15

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IEGPTLRQWLAARA IEGPTLROWLAARA 14

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the bone marrow stem cells or the stem cells in the peripheral circulation, and transplanting the harvested stem cells into the subject. A method (M3) is also provided for reducing a time to engraftment compound to the subject, enhancing the expansion of the stem cells in a subject, involves administering a compound to the subject, enhancing the expansion of the stem cell population within bone marrow and/or mobilizing the stem cells in cells or one or more of the stem cells in the peripheral circulation, harvesting one or more of the bone marrow stem cells or one or more of the stem cells into the subject. The cells or one or more disclosed as peptides, including cyclic or modified peptides. (M1) is useful for increasing haematopoietic stem cell compounds are disclosed as peptides, including cyclic or modified peptides. (M1) is useful for increasing haematopoietic stem cell congraftment following reinfusion of stem cells, reducing the incidence of cells are the production and reducing the incidence of secondary failure of platelet production and reducing the time of platelet and/or cells in also useful for increasing the number of stem cells in a subject. CC whose cells are then used for rescue of recipient subject. Also useful in the treatment of thrombocytopenia. (M1) enables transplantation to
                                                                                                                                                                                                                                                                                                                                                                                                                    cell production in a subject which involves administering a Thrombopoietin (TPO) mimetic compound to the subject. Also included is another method (M2) of providing haematopoietic stem cells to a subject which involves administering a TPO mimetic compound to a subject to enhance expansion of a stem cell population within bone marrow and/or mobbilize stem cells in peripheral circulation, harvesting one or more of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO;
proceed in patients who would not otherwise be considered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing hematopoietic stem cell production in subject, useful reducing the incidence of delayed primary engraftment, comprises administering a Thrombopoietin mimetic compound e.g., a peptide {\tt i}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaushansky K,
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18-SEP-2002; 2002US-0411779P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stem cell therapy; HSC; transplantation; engraftment; mimetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPO mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM72479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM72479 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-283153/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (THRE-) 3-DIMENSIONAL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to a method (M1) for increasing haematopoietic stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haematopoietic stem cell; thrombopoietin; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003WO-US029701.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macdonald BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "beta-alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    because of unacceptably high risk of failed engraftment, reduces the number of aphereses required to generate a minimum acceptable harvest, reduces the incidence of primary and secondary failure of engraftment by increasing the number of haematopoietic stem cells (HSCs) available for transplantation and reduces the time required for primary engraftment. The present sequence represents an example of TPO mimetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM72478 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 AA
                                                                                                                         Disclosure; Fig 2; 32pp; English.
                                                                                                                                                         administering
                                                                                                                                                                       reducing
                                                                                                                                                                               Increasing
                                                                                                                                                                                                        WPI; 2004-283153/26
                                                                                                                                                                                                                             Kaushansky K,
                                                                                                                                                                                                                                                                          18-SEP-2002;
18-SEP-2002;
                                                                                                                                                                                                                                                                                                            18-SEP-2003; 2003WO-US029701
                                                                                                                                                                                                                                                                                                                                   01-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM72478;
                                                                                                                                                                                                                                                    (THRE-) 3-DIMENSIONAL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haematopoietic stem cell; thrombopoietin; haemostatic; cell therapy; HSC; transplantation; engraftment; mimet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                         ng hematopoietic stem cell production in subject, useful the incidence of delayed primary engraftment, comprises ering a Thrombopoietin mimetic compound e.g., a peptide t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                          2002US-0411700P.
2002US-0411779P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                             Macdonald BR;
                                                                                                                                                                                                                                                                                                                                                                             group"
                                                                                                                                                                                                                                                                                                                                                                                      /note= "Lys (15) is peptide through the copy of the peptide
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 8;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          linked to one copy of the TPO mim alpha amino group and to a second (not shown) via the omega amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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cell production in a subject which involves administering a Thrombopoietin (TPO) mimetic compound to the subject. Also included is another method (M2) of providing haematopoietic stem cells to a subject which involves administering a TPO mimetic compound to a subject to enhance expansion of a stem cell population within bone marrow and/or mobilize stem cells in peripheral circulation, harvesting one or more of the bone marrow stem cells or the stem cells in the peripheral circulation, and transplanting the harvested stem cells into the subject A method (M3) is also provided for reducing a time to engraftment

the subject

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The invention relates to a method

(M1) for increasing haematopoietic stem

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RESULT 32
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPO; haematopoietic stem cell; thrombopoietin; haemostatic; stem cell therapy; HSC; transplantation; engraftment; mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPO mimetic peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-2004
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Increasing hematopoietic stem cell production in subject, useful in reducing the incidence of delayed primary engraftment, comprises
                                                                                                                         WPI; 2004-283153/26
                                                                                                                                                                                                                                                                                                                                                           18-SEP-2002; 2002US-0411779P.
18-SEP-2002; 2002US-0411779P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-2003; 2003WO-US029701
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                                                                                                                                                                                                Kaushansky K,
                                                                                                                                                                                                                                                                                    (THRE-) 3-DIMENSIONAL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEGPTLROWLAARA 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                     Macdonald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note = connected to a cysteine residue of a similar TPO mimetic peptide (not shown) by a disulphide bridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 73; DB 8; 100.0%; Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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cc which involves administering a TPO minetic compound to a subject to combilize stem cells in peripheral circulation, harvesting one or more of the bone marrow stem cells or the stem cells in the peripheral circulation, harvesting one or more of circulation, and transplanting the harvested stem cells into the subject. A method (M3) is also provided for reducing a time to engraftment compound to the subject, enhancing the expansion of the stem cells in a subject, involves administering a compound to the subject, enhancing the expansion of the stem cell population within bone marrow and/or mobilizing the stem cells in cell population within bone marrow and/or mobilizing the stem cells in cells or one or more of the stem cells in the peripheral circulation, and transplanting the one or more harvesting one or more of the bone marrow stem cells or one or more of the stem cells into the subject. TPO transplanting the one or more harvested stem cells into the subject. TPO transplanting the one or more harvested stem cells into the subject. TPO cells or one or more disclosed as peptides, including cyclic or modified comparatiment following reinfusion of stem cells into the subject. TPO cells engraftment following reinfusion of stem cells in a subject. Cells are then useful for increasing the time of platelet and/or cells are then used for rescue of latelet and/or cells in a subject. The present stem cells from a donor the treatment of thrombocytopenia. (M1) enables transplantation to cell considered as candidates because of unacceptably high risk of failed engraftment, reduces the incidence of paraftment by increasing the number of stem cells from a considered to generate a minimum acceptable harvest, cells present sequence represents an example of TPO mimetic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin (TPO) mimetic compound to the subject. Also included is another method (M2) of providing haematopoietic stem cells to a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   administering a Thrombopoietin mimetic compound e.g., a peptide to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    production in a subject which involves administering a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a method (M1) for increasing haematopoietic stem
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δ Matches Best Local Query Match 1 IEGPTLRQWLAARA 14 14; Conservative Similarity 100.0%; Score 73; 100.0%; Pred. No. vative 0; Mismatch Mismatches 1.5e-05; hes 0; DB 8; Length 15; Indels 0 Gaps 0

Sequence 15 AA;

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ADM72522 standard; peptide; 15 AA
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TPO mimetic peptide fragment. 17-JUN-2004 (first entry)

TPO; haematopoietic stem cell; thrombopoietin; haemostatic; stem cell therapy; HSC; transplantation; engraftment; mimetic

Synthetic. Modified-site Location/Qualifiers

/note= "Ly8 (15) is 1 peptide through the a copy of the peptide (group" linked to one copy of the TPO mimetic alpha amino group and to a second (not shown) via the omega amino

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RESULT 34
ADM72523
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                                                                                                                                                                                                                                                                                                                                                                                                 CC Thrombopoietic (TPO) mimetic compound to the subject. Also included is another method (M2) of providing haematopoietic stem cells to a subject to which involves administering a TPO mimetic compound to a stubject to combilize stem cells in peripheral circulation, harvesting one or more of the bone marrow stem cells or the stem cells in the peripheral circulation, and transplanting the harvested stem cells into the subject. CC A method (M3) is also provided for reducing a time to engraftment CC following reinfusion of stem cells in a subject, involves administering a CC TPO mimetic compound to the subject, enhancing the expansion of the stem CC ll population within bone marrow and/or mobilizing the stem cells in CC peripheral circulation, harvesting one or more of the stem cells into the subject. TPO mimetic compounds are disclosed as peptides, including cyclic or modified CC production in a subject e.g., human. (M3) is useful for increasing haematopoietic stem cell comparatiment following reinfusion of stem cells, reducing the incidence of delayed primary engraftment, reducing the time of platelet and/or neutrophil engraftment following reinfusion of stem cells in a subject. (M1) is also useful for increasing the number of stem cells in a subject. CC whose cells are then used for rescue of recipient subject. Also useful in the treatment of thrombocytopenia. (M1) enables transplantation to proceed in patients who would not otherwise be considered as candidates concerns the incidence of paraftment by increasing the number of aphereses the incidence of necessary and secondary failure of engraftment by increasing the number of haematopoletic stem cells (HSCs) available for reduces the incidence of primary and secondary failure of engraftment by increasing the number of haematopoletic stem cells (HSCs) available for transplantation and reduces the time required for primary appraftment.
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                              Query Match
Best Local
ADM72523,
                                      ADM72523 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                          Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-2002; 2002US-0411770P.
18-SEP-2002; 2002US-0411779P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method (M1) for increasing haematopoietic stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaushansky K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                   transplantation and reduces the time required for primary engraftment. The present sequence represents an example of TPO mimetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             production in
                                                                                                                                                                                     1 IEGPTLRQWLAARA 14
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macdonald BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a subject which involves administering a o) mimetic compound to the subject. Also
                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                              Score 73; DB 8;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                           <u>.</u>.
                                                                                                                                                                                                                           Gaps
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CC the bone marrow stem cells or the stem cells in the peripheral circulation, and transplanting the harvested stem cells into the subject.

CC A method (M3) is also provided for reducing a time to engraftment compound to the subject, involves administering a following reinfusion of stem cells in a subject, involves administering a feel population within bone marrow and/or mobilizing the expansion of the stem cell population within bone marrow and/or mobilizing the stem cells in cells or one or more of the stem cells in the peripheral circulation, harvesting one or more of the bone marrow stem cells or one or more or more harvested stem cells into the subject. TPO cells or one or more harvested stem cells into the subject. TPO cells or one or more harvested stem cells into the subject. TPO cells or one or more harvested stem cells into the subject. TPO cells or one or more harvested stem cells into the subject. TPO cells or one or more peripheral circulation, and cells or one or more harvested stem cells into the subject. TPO cells or one or more cells or increasing haematopoietic stem cell cells production in a subject e.g., human. (M3) is useful for reducing time to cell subject e.g., human. (M3) is useful for reducing time to cell subject or of platelet production and reducing the time of platelet and/or cells in a subject. (M1) is also useful for increasing the number of stem cells in a subject. (M1) is also useful for increasing the number of stem cells in a subject. Cells are then used for rescue of recipient subject. Also useful in the treatment of thromboytopenia. (M1) enables transplantation to compose cells in a subject and/or cells in cells in a subject. The cell cells in the transplantation to cells in the transplantation to cells in the transplantation to cells in the transplantation to cells in the transplantation to cells in the cells in the cells in the cells in the cells in the cells in the cells in the cells in the cells in the cells in the cells in the cells in the cells in the cells in the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell production in a subject which involves administering a Thrombopoietin (TPO) mimetic compound to the subject. Also included is another method (M2) of providing haematopoietic stem cells to a subject which involves administering a TPO mimetic compound to a subject to enhance expansion of a stem cell population within bone marrow and/or mobilize stem cells in peripheral circulation, harvesting one or more of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing hematopoietic stem cell production in subject, useful reducing the incidence of delayed primary engraftment, comprises administering a Thrombopoietin mimetic compound e.g., a peptide t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 32pp; English.
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                                                                  The present sequence represents an example of TPO mimetic
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CC cell production in a subject which involves administering a subject which involves administering a recompound to the subject. Also included is CC which involves administering a TPO mimetic compound to a subject to a subject combilize stem cells in peripheral circulation, harvesting one or more of the bone marrow stem cells or the stem cells in the peripheral CC circulation, and transplanting the harvested stem cells into the subject. CC A method (M3) is also provided for reducing a time to engraftment CC following reinfusion of stem cells in a subject, involves administering a CC cell population within bone marrow and/or more of the subject. TPO mimetic compound to the subject, enhancing the expansion of the stem cells or one or more of the stem cells in the peripheral circulation, harvesting one or more of the stem cells in cells or one or more of the stem cells in the peripheral circulation, and transplanting the one or more of the stem cells in the peripheral circulation, and transplanting the one or more harvested stem cells into the subject. TPO mimetic compounds are disclosed as peptides, including cyclic or modified peptides. (M1) is useful for increasing haematopoietic stem cell congraftment following reinfusion of stem cells, reducing the incidence of the subject e.g., human. (M3) is useful for reducing time to
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18-SEP-2002; 2002US-0411779P.
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                             comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoslobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents a TPO mimetic neartife.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      whose cells are then used for rescue of recipient subject. Also useful in the treatment of thrombocytopenia. (M1) enables transplantation to proceed in patients who would not otherwise be considered as candidates because of unacceptably high risk of falled engraftment, reduces the number of aphereses required to generate a minimum acceptable harvest, reduces the incidence of primary and secondary failure of engraftment by increasing the number of haematopoietic stem cells (HSCs) available for transplantation and reduces the time required for primary engraftment. The present sequence represents an example of TPO mimetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         delayed primary engraftment, reducing the time of platelet and/or of platelet production and reducing the time of platelet and/or neutrophil engraftment following reinfusion of stem cells from a donce (MI) is also useful for increasing the number of stem cells from a donce the constant subject. Also useful stem cells are then used for rescue of recipient subject. Also useful the constant subject is a constant subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunoglobulin molecule comprising a region, where two complementarity determining regions (CDRs) are replaced wi or a TPO mimetic, useful for treating thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin; complementarity determining region; CDR; peptide
erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
immunotherapy; thrombocytopenia.
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                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 2; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-460973/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowdish KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2003; 2003WO-US036894
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07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                                             The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It is part of a dimer linked by the omega amino acid to the omega amino acid in the sequence in AAWO9468. The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                                                                     Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp thrombocytopenia resulting from chemotherapy, etc.
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Sequence 16
                                                                                                                                                                                                                                                                         Claim 30; Page 91; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dower WJ, Barrett RW, Cw
Mattheakis LC, Schatz PJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; thrombocytopenia; TPO; TR; proliferation; transfusion; chemotherapy; radiation thera
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Pred. No. 1.5e-05;
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iton NC;
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Query Match Best Local Similarity

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DB 2; 1.6e-05;

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                                                                                                                                                                                                                                            Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                   Sequence 16 AA;
                                                                                      resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate th mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent
                                                                                                                                                       The present peptide binds the thrombopoietin receptor (TR), has a molecular weight of less than 8000 Da and a TR binding affinity as expressed by an IC50 of no more than about 100 microM. It can be used to treat disorders which are susceptible to treatment with a thrombopoietin
                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombopoietin receptor; binding peptide; treatment; agon: haematological disorder; thromboposenia; chemotherapy; haematological disorder strow transfusion; diagnossis; radiation therapy; bone marrow transfusion; diagnossis; signal transduction; receptor activation; cell culture.
                                                                                                                                           agonist, preferably haematological disorders and thrombocytopaenia
                                                                                                                                                                                                                     Claim 30; Page 91; 106pp;
                                                                                                                                                                                                                                                                                                  WPI; 1997-052226/05.
                                                                                                                                                                                                                                                                                                                             Mattheakis
                                                                                                                                                                                                                                                                                                                                           Dower WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin receptor binding peptide
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                                                                                                                                                                                                                                                                                                                                                                   (GLAX ) GLAXO
              Local Similarity
14;
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                                                                                                                                                                                                                                                                                                                            LC,
                                                                                                                                                                                                                                                                                                                                        Barret RW,
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                     GROUP LID.
                                                                                                                                                                                                                                                                                                                                                                                           95US-00478128
95US-00485301
                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US009623
                                                                                                                                                                                                                                                                                                                             Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
/label= bAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carboxy group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
             100.0%;
                                                                                                                                                                                                                                                                                                                            Cwirla SE, Duffii
PJ, Wagstrom CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "epsilon amino group of Lys16 linked to terminal
y group of AAW33034"
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                                                                                                                                                                                                                     English.
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             Score 73; DB 2;
Pred. No. 1.6e-05;
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 Mismatches
                                                                                                                                                                                                                                                                                                                            Duffin DJ, Gates CM, om CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                         Length 16;
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  Indels
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RESULT 40
AAW36771
ID AAW36
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AC AAW36
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DT 11-MA
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                                                                                                                          Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin receptor; binding peptide; treatment; agon: haematclogical disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                         Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36775 standard; peptide; 16
                                                                                                                                                               Sequence 16
                                                                                                                                                                                                  The present peptide, which binds the thrombopoietin receptor (TR), cused to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombopoytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and investigate the mechanism of thrombopoietin signal transduction and
                                                                                                                                                                                                                                                                       Example 9; Page 77; 106pp; English.
                                                                                                                                                                                                                                                                                                                                 WPI; 1997-052226/05.
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Mattheakis LC, Schatz PJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1998
  11-MAR-1998
                                                                                                                                                                                receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                (GLAX ) GLAXO GROUP LTD.
                                     AAW36771
                                                                                                                          l Similarity
14; Conserv
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                                                                                    N
                                      standard;
                                                                                               IEGPTLROWLAARA 15
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                                                                                                                           Conservative
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 (first entry)
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95US-00485301.
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1. .16
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "NH2-Cys"
                                     peptide;
                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                   Cwirla SE, Du
PJ, Wagstrom
                                      16
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                                                                                                                                    Score 73; DB 2; 1
Pred. No. 1.6e-05;
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                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                    Duffin DJ, Gates CM, om CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment; agonist;
                                                                                                                                             Length 16;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                               Johnson SS;
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present peptide, which binds the thrombopoietin receptor (TR), (used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin receptor; binding peptide; treatment; agon; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dower WJ,
Mattheakis
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07-JUN-1995;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Page 76; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-052226/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin receptor binding
Key
                                  Synthetic
                                                                 thrombopoietin receptor; haematological disorder; screening; agonist; assay; megakaryocyte; blood disorder; thrombocytopaenia; TPO.
                                                                                                                     Peptide chain of compound attached to
                                                                                                                                                         01-DEC-1998
                                                                                                                                                                                          AAW66709;
                                                                                                                                                                                                                            AAW66709
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                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                   IEGPTLROWLAARA
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LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00478128
95US-00485301
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1. .16
16
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "NH2-Cys"
                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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PJ, Wagstrom
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                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                        Score 73;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                       hydrophilic polymer.
                                                                                                                                                                                                                                                                                                                                                                                     . 1.6e-05;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 16;
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RESULT 42
AAW66713
ID AAW66
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                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 14
01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide compound(s) which can bind and activate thrombopoietin receptor - may be used in treating haematological disorders and in methods for screening for new thrombopoietin receptor agonists.
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                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1 and 10; Page 59; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Balasubramanian
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                                                                   AAW66713 standard;
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                                                                                                                                                                                               1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                           16
                                                                                                                                                             IEGPTLROWLAARA 14
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                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                    Conservative
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .14
/note= "thrombopoietin receptor agonist"
15
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                                                                     peptide; 16 AA
                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                  Score 73; DB
Pred. No. 1.6
0; Mismatches
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Hendren RW,
                                                                                                                                                                                                                                    . 1.6e-05;
thes 0;
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Deprince RF
                                                                                                                                                                                                                                                                        Length 16
                                                                                                                                                                                                                                    Indels
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IEGPTLROWLAARA 14 IEGPTLROWLAARA 14 Query Match Best Local S Matches 14

Similarity

100.0%;

Conservative

0

Score 73; DB 2; Pred. No. 1.6e-05; Mismatches 0;

Length 16;

<u>.</u>

Gaps

0

Sequence 16 AA;

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The invention relates to peptide compounds composed of two peptide chains attached to each of the amino groups of a single Lys in the amide form. CC The compounds are of formula (Pep1) (Pep2)K(NH2), where Pep1 is of CC formula: X1-I-B-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9-X10; and pep2 is of CC formula: X1-I-B-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9-X10; and pep2 is of CC acetyllysine; X4 = Gln or Gli; X5 = Txp, L1-naphthylalanine or Phe; X6 = CC Ala, 5-aminopentanoic acid or 2-aminobutyric acid; X7 = Ala, N-methyl-alanine, Or is absent; X8 = Arg, p- amino-phenylalanine, N-CC acetyl-lysine, or is absent; X9, x9' = Ala, beta Ala, N-methyl-alanine, CC Sar, or is absent; X10, X10' = beta Ala or is absent. The new peptides CC are capable of binding to, and activating, the thrombopoietin (TP0) CC receptor. They may be used in vitro as tools for understanding the CC biological role of TPO. They may be used as competitive binders in assays to screen for new TPO receptor agonists. They may be used as reagents for detecting TPO receptors in living cells, biological fluids, etc. They may be used to maintain growth and proliferation of TPO-dependent cells and CC por in vitro expansion of megakaryocytes. They may be used to activate thrombocytopaenia associated with bone marrow transfusions, radiotherapy or chemotherapy. The present sequence represents a specific example of CC (Pen1)K(NH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide compound(s) which can bind and activate thrombopoietin receptor - may be used in treating haematological disorders and in methods for screening for new thrombopoietin receptor agonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
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anian P, Wagstrom CR, Hendren
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Deprince RB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide compound(s) which can bind and activate thrombopoietin receptor - may be used in treating haematological disorders and in methods for screening for new thrombopoietin receptor agonists.
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Balasubramanian P,
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peptide chain identical to the region (residues 1-15)
the present peptide"
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Hendren
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identical to the region
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         The invention relates to peptide compounds composed of two peptide chains cattached to each of the amino groups of a single Lys in the amide form. CC The compounds are of formula (Pepl) (Pep2) K(NH2), where Pepl is of CC formula: X1-1-E-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9-X10; and pep2 is of CC endla: X1-1-E-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9-X10; and pep2 is of CC endly or Sar (sarcosine); X3 = Arg, Ala, Nle (norleucine) or N-CC acetyllysine; X4 = Gln or Glu; X5 = Trp, L-1-naphthylalanine or Phe; X6 = CC Ala, 5-aminopentanoic acid or 2-aminobutyric acid; X7 = Ala, N-actyllysine, or is absent; X8 = Arg, p-amino-phenylalanine, N-CC diphenylalanine, or is absent; X9, X9' = Ala, beta Ala, N-methyl-alanine, CC Sar, or is absent; X10, X10' = beta Ala or is absent. The new peptides CC are capable of binding to, and activating, the thrombopoietin (TPO) CC receptor. They may be used in vitro as tools for understanding the biological role of TPO. They may be used as competitive binders in assays to screen for new TPO receptor agonists. They may be used as reagents for detecting TPO receptors in living cells, biological fluids, etc. They may be used to maintain growth and proliferation of TPO-dependent cells and CC be used to maintain growth and proliferation of TPO-dependent cells and CC thrombocytopaenia associated with bone marrow transfusions, radiotherapy correspond transfusions, radiotherapy correspond transfusions, radiotherapy correspond to activate or thrombocytopaenia associated with bone marrow transfusions, radiotherapy correspond to activate or the present semisors represents a meerific example of
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15
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attached to another peptide chain identical to
(residues 1 to 14) of this peptide"
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Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that contact and activate the human thrombopoietin receptor (PPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and cenzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dower WJ,
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Manian P, Wagstrom CR, Hendren RW,
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serine-threonine glyceraldehyde-3-p baf protein hypothetical

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ALIGNMENTS

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probable membrane protein YPO1203 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0147
C;Accession: AG0147
R; Prackhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P25545; EMBL:Z22705; NID:g297851; PIDN:CAA80406.1; R;Meijer, W.G.; Arnberg, A.C.; Enequist, H.G.; Terpstra, P.; Lidstrom, M.E.; Di Mol. Gen. Genet. 225, 320-330, 1991
A;Title: Identification and organization of carbon dioxide fixation genes in Xa A;Reference number: S13573; MUID:91172133; PMID:1900916
A;Accession: S13578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Start codon: GTG
C;Superfamily: transcript
C;Keywords: DNA binding;
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C;Genetics:
A;Gene: cbbR
                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AG0147
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A; Residues: 1-150 < MEI >
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A; Residues: 1-296 < KI
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Matches 9
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81.8%;
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UTP-glucose-1-phosphate uridylyltransferase

(EC

2.7.7.9) galU [similarity] - Mycobacteri

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C;Species: Mycobacterium tuberculosis
C;Accession: D70601
C;Accession: D70601
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70601
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-306 CCOL>
A;Cross-references: UNIPROT:005576; GB:Z94752; GB:AL123456; NID:g3261731; PIDN:CAB08153
A;Experimental source: strain H37Rv
probable glutathione transferase (EC 2.5.1.18) GST3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T37464
R;Tawe, W.N., Eschbach, M.L.; Walter, R.D.; Henkle-Duehrsen, K. submitted to the EMBL Data Library, June 1997
A,Description: Paraquat mediates differential gene expression in C. elegans. A;Reference number: Z21702
A;Accession: T37464
A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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C;Superfamily: Escherichia coli UTI
C;Keywords: nucleotidyltransferase
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A;Introns: 45/1; 76/1; 111/3
C;Superfamily: glutathione transferase
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C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T23485
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A; Residues: 1-200 <WIL>
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Pred. No.
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Pred. No.
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N;Alternate names: 2,3-dihydroxybenzoate-AMP ligase [misnomer]; dihydroxybenzoic a C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 31-Dec-1989 #sequence revision 21-Nov-1997 #text_change 09-Jul-2004
C;Accession: H64792; A48308; Ā32047; I41058; S08076
R;Blattner, F;R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley,
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Tetle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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C; Superfamily: glutathic
C; Keywords: transferase
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A;Cross-references: UNII
A;Experimental source: C;Genetics:
                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 393-536 <LIU>
A;Residues: 393-536 <LIU>
A;Cross-references: GB:M24148; NID:g304949; PIDN:AAA16101.1; PID:g450380
C;Comment: The enzymatic steps in the condensation of L-serine and 2,3-dihydroxybenzoic ty is based on its recognized homology with 4-coumarate-CoA ligase and by analogy with tC;Comment: The formation of 2,3-dihydroxybenzoyl-AMP has been observed. The rapid reacticarrier protein) to release AMP, has also been observed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A48308
A;Molecule type: DNA
A;Residues: 1-368,'ECRRKSTAAR',379-536 <STA>
A;Residues: GB:MZ7490; EMBL:X15058; N
R;Liu, J.; Duncan, K.; Walsh, C.T.
J. Bacteriol. 171, 791-798, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Staab, J.F.; Elkins, M.F.; Earhart, C.F.
FEMS Microbiol. Lett. 59, 15-19, 1989
A;Title: Nucleotide sequence of the Escherichia coli entE
A;Reference number: A48308; MUID:89290355; PMID:2525505
A;Note: in MedLine 89290355 this citation is erroneously c
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                                                                                                4 C C
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A;Map position:
C;Function:
                                                                                                                                                                                                                                                                                                                              carrier protein)
C;Genetics:
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A; Experimental source: strain K-12,
                                                                                                                                                                                      A; Note: this is one component of a membrane-bound multienzyme
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                                                                                                                                                           for transport into the cell
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                                                                                      Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology; Keywords: acid-thiol ligase; enterobactin biosynthesis; membrane-associated; 69-526/Domain: acetate-CoA ligase homology <ACL>
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Pred. No. 5
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IEGPTLRQWLAARA 14

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; C they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Chidambaram,

0.,

Sutton,

G.G.; Dodson, M.; Utterback,

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MCE

probable dimethyladenosine transferase (ksgA) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: G71337

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A; Reference number: A99629; A; Accession: A99708
                                                                                                                                                                                                                                                                                       DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 01-Mar-2002
C;Accession: E85558
                                                                                                                                 A;Gene: ECs0633
C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA
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                                                                                                                                                                                                                                                                                                                                                                                                                     2,3-dihydroxybenzoate-AMP ligase [imported] - C;Species: Escherichia coli
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C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA
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A; Residues: 1-536 <STO>
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Nature 409, 529-533, 2001
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                                                                                                                                                                                          A; Experimental source:
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A; Residues: 1-536 < HAY>
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;Experimental source: strain O157:H7, substrain RIMD 0509952
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Pred. No. 13;
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Shiba, T.;
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A.; Dimalanta,
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Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: B71325
                                                                                                                                                                                                                                                                 Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84853
                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: E84853
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Taleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Verense, D.; White, D.; W
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                                                                           A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein At2g42400 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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A;Gene: TP0421
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A; Residues: 1-683 < COL>
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A; Residues: 1-285 < COL>
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                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-473 <STO>
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Best Local S
Matches 9
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                                           ;Gene: At2g42400
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                                                                                                                  UNIPROT: Q9SLB9; GB: AE002093; NID: g4567312; PIDN: AAD23723.1; GSPDB: GN
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50; MUID:98332770; PMID:9665876
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69.2%;
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polyprotein - simian immunodeficiency virus SIVsm (strain E543) (fragme C;Species: simian immunodeficiency virus SIVsm A;Variety: strain E543 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T11560
                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-195 <-HAY>
A;Cross-references: UNIPROT:Q8X5U4; GB:BA000007;
A;Experimental source: strain O157:H7, substrain
C;Genetics:
probable phosphopantetheinyltransferase [imported] -
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #sequence_revision 16-Feb-2001
                                                         RESULT
F86017
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable phosphopantetheinyltransferase [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
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F91171
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C;Keywords: AIDS; immunodeficiency
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A; Residues: 1-1019 <HIR>
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A;Title: A molecularly cloned, pathogenic, neutralization-resistant simian immuno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T11560
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                                                                                                                                                                                                                                                                                A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z17285;
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 6
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                   EGPTLRQWLAARA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGPKLROW 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii,
Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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87.5%;
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53.8%;
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MUID:97151152;
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                                                                                                                                                                                                                          Score
Pred.
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No.
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15;
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RIMD 0509952
 #text_change 09-Jul-2004
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                                       Escherichia coli (strain 0157:H7,
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M.; Shinagawa,
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A;Cross-references: GB:AE000423; GB:U00096; NID:g1789880; PIDN:AAC76500.1; PID:g1789886; A;Experimental source: strain K-12, substrain MG1655 C;Genetics: A;Gene: yhhU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical 21.8K protein (ftsy-nika intergenic N;Alternate names: hypothetical protein o195 (Species: Escherichia coli C;Date: 27-Jan-1995 #seguence_revision 27-Jan-199 C;Accession: $47694; F65144 R;Plunkett, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: F86017
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau. B.; Glasner, J.D.; R
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F86017
A;Statue; preliminary
A;Molecule type: DNA
A;Residues: 1-195 <570>
                                                                                                                                                                             RESULT 16
E87575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F65144
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A;Experimental source: strain O157:H7, substrain
C;Genetics:
A;Gene: Z4867
                  R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
                                                                                              ABC transporter, ATP-binding protein CC2634 [imported] - Caulobacter cresces C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: E87575
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A; Residues: 1-195 < PLU>
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A;Status: prelimina
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                                                                                                                                   BC transporter, ATP-binding protein CC2634 [imported] - Species: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
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Best Local :
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Best Local :
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Complete
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7; Conserve
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Genome Sequence of
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53.8%;
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Pred. No.
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Pred. No.
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Bloch, C.A.;
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Caulobacter crescentus
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15;
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Perna, N.T.;
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Burland, V.; Riley, M.; Co
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Potamousis,
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K.; A
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RESULT
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A;Molecule type: DNA
A;Residues: 1-249 <ST
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                                                                                                C; Superfamil
C; Keywords:
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A;Title: Evidence in favor of the symbiotic origin of chloroplasts:
A;Reference number: A90888; MUID:87002494; PMID:3757034
A;Accession: C24430
                                                                                                                                                                                                                                                                                                               glyceraldehyde-3-phosphate dehydrogenase (NADP)
C;Species: Nicotiana tabacum (common tobacco)
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C; Keywords:
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C;Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
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C;Species: Mycobacterium leprae
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                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-326 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9Z5G1;
A;Experimental source: cosmid L373
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Best Local :
                                                                                              Superfamily: glyceraldehyde-3-phosphate dehydrogenase Keywords: cytosol; NADP; oxidative phosphorylation; o:
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      IEGPTLROWLAARA 14
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                                    Conservative
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Pred. No. 20;
2; Mismatches
                                    5
                                                   Score 41; DB
Pred. No. 26;
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Pred. No.
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February 1998
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VDGPSMKDWRGGRA 192

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R;Martin, W.; Gierl, A.; Saedler, H.
Nature 339, 46-48, 1999
A;Title: Molecular evidence for pre-Cretaceous
A;Reference number: S17991
A;Accession: S18484
                                                                                                                              glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)
N;Alternate names: triosephosphate dehydrogenase
C;Species: Sinapis alba (white mustard)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_cl
C;Accession: A24796
C;Accession: A24796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross references: UNIPROT: D26519; EMBL: X60344; NID: g20548; PIDN: CAA42902.1; PID: g20549
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1991
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase
F;4-34/Region: beta-alpha-beta NAD nucleotide-binding fold
F;153,180/Active site: Cys, His #status predicted
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DEIS3C
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C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: oxidoreductase
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A;Molecule type: mRNA
A;Residues: 1-337 <OST>
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R;Ostrem, J.A.; Vernon, D.M.; E
J. Biol. Chem. 265, 3497-3502,
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A; Molecule type: mRNA
                    Eur. J. Biochem. 159, 323-331, 1986
A;Title: Prokaryotic features of a nucleus-encoded enzyme.
A;Reference number: A24796; MUID:87004643; PMID:3530755
A;Accession: A24796
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A; Accession: A35080
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A35080
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A; Residues: 1-336 < MAR>
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                                                                                                           W.; Cerff, R.
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A;Cross-references: UNIPROT:Q92ZH9; GB:AE006469; PIDN:AAK65164.1; PII A;Experimental source: strain 1021, megaplasmid pSymA R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
                                                                                                                                                                                                                R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: B95325
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A;Introns: 2/1; 12/1; 45/3; 84/2; 117/3; 167/2; 187/1; 267/2
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: cytosol; oxidoreductase
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A;Title: Cloning and chromosomal mapping of nuclear genes
A;Reference number: JQ1285; MUID:92009205; PMID:1916285
A;Accession: JQ1287
A;Molecule type: DNA
A;Residues: 1-338 <SHI>
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JQ1287
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A;Cross-references: UNIPROT:P04796; GB:X04301; NID:g21142; PIDN:CAA27844.1;
A;Cross-references: UNIPROT:P04796; GB:X04301; NID:g21142; PIDN:CAA27844.1;
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase
C;Csywords: glyceraldehyde-3-phosphate dehydrogenase #status experiment
E;2-338/Product: glyceraldehyde-3-phosphate dehydrogenase #status experiment
E;7-37/Region: beta-alpha-beta NAD mucleotide-binding fold
E;156,183/Active site: Cys, His #status predicted
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R; Shih, M.C.; Heinrich, P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_ch
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001
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A; Residues: 1-338 < SHI1>
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A; Residues: 1-719 < KUR>
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Pred. No.
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Pred. No.
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                                                                        Abola, P.; Ampe,
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                                                    F.; Barloy-Hubler
N.A.; Fisher, R.F.
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RESULT 25
AE2719
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A; Map position: circular chromoso C; Superfamily: DNA topoisomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, (hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A97359;
A;Accession: A97501
A;Status: preliminary
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrol
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                                                                                                                                                                         A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                         R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Dhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A; Map position:
C; Superfamily:
                                                                               A;Cross-references: UNIPROT:Q8UG82; A;Experimental source: strain C58 (
                                                                                                                                                                                                                                                                                                                                                                              topoisomerase IV subunit A parC [imported] - Agrobacterium tumefaciens (str C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-750 < KUR>
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Best Local
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ONA topoisomerase (A
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46.2%;
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66.7%;
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Pred. No.
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(ATP-hydrolyzing)
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kelz, B.
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                                                        probable permease NMA0414 [imported] - Neisseria meningitidis (strain Z2491 serogroup C;Species: Neisseria meningitidis (c;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 C;Accession: A81958 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mor; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea Nature 404, 502-506, 2000
                                                                                                                                                                                                    RESULT
A81958
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    A;Reference number: A81775;
A;Accession: A81958
                                           A; Title: Complete DNA sequence of a serogroup A strain of Neisseria
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hypothetical protein A - Bacillus firmus
C;Species: Bacillus firmus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
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R;Geistlich, M.; Losick, R.; Turner, J.R.; Rao, R.N.
Mol. Microbiol. 6, 2019-2029, 1992
A;Title: Characterization of a novel regulatory gene governing
A;Reference number: S25202; MUID:92374852; PMID:1508047
A;Accession: S25204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Streptomyces ambofaciens
C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change
C;Accession: S25204; S21599
                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-463 <QUI>
A;Cross-references: UNIPROT:P30267; GB:L02548; EMBL:M74194; NID:g143118; PIDN:AAA22559.
                                                                                                                                                                                                              A; Reference number: S27490
A; Accession: S27491
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F;39-139/Domain: bioC homology <BIOC>
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A; Residues: 1-239 < GEI>
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Pred. No.
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MUID:20222556; PMID:10761919

menigitidis

Z2491

S.R.; More Rajandream

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submitted to the EMBL Data Library, December 1992
A;Description: Human infection by genetically diverse SIVSM-related HIV-2 in west A;Reference number: S30460
A;Retession: S30484
A;Status: preliminary
A;Molecule trace.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-530 <PAR>
A;Cross-references: UNIPROT:Q9JWE3; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB837;
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA0414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. T.; H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
                                                                                                                                                     A;Cross-references: EMBL:M87114
C;Superfamily: pol polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Neisseria meningitidis serogroup A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: E81015
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A; Residues: 1-656 < GAO>
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A; Residues: 1-531 <TET>
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                                                                                                                                                                                                                                                                                                                                                               ol polyprotein - human immunodeficiency virus type 2;Species: human immunodeficiency virus type 2, HIV-2;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 23-Mar-2001
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8; Conserv
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Pred. No.
                                                                                            Pred. No. 77;
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Pred. No. 62;
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strain MC58
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A; Molecule type: DNA
A; Residues: 1-721 «KORI»
A; Residues: 1-721 «KORI»
A; Cross-references: UNIPROT: P16452; GB: L06519; NID: g306738; PIDN: AAA52385.1; PID: g30674
A; Experimental source: cell type erythrocyte; tissue type peripheral blood; tissue lib
A; Experimental source: cell type erythrocyte; K.; Bliss, S.A.; Bouhassira, E.E.; Nagel
R; Sung, L.A.; Chien, S.; Chang, L.S.; Lambert, K.; Bliss, S.A.; Bouhassira, E.E.; Nagel
Proc. Natl. Acad. Sci. U.S.A. 87, 955-959, 1990
A; Title: Molecular cloning of human procein 4.2: a major component of the erythrocyte m
A; Reference number: A34865; MUID: 90138995; PMID: 1689063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Contains: erythrocyte membrane band 4.2 protein, long C; Species: Homo sapiens (man) C; Date: 29-Oct-1999 #sequence revision 29-Oct-1999 #text C; Accession: A39707; A34865; B34865; A34883 R; Korsgyren, C:; Cohen, C.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 4840-4844, 1991 A, Title: Organization of the gene for human erythrocyte A, Reference number: A39707; MUID:91271288; PMID:2052563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 31
S30483
                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-3,34-364, KRGLPC',371-379,'H',381-405,'L',407-721 <SUN2>
A;Residues: 1-3,34-364, KRGLPC',371-379,'H',381-405,'L',407-721 <SUN2>
A;Cross-references: GB:M30646; NID:g189435; PIDN:AAA36402.1; PID:g189436
A;Cross-references: isolate Sickle cell partient; cell type reticulocyte
A;Note: parts of this sequence were determined by protein sequencing
R;Korsgren, C:; Lawler, J:; Lambert, S:; Speicher, D:; Cohen, C:M.
Proc. Natl. Acad. Sci. U.S.A. 87, 613-617, 1990
A;Title: Complete amino acid sequence and homologies of human erythrocyte 1
A;Reference number: A34883; MUID:90138879; PMID:2300550
A;Accession: A34883
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A;Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa, Reference number: S30460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-364,'KRGLPC',371-379,'H',381-405,'L',407-721 <SUN1>A;Cross-references: GB:M30647; NID:g189433; PIDN:AAA36401.1; PID:GA;Accession: B34865
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A39707
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A;Molecule type: nucleic acid
A;Residues: 1-656 <GAO>
A;Cross-references: EMBL:M87111
A;Gene: GDB:EPB42; PA
A;Cross-references: GDB:127385; OMIM:177070
A;Map position: 15q15-15q15
                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-3,34-721 <KOR2>
A; Cross-references: GB: M29399; NID: g182083; PIDN: AAA35798.1; PID: g182084
C; Comment: This protein is a major constituent of the erythrocyte membran
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                                                                                                      Genetics:
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Pred. No.
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C;Superfamily: protein-glutamine gamma-glutamyltransferase C;Keywords: alternative splicing; blocked amino end; glycoprotein; lipoprotein; F;2-721/Product: erythrocyte membrane band 4.2 protein, long splice form #status

myristy

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telomerase reverse transcriptase - Arab N;Alternate names: protein F5E19 190 C;Species: Arabidopsis thaliana (mouse-C;Date: 18-Aug-2000 #sequence_revision C;Accession: T51917 R;Sato, S.; Nakamura, Y.; Kaneko, T.; K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 33
T51517
                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 2(IV) chain precursor - human
N;Alternate names: procollagen alpha 2(IV) chain
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A32024; S00007; S02624; S00246; S17678; S16911; B32117; S16877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-1123 <SAT>
A; Cross-references: UNIPROT: Q9SPU7; EMBL: AL391147
A; Experimental source: cultivar Columbia; BAC clo
C; Genetics:
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F;298-316/Domain: transmembrane #status predicted <TRM>
F;518-520/Kegion: cell attachment (R-G-D) motif
F;27Modified site: myristylated amino end (cly) (in mature form) #status predicted F;103,420,447,529,604,705/Binding site: carbohydrate (Asn) (covalent) #status predicted F;278/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
                                                                                                                                                                                                                                                                                        J. Biol. Chem. 263, 19488-19493, 1988
A;Title: The complete primary structure of the alpha2 c
A;Reference number: A32024; MUID:89066769; PMID:3198637
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                                                                                                                                                                        R;Hostikka, S.L.; Kurkinen,
FEBS Lett. 216, 281-286, 19
                                                                                                                                                                                          A;Cross-references: UNIPROT:P08572; EMBL:J04210; R;Hostikka, S.L.; Kurkinen, M.; Tryggvason, K.
                                                                                                                                                                                                                                                                                                                                           R;Hostikka, S.L.; Tryggvason, K.
J. Biol. Chem. 263, 19488-19493, 1988
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A;Accession: T51517
A;Status: preliminary
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                                                 A; Molecule type: mRNA
A; Residues: 1254-1398, 'V', 1400-1712 <HOS2>
                                                                                         A;Reference number: S00007; MUID:87219158; PMID:3582677 A;Accession: S00007
                                                                                                                                    ated region.
                                                                                                                                                     A; Title: Nucleotide sequence coding
                                                                                                                                                                                                                                      A;Residues: 1-1712 <HOS1>
                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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          A; Note: 1399-Ile was also found
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                                Cross-references: EMBL:J04210; EMBL:X05610;
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August 2000
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                                    PIDN: CAA29098.1;
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A;Molecule type: protein
A;Residues: 490-492,'X',494-496;675-677,'G',679-680,'G',682,684-685,
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                                        A; Accession: S16912
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A; Molecule type: protein
A; Residues: 407-570 < EBL>
R; MacWright, R.S.; Benson, V.A.; Lovello
Biochemistry 22, 4940-4948, 1983
A; Title: Isolation and characterization
A; Reference number: S16910; MUID: 8405334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:J04217; NID:g180759; PIDN:AAA53097.1; PID:g553233; EMBL:J05039 A;Note: this sequence was submitted to the EMBL Data Library, October 1988 R;Siebold, B.; Qian, R.Q.; Glanville, R.W.; Hofmann, H.; Deutzmann, R.; Kuehn, K. Eur. J. Biochem. 168, 569-575, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:J04217; EMBL:J05039; NID:g180759; PIDN:AAA53097.1; R;Soininen, R.; Huotari, M.; Ganguly, A.; Prockop, D.J.; Tryggvason, K. J. Biol. Chem. 264, 13565-13571, 198
A;Title: Structural organization of the gene for the alpha-1 chain of human A;Reference number: S16876; MUID:89340433; PMID:2701944
A;Accession: S16877
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A;Title: The structural genes for alphal and alpha2 chains of human type A;Reference number: A92690; MUID:89034231; PMID:3182844
A;Accession: B32117
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                                                                                                                                                                                                       A;Note: the sequence from Fig. 4 is R;Eble, J.A.; Golbik, R.; Mann, K.; EMBO J. 12, 4795-4802, 1993
A;Title: The alpha-1-beta-1 integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO J. 7, 2687-2695, 1988
A;Title: The genes for the alpha1(IV) and alpha2(IV) characterence number: S02738; MUID:89030632; PMID:2846280
A;Accession: S16911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Poeschl, E.; Pollner, R.; Kuehn, K. EMBO J. 7, 2687-2695, 1988
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A;Cross-references: EMBL:X05562; NID:g30075; PIDN:CAA29076.1;
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A; Residues: 1-682, 'G'
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                                                                                                                                                            A; Reference number: S39614; A; Accession: S39615
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A; Residues: 1-33 <SOI1>
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A; Residues: 1-33 < POE>
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A;Residues: 1-470,'P'
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        acterization of MUID:84053346;
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                                                                                   Lovello,
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                                                                                      K.T.; van der Rest,
          pepsin-solubilized
PMID:6416291
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C;Reywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycoprof; basement membrane; cell binding; coiled csIG>
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1712/Product: collagen alpha 2(IV) chain #status predicted <MAT>
F;29-1712/Product: collagen alpha 2(IV) chain #status predicted <MAT>
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Hoppe-Seyler's Z. Physiol. Chem. 362, 943-951, 1981
A;Title: Peppin fragments of human placental basement-membrane collagens showing A;Reference number: S16908; MUID:82005835; PMID:6792033
A;Accession: B58517
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A;Introns: 15/2; 33/3; 1347/1; 1380/1; 1429/1; 1468/1; 1532/1; 1527/3 #status incomplete A;Note: the alpha 1(IV) and alpha 2(IV) chain genes are encoded on opposite strands with C;Complex: Type IV collagen is a heterotrimer of two alpha 1(IV) chains (see PIR:CGHU4B) domains (with disulfide and desmosine cross-links), dimeric associations among trimer carrupted helical domain (with disulfide and desmosine cross-links).
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A;Residues: 1480-1535;1545-1614;1617-1662,'H',1664-1700,'G';1705-1708;1710-1712
A;Residues: 1480-1535;1545-1614;1617-1662,'H',1664-1700,'G';1705-1708;1710-1712
A;Note: the sequence form Fig. 7 is inconsistent with that shown in Fig. 11 in h
R;Myers, J.C.; Howard, P.S.; Jelen, A.M.; Dion, A.S.; Macarak, E.J.
J. Biol. Chem. 262, 9231-9238, 1987
A;Title: Duplication of type IV collagen COOH-terminal repeats and species-speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: structural component of basement membrane C;Superfamily: collagen alpha 1(IV) chain
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A; Residues: 1486-1574, 'I', 1576-1712 < MYE>
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A;Reference number: S01450; MUID:88085168; PMID:3692475
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A;Residues: 490-492,'X',494-501,'P',503-507;952-957,'X',959-966,'X',968;984-986,'X'
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A; Residues: 1040, 'L',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: 1040,'L',1042-1398,'V',1400-1418,'M',1420-1635,'V',1637-1712 <KIL:
Cross-references: EMBL:M24766; NID:g537328; PIDN:AAA52043.1; PID:g537329;Siebold, B.; Deutzmann, R.; Kuehn, K.
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A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; I. A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11018950
A;Accession: A84326
                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P72684; EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA166 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: Synechocystis hypothetical protein slr0740
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A; Residues: 1-131 < KAN>
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A; Residues: 1-325 <STO>
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Pred. No. 4
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Pred. No. 2e+02;
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.G.; Jablı
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A;Molecule type: DNA
A;Residues: 239-267 <ALL>
A;Cross-references: EMBL:X90711; NID:g992967; PIDN:CAA62242.1; PID:g992968
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Aug C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-267 <RES-
A;Cross-references: UNIPROT:Q45338; EMBL:U12020; NID:g687228; PIDN:AAA75361.1;
A;Cross-references: UNIPROT:Q45338; EMBL:U12020; NID:g687228; PIDN:AAA75361.1;
A;Cross-references: UNIPROT:Q45338; EMBL:U12020; NID:g687228; PIDN:AAA75361.1;
A;Cross-references: UNIPROT:Q45338; EMBL:U12020; NID:g687228; PIDN:AAA75361.1;
A;Cross-reference number: S70669; MUID:96419162; PMID:8821935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V. EMBO J. 13, 2935-2947, 1994
A;Title: Mossic genome structure of simian immunodeficiency virus from West African A;Reference number: 846335; MUID:94298785; PMID:8026477
A;Accession: $46354
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C;Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) C;Specias: Leishmania mexicana C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_ch C;Accession: B48445; S25142
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A. Title: Identification of a Bordetella pertussis regulatory
A.Reference number: 140327; MUID:95325323; PMID:7601846
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A;Experimental source: isolate SABD37; sabaeus monkey
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December
                                                                                         B48445
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I40327
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Best Local
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Best Local
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Pred. No.
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Pred. No.
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                                                                                                                                                                           R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, I A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUJD:21128732; PMID:11234002
A;Accession: C87021
                         A;Gene: ML0897
C;Superfamilia
                                                                                                                                                                                                                                                                                                                                                             serine-threonine protein kinase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence revision 20-Apr-2001 #text_change 0: C;Accession: C87021
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                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <STO>
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                                                                   C; Genetics:
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                                                                                         A;Cross-references: UNIPROT:069568; GB:AL450380; NID:g13092968; PIDN:CAC31278.1;
                       ;Superfamily: Mycobacterium tuberculosis probable serine/threonine-specific
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#text_change 09-Jul-2004

Thomson, N.R.; Wheeler, Fraser, A.; Hamlin, N.;

P.R.; H

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Skelton,

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Squares,

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protein

GSPDB

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hypothetical protein APE2086 - Aeropyrum pernix (strain ki)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q01558; EMBL:X65220; NID:g9552; PIDN:CAA46323.1; C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: B48445
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Hannaert, V.; Blaauw, M.; Kohl, L.; Allert, S.; Opperdoes, F.R.; Michels, Mol. Biochem. Parasitol. 55, 115-126, 1992
A;Title: Molecular analysis of the cytosolic and glycosomal glyceraldehyde-3A;Reference number: A48445; MUID:93063042; PMID:1435864
                                                                                                                                C; Superfamily:
                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-331 < KAW>
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R;Kawarabayasi, Y.;
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                                                                                                                                                  A;Gene: APE2086
                                                                                                                                                                                 A; Experimental source:
                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9YA52; DDBJ:AP000063; NID:g5105654; A;Experimental source: strain K1
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5; Conserva
                                                                Similarity 6; Conserv
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 GPVVREWFRRRA
                                                                                                                                  conserved
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                                                                   Conservative
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                                                                                                                                hypothetical protein MJ1157
                                                                                 53.4%;
 317
                                                                  Score 39; DB Pred. No. 57; 2; Mismatches
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Pred. No.
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RESULT 44
GNLJCA
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C83221
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A;Molecule type; DNA
A;Residues: 1-791 <HEI>
A;Cross-references: UNIPROT:Q9KU26; GB:AE004157; GB:AE003852; NID:g9655148; PIDN:AAF9386
A;Cross-references: Berogroup O1; Strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                           R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D., Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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Thehas 7; Conserve
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A;Residues: 1-600 <STO>
A;Crose-references: UNIFROT:09HYJ8;
A;Experimental source: strain PAO1
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A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83221
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004
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Pred. No. 1e+02;
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HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 2 (isolate CAM2/Gun N;Contains: endonuclease (EC 3.1.--); retropepsin (EC 3.4.23.16); RNA-directed DNA poly C;Species: human immunodeficiency virus type 2, HIV-2 A;Note: host Homo sapiens (man) (C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004 C;Accession: B38475; JQ0974 R;Tristem, M; Hill, F; Karpas, A. J. Gen. Virol. 72, 721-724, 1991 A;Tritle: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type A;Accession: B38475; MUID:91170959; PMID:2005437 A;Accession: B38475; MUID:91170959; PMID:2005437 A;Accession: B38475; MUID:91170959; PMID:2005437
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HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 2 (isolate GH-1) N;Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA pc C;Species: human immunodeficiency virus type 2, HIV-2 A;Note: host Homo sapiens (man) C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004 C;Accession: JS0328
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A;Residues: 1-1034 <TRI>
A;Cross-references: UNIPROT:P24107
A;Cross-readthrough of the terminator TGA may occur between codons ATT for 564-Ile and C;Comment: The cleavage sites of this polyprotein have not been determined.
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-1035 <HAS>
A;Cross-references: UNIPROT:P18042
A;Note: this sequence was submitted
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F; 85-183/Product: retro
F; 109/Active site: Asp
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A;Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant divergence A;Reference number: JS0327; MUID:90122350; PMID:2611042
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C; Superfamily:
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A;Start codon: ACA
                                                                                                                                                                                                          ;Superfamily: pol polyprotein
;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; nucleo!
;85-183/Product: retropepsin #status predicted <RTP>
;109/Active site: Asp (shared with dimeric partner) #status predicted
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05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                      01-MAY-1992 (Rel. 22, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
HTH-type transcriptional regulator cbbR (RuBisCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                        "Identification and organization of carbon dioxide Xanthobacter flavus H4-14."; Mol. Gen. Genet. 225:320-330(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 302 AA;
                                                                                              MEDLINE=91172133;
Meijer W.G., Arnbe
Dijkhuizen L.;
                                                                                                                                   STRAIN=H4-14;
                                                                                                                                                                                           MEDLINE=94012468; PubMed=8407781; van den Bergh E., Dijkhuizen L., Meijer W.G.; "CbbR, a LyRer-type transcriptional activator, is reexpression of the autotrophic CO2 fixation enzymes
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Hyphomicrobiaceae; Xanthobacter.
                                                                                                                                                                                                                                                                                                                     Name=cbbR; Synonyms=cfxO;
Xanthobacter flavus.
                                                                                                                                                                                                                                                                                                                                             transcriptional regulator).
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                                                                                                                                               SEQUENCE OF
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                                                                                                                                                                       Bacteriol.
       . Gen. Genet. 225:320-330(1991).

FUNCTION: Transcriptional activator for the cbb operon (cbbis for RuBisCO and other Calvin cycle genes. Binds specifically two binding sites in the cbbr-cbbi intergenic region.

SIMILARITY: Contains 1 HTH lysr-type DNA-binding domain.
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                                                                                                          Arnberg A.C.,
                                                                                                                                                                      175:6097-6104(1993).
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Pred. No. 2
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Best Local S
                                                            "Complete genome sequence of the model actinomyce coelicolor A3(2).";
Nature 417:141-147(2002).

-!- SIMILARITY: Contains 1 HTH merr-type DNA-bind EMBL; AL393918; CAB5G383.1; -.
GO; GO:000562; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0003705; F:regulation of transcription, DNI
InterPro; IPR000551; P:regulation of transcription, DNI
InterPro; IPR000551; Putativ_DNA_bind.
Pfam; PF00376; Merrk; 1.
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                                                                                                                                                                                                                                                    SEQUENCE FROM 145;

STRAIN=A3(2) / M145;

MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.B., Sarown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

Saeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Seeger K., Saunders D., Woodward J.R., Barrell B.G., Parkhill J.,

Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
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Q9RKM5;
01-MAY-2000
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DNA_BIND
SEQUENCE
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01-MAY-2000 (TYEMBLTE1. 13, Last seq.
01-MAR-2004 (TYEMBLTE1. 26, Last anno
Putative MerR family transcriptional
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EMBL; X17252; -; NOT ANNOTATED_CDS.
PIR; A36925; A36925.
InterPro; IPR000847; HTH Lysr.
InterPro; IPR0005119; Lysr subst.
InterPro; IPR009518; Wing_hlx_DNA_bnd.
Descriptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomycineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORFNames=SCD17.06c;
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Activator; DNA-binding; Transcription regulation
DOMAIN 5 62 HTH lysR-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00126; HTH 1; 1.
Pfam; PF03466; LysR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
Complete proteome; DNA-binding.
                 SMART; SM00422; HTH_MERR; 1.
PROSITE; PS50937; HTH_MERR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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H-T-H motif ()
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                                                                                                          factor activity; LDA.

factor mation, DNA-dependent;
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(See http://www.isb-sib.ch/announce/
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Hypothetical protein (Fragment).
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Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
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EMBL; AF371960; AAL98838.:
SEQUENCE 941 AA; 10670:
                                                                                                                                                                                                                                         "Complete genome analysis of kidney necrosis iridovirus.";
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AA; 106703 MW;
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Best Local S
Matches 9
                                STRAIN=CO-92 / Biovar Orientalis;

MEDLINB=21470413; PubMed=11586360; DOI=10.1038/35097083;

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"Genome sequence of Yersinia pestis, the causative agent of plague."
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SIGNAL
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InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 2.
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       Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae;
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ane protein). y2985;

Enterobacteriales;

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Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Storegasta W.M., Georgescu A.M., Vergez L.M., Land M.L., Mot Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., V. Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Derbise A., Hauser L.J., Garcia E., "Insights into the genome evolution of Yersinia pestis t genome comparison with Yersinia pseudotuberculosis."; Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yersinia pseudotuberculosis IP 32953.
Bacteria; Proteobacteria; Gammaproteobacteria;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative drug/metabolite (DME family) efflux pump p
Score 47; DB 2
Pred. No. 8.2;
0; Mismatches
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M., Medigue C.,
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SEQUENCE FROM |
STRAIN=KIM5 /
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STRAIN=CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

MEDLINE=22206494; PubMed=12218036;

DOI=10.1128/GB.184.19.5479-5590.2002;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Peterson J.D., DeBoy R.T., Nolson W.C., Umayyam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Salzberg M.R., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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SEQUENCE
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7,
Name=galU; OrderedLocusNames=MTI022;
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DOI=10.1128/JB.184.16.4601-4611.2002;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Schwartz D.C., McDonough K.A., Nilles M.L., Matson J.S., B
                    TIGR; MT1022; -.
GO; GO:0016740; F:transferase activity; IE
GO; GO:0003983; F:UTP-glucose-1-phosphate
GO; GO:0009058; P:biosynthesis; IEA.
InterPro; IPR005835; NTP transferase.
Pfam; PF00483; NTP_transferase; 1.
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Nucleotidyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
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J. Bacteriol. 184:4601-4611(2002).
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                                                                                                                                                              teriol. 184:5479-5490(2002)
AE000516; AAK45269.1; -.
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Biovar Mediaevalis;
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Qin H., Wang J., Li S
J., Yang H., Wang J., I
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01-JUL-1997
01-JUL-1997
01-JUN-2003
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PIR; D70601; D70601.

Tuberculist; Rv0993; --
G0; G0:0016779; F:nucleotidyltransferase
G0; G0:0009058; P:biosynthesis; IEA.
G0; G0:0009058; N:D:Cransferase.
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Complete
SEQUENCE
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01-JUL-1997 (TYEMBLYE1. 04, Last sequence update)
01-JUN-1997 (TYEMBLYE1. 24, Last sequence update)
01-JUN-2003 (TYEMBLYE1. 24, Last annotation update)
01-JUN-2003 (TYEMBLYE1. PHOSPHATE URIDYLYLTRANSFERASE GALU (UDP-
PROBABLE UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHATE
URIDYLYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE)
                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE UTP--GLICOSE-1-PHOSPHATE URIDYLYLTRANSFERASE GALU
GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOS
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2.7.7.9).
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Name=galU;
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steriaceae; Mycobacterium
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Pred. No.
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AGARNIE-22705(107; PubMed-12788972; DOI=10.1073/pnas.1130426100;

AGARNIE-2705(107; Medina N., Mansoor H.,

AGARNIE B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

AGARNIE B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

The complete genome sequence of Mycobacterium bovis.";

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The complete genome sequence of Mycobacterium bovis.";

BMBL; BX248337; CAD93881.1;

CG; GO:0016779; F:mucleotidyltransferase activity; IEA.

BGG; GO:0016796; F:transferase activity; IEA.

BGG; GO:0016796; F:transferase activity; IEA.

BGG; GO:0016796; F:biosynthesis; IEA.

InterPro; IPR005835; NTP transferase.

BFam; PF00483; NTP transferase; Transferase.

Complete proteome; Nucleotidyltransferase; Transferase.
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Q89RH2;
Q1-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR 2004 (TrEMBLrel. 26,
     Complete
SEQUENCE
                                                    PROSITE;
                                                                                                                                                                                 EMBL; AP005945; BAC48065.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003824; F:Cate binding; IEA.
GO; GO:0003824; F:Cate binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0004668; P:protein amino acid phosphorylation;
InterPro; IPR00109; Kinase like.
InterPro; IPR001932; PP2C-like.
InterPro; IPR000719; Prot kinase.
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"Complete genomic sequence of nitrogen-fixing "Eradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
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Kaneko T., Nakamura Y., Sato S., Minamisawa
Sasamoto S., Watanabe A., Idesawa K., Iriguc
Kohara M., Matsumoto M., Shimpo S., Tsuruoka
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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SMART; SM00332; PP2Cc;
SMART; SM00331; PP2CS;
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STRAIN=MBIC3019;
MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston
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Sphingomonadaceae; Erythro
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PRINTS; PR00256; REACTNCENTRE.
TIGRFAMS; TIGR01157; PufL; 1.
PROSITE; PS00244; REACTION CENTER;
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Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Pre
Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
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GO:0045156; F:electron transporter,
GO:0006118; P:electron transport; I
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ABeja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
A Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
T' "Unsuspected diversity among marine aerobic anoxygenic phototrophs."

L Nature 415:630-633(2002).
R EMBL; AB027515; BAA78672.1; -.
R HSSP; P02954; 1YST.
R GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte...; GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte...; BR GO; GO:00051156; F:electron transporter, transferring electron...; BR GO; GO:00061156; F:electron transporter; LEA.

DR GO; GO:00061156; F:electron transporter; BEA.

R GO; GO:00061156; F:electron transporter; BEA.

DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.

R InterPro; IPR00587; Photo L.

R InterPro; IPR000484; Photo RC.

DR Pfam; PF00124; Photo RC; 1.

PFam; PF00124; Photo RC; 1.

PR PRINTS; PR00256; REACTION CENTER; 1.

DR PROSITE; PS00244; REACTION CENTER; 1.

SEQUENCE 278 AA; 30735 MW; OBE618844B3C54FB CRC64;
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HSSP; P02954; 1YST.

GO; GO:0030077; C:light-harvesting complex (se GO; GO:0030077; C:light-harvesting complex (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans) (rans)
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STRAIN=12822 / ATCC BAA-587;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

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Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

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Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

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Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

GCorporative and the first of the Genome Semiences of Rorderella pertussis.
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EMBL; BX640423; CAB3964.1; GO; GO:0016874; F:ligase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative phenylacetate-CoA ligase.
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=519;
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                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                      Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00501; AMP-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 PSLRDWLAAR 230
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8; Conserv
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421 AA; 45579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTLROWLAAR
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                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella.
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80.0%;
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Betaproteobacteria; Burkholder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB
Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
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                                                          Stevens K.,
       pertussis
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RESULT 18
GTS3_CAEEL
ID GTS3_C
AC 016116
DT 10-OCT
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Q885P2
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Best Local S
Matches 8
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Best Local
  GTS3 CAEEL (
016116; Q21357;
10-OCT-2003 (Re
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EMBL;
HSSP;
TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100; Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Witterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Martin G.B., Schmeider D.J., Tang X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, Dimethylsulfoxide reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00501; AMP-binding; 2.
Complete proteome; Ligase.
SEQUENCE 421 AA; 45558 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella parapertussis and Bordetella bronchiseptica.";
Nat. Genet. 35:32-40(2003).
EMBL; BX640437; CAB30725.1; -.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
Interpro; IRR000873; AMP-bind.
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR009010; Asp_decarb fold InterPro; IPR006657; Mol_dinuc_bind. Pfam; PF01568; Molydop_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider Bender C.L., White O., Fraser C.M., Collmer A., "The complete genome sequence of the Arabidopsis and tpseudomonas syringae pv. tomato DC3000.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=DC3000;
MEDLINE=22834015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas syringae pv. Proc. Natl. Acad. Sci. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=PSPTO1789;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0030151; F:molybdenum ion binding; IEA. GO:0016491; F:oxidoreductase activity; IEA. erPro; IPR009010; Asp_decarb_fold.
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PSPTO1789;
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756 AA;
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                                                                                                                                                                                                                            IEGPTLRQWLAAR 13
     (Rel. 42, Created)
                                                                                                                                                                                                                                                                             Conservative
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80.0%;
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61.5%;
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Last annotation updat
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Pred. No. 26;
1; Mismatches
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                                                                                                                                                                                                                                                                                                    Score 45;
Pred. No.
                                                      PRT;
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Best Local S
Matches 8
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GO; GO:0004364; F:glutathione tran GO; GO:0004364; F:glutathione tran InterPro; IPR010987; GST_Clike.

InterPro; IPR004046; GST_Cterm.

InterPro; IPR004045; GST_Nterm.

Pfam; PF00798; GST_N; 1.

Pfam; PF02798; GST_N; 1.

Transferase.
                     ECO57
ENTE ECO57
Q8XBV3;
Q8XBV3;
28-FEB-2003
28-FEB-2003
25-OCT-2004
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25-OCT-2004
Glutathione
Name=gst-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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Submitted
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REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. e
investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tawe W.N., "Paraquat m
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence v
28-FEB-2003 (Rel. 45, Last annotation content and component E (
[Includes: 2,3-dihydroxybenzoate-AMP]
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF010241; AAB65419.1; EMBL; Z68879; CAA93088.2; -. PIR; T37464; T37464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Son send an email to license@isb-sib.ch).
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Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
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ORFNames=K08F4.11;
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Enterobacteriaceae; Escherichia.

Bacteria; Proteobacteria; Gammaproteobacteria;

Escherichia coli 0157:H7.

Name=entE; OrderedLocusNames=z0736,

EC80633;

Enterobacteriales;

(Dihydroxybenzoic acid-activating enzyme); S-dihydroxybenzoyltransferase (EC 2.3.1.-)].

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
-!- FUNCTION: Activates the carboxylate group of 2,3-dihydroxy-benzoate (2,3-DHB), via ATP-dependent PPi exchange reactions, to the acyladenylate. Then, catalyzes the acylation of holo-entB with 2,3-DHB adenylate, preparing that molecule for amide bond formation with L-serine (By similarity).
-!- CATALYTIC ACTIVITY: ATP + 2,3-dihydroxybenzoate = diphosphate + (2,3-dihydroxybenzoyl)-adenylate.
-!- CATALYTIC ACTIVITY: (2,3-dihydroxybenzoyl)-adenylate + holo-entB = adenosine 5'-monophosphate + acyl-holo-entB.
-!- PATHWAY: Siderophore biosynthesis; enterobactin biosynthesis.
-!- PATHWAY: Siderophore biosynthesis; enterobactin biosynthesis.
-!- SIDBUNIT: Proteins entB, entD, entE, and entF form a multienzyme complex called enterobactin synthetase (By similarity).
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family. EntE subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Kurokawa T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
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[2]
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Acyltransferase; Complete proteome; Enterobactin biosynthesis;
Iron transport; Ligase; Multifunctional enzyme; Transferase;
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pfam; pF00501; AMP-binding; 1.
TIGRRAMs; TIGR0173; AA-adenyl-dom;
TIGRFAMs; TIGR01923; menE; 1.
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57.1%;
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                                                          Gehring A.M., Bradley K.A., Walsh C.T.;

"Enterobactin biosynthesis in Escherichia coli: isochorismate lyas (EntB) is a bifunctional enzyme that is phosphopantetheinylated by EntD and then acylated by EntE using ATP and 2,3-dihydroxybenzoate Biochemistry 36:8495-8503(1997).

-I-FUNCTION: Activates the carboxylate group of 2,3-dihydroxybenzoate (2,3-DHB), via ATP-dependent PPI exchange reactions, the acyladenylate. Then, catalyzes the acylation of holo-entB 2,3-DHB adenylate, preparing that molecule for amide bond formation with L-serine.

-I-CATALYTIC ACTIVITY: ATP + 2,3-dihydroxybenzoate = diphosphate
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Name=entE; OrderedLocusNames=b0594;
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SEQUENCE FROM N.A., Allen E., Araujo R., Aparicio A., Davis K., Duncan Chung E., Allen E., Araujo R., Kalman S., Komp C., Kurdi O., Lew H. Federspiel N., Hyman R., Kalman S., Schramm S., Davis R.W.;

Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;

Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of a cluster of Escherichia coli enterobactin biosynthesis genes: identification of entA and purification of its product 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase."; 1. Bacteriol. 171:791-798(1989).
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         (2,3-dihydroxybenzoyl)-adenylate. CATALYTIC ACTIVITY: (2,3-dihydrox
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EMBL; U82598; AAB40794.1; -.
EMBL; X15058; CAA33158.1; -.
EMBL; M24148; AAA16101.1; -.
EMBL; M36700; AAA18492.1; -.
PIR; H64792; SYECEB.
HSSP; P40871; IMD9.
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EcoGene; EG10263; entE.
EcoGene; EG10263; entE.
InterPro; IPR000873; AMP-bind.
Pfam; PP00501; AMP-binding; 1.
PFINTS; PR00154; AMPBINDING.
TIGRPAMs; TIGR01733; AA-adenyl-dom; 1.
TIGRPAMs; TIGR01733; BA-adenyl-dom; 1.
PROSITE; PS00455; AMP BINDING; 1.
ACYltransferase; Complete proteome; Enterobactin biosynthesis;
Iron transport; Ligase; Multifunctional enzyme; Transferase;
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                                                                                                                                                                           STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
Jin QO, Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., I
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Qu D.
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y.,
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01-JUN-2003 (TrEMBLrel. 24,
25-OCT-2004 (TrEMBLrel. 28,
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=301 / Serot
                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2,3-dihydroxybenzoate-AMP ligase.
Name=entB; OrderedLocusNames=S0514, SF0508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q83M10;
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  STRAIN=2457T;
                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shigella flexneri.
                                                                                                                               "Genome sequence
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PATHWAY: Siderophore biosynthesis; enterobactin biosynthesis.
SUBUNIT: Proteins entB, entD, entB, and entF form a multienzyncomplex called enterobactin synthetase.
SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family. EntE subfamily.
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536 1
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                                                                            of Shigella flexneri 2a: insights into pathogenicity on with genomes of Escherichia coli K12 and O157."; s. 30:4432-4441(2002).
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, Ding K., Chen S.,
B., Wen Y., Hou Y.,
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last samotation update)
Putative gag/pol polyprotein (Putative gag-pol polyprotein).
ORFNames=OSJNBb003BH12.4;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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DOI=10.1128/IAI 71.5.2775-2786.2003;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., De
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J.,
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., i
Schwartz D.C., Blattner F.R.;
                                 Buell C.R., Wing R.A., McCom
Submitted (MAY-2003) to the
EMBL; AC105932; AAN04966.1;
EMBL; AE017067; AAP52546.1;
Gramene; QBLMK9;
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Overton II L.I., Tsitrin T., Kim M.M., Bera J.J., Jin S. S
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbus
White O., Salzberg S.L., Fraser C.M.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016874; F:ligase activity; GO; GO:0008152; P:metabolism; IEA.
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GO; GO:0016874; F:1
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                                                                                                                                                                                                                                                                                                                                                        "In-depth view of structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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PROSITE; PS00455; AMP_BINDING;
Ligase; Complete proteome.
SEQUENCE 536 AA; 58851 MW;
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                  chromosome 10
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8; Conserv
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cture, activity, and evolution of
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T.V.,
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Polyprotein.
SEQUENCE 760
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Science 281:3'
-!- FUNCTION:
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28-FEB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N',
N'-adenosyl(rRNA) dimethyltransferase) (16S __RNA dimethylase) (High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R.J., Gwinn M.L., Hickey E.K., Clayron R.A., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J. Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M., Utterback T.R., McDonald L.A., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky Weidman J.F., Smith H.O., Venter J.C.; "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institumodified and this statement entities requires a license
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Name=ksgA; OrderedLocusNames=TP0337.
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                                                                                                                                                                                                                                       HAMAP; MF_00607; ; 1.
InterPro; IPR001737; RRNA A di
InterPro; IPR000051; SAM bind.
Pfam; PF00398; RrnaAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponema pallidum.
Bacteria; Spirochaetes;
                                                                                                                                 NART; SMO0650; rADc; 1.
TIGREAMS; TIGRO0755; KBGA; 1.
PROSITE; PSO1131; RRNA A DIMETH; FALSE NEG.
Antibiotic resistance; Complete proteome; M
                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001213; AAC65323.1; PIR; G71337; G71337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
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nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ence 281:375-388 (1998).

FUNCTION: Specifically dimethylates two adjacent adenosines FUNCTION: Specifically dimethylates two adjacent adenosines loop of a conserved hairpin near the 3'end of 16S rRNA in the particle. Its inactivation leads to kasugamycin resistance (similarity).

SIMILARITY: Belongs to the rRNA adenine N-6-methyltransferas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family. KsgA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                             processing; T:
ENCE 285 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    license agreement (See http://www.isb-sib.ch/announce/
                                                                                  32275
     58.9%;
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MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749; MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749; Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W. Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A., Clayton R.A., Meyer T., Tsapin A., Scott J., Benanan M.J., Durkin A.S. Brinkac L.M., Daugherry S.C., DeBoy R.T., Dodson R.J., Durkin A.S. Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M., Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
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Ludwig W., Gade D.,
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OrderedLocusNames=RB6375;
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01-MAR-2003
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InterPro; IPR003169; GYF.
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Natl. Acad. Sci. U.S.A. 100:8298-8303(2003)
BX294144; CAD74759.1; -.
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297 AA; 31805 MW;
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Beck A., Borzym K.,
R., Reinhardt R.;
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n K., Heitmann
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01-MAR-2002 (TrEMBLrel. 20, L
01-JUN-2003 (TrEMBLrel. 24, L
Hypothetical protein PAE0634.
OrderedLocusNames=PAE0634;
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Nat. Biotechnol. 20:11
                                STRAIN=MA-4680; MEDLINB=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
                                                                                                                                                                                                                                                                                    Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteria; Actinobacteria; Actinobacteria;
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Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002)
EMBL; AE009776; AAL62908.1; -.
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MEDLINE=21664397;
Fitz-Gibbon S.T.,
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Archaea; Crenarchaeota; Thermoprotei;
Thermoproteaceae; Pyrobaculum.
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SO0675; -.
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PubMed=11792869;
Ladner H., Kim U.
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C5799F975B972941 CRC64;
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.-J., Stetter K.O., Simon M.I.,
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Pfam; PF01436; NHL; 5.
PRINTS; PR01415; ANKYRIN.
PROSITE; PS50005; TPR; 1.
PROSITE; PS50093; TPR_REGION; 1.
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083436;
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SEQUENCE
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Science 281:375-388(1998).
Science 281:375-388(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99332770; PubMed=9665876; DOI=10.1126/science.281.5375.3' Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Bodson R.J., Gwinn M.L., Hickey B.K., Clayton R.A., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson Schalak H.G., Richardson D.L., Howell J.K., Chidambaram M., Utterback T.R., McDonald L.A., Artiach P., Bowman C., Cotton M.D. Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusl
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PIR; B71325; B71325.
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Weidman J.F., Smith H.O., Venter J.C.;
"Complete genome sequence of Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=160;
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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EMBL; AP005023; BAC68457.1;
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STRAIN=MA-4680
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STRAIN-BRISTOL N2;
JONES K., MUTTAY J., Graves
"The sequence of C. elegans
"The sequence of C. elegans
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GO; GO:00
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                   WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; ACOG6712; AAK39324.1; -.
WormBase; WBGene00022471; Y119C1B.5.
WormPep; Y119C1B.5; CE27234.
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"Genome sequence of the nematode C. elegans: a pl
investigating biology, The C. elegans Sequencing
Science 282:2012-2018(1998).
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MEDLINE=99069613; 1
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GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
InterPro; IPR001841; Znf ring.
Pfam; PP00097; zf-C3HC4; 1.
SMART; SM00104; RING; 1.
PROSITE; PS00089; ZF_RING; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 754 AA; 85323 MW; 41BAA9297FA3BF05 CRC64;
                                                                                                                                                                                                                                                                Q8N9N4
Q8N9N4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJINE_1681879; PubMed=11823852; DOI=10.1038/415497a; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S. Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Arlat M., Bhilsane N., Claudel-Renard C., Cunnac S., Demang Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum Nature 415:497-502(2002).
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01-MAR-2002 (TrEMBLrel. 20, Last sequenc
01-MAR-2002 (TrEMBLrel. 20, Last annotat
Hypothetical protein RSc1059.
Name=RS04149; OrderedLocusNames=RSc1059;
                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                      Hypothetical protein FLJ36840. Homo sapiens (Human).
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Burkholderiaceae; Ralstonia.
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SEQUENCE FROM N.A.
PubMed=14702039; DOI=10.1038/ng1285;
Ota T., Suzuki Y., Nishikawa T., Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                      NCBI_TaxID=9606;
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91 AA;
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X MEDLINE-2161879; PubMed=11823852; DOI=10.1038/415497a;
A Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
A Weissenbach J., Boucher C.A.;
Tegenome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
C. -!- SIMILARITY: Contains 1 HTH luxR-type DNA-binding domain.
BEMBL; AL646085; CAD18730.1; -.
BR GO; GO:0005700; F:transcription factor activity; IEA.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 25, Last annotation update)
PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
Name=RS02135; OrderedLocusNames=RSp1579;
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Sekine M., Obayashi M., Nishi T., Shibahara T., Tana
Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura
Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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AK094159; BAC04297.1;
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, Shiratori A.,
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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PFAM; PF00078; RVT 1; 1.
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PROSITE; PS50175; ASP_PROT_RETROV; 1.
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MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;

Pedulla M.L., Pord M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,

Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,

Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,

Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,

Hatfull G.F.;

"Origins of highly mosaic mycobacteriophage genomes.";

Cell 113:171-182(2003).

EMBL; AY129336; AAN07992.1;

EMBL; AY129336; AAN07992.1;

SEQUENCE 325 AA; 35999 MW; 04265796D0B4FC1D CRC64;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobia
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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67;
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                                                                                                                                                                                                                                          Length 326;
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RESULT
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Matches 8
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QSSIB9, QSASU2;

QSSIB9, QSASU2;

01-MAY-2000 (TrEMBLrel. 13, Created)

01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00917; MATH; 1.
SMART; SM00025; BTB; 1.
SMART; SM00061; MATH; 1.
PROSITE; PS50097; BTB; 1.
PROSITE; PS50144; MATH; 1.
SEQUENCE 375 AA; 41043 M
                     Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Barnstead M.E., Mason T.M., Bowman C.L., Ronning (Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Fraser C.M., Venter J.C.; Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12447439; DOI=10.1038/nature01183; Feng C., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J., Feng O., Zhang Y., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y., Li Y., Hu X., Jia P., Zhang Y., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D., Li X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Li X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J., Mu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H., Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y., Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W. Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y., Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
0SJNBa0053KL9.27 protein (OSJNBb0060E08.2 protein).
Name=OSJNBa0053KL9.27; Synonyms=OSJNBb0060E08.2;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poa
Ehrhartoideae; Oryzeae; Oryza.
NCBI TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

PubMed=12447439; DOI=10.1038/nature01183;
PubMed=12447439; PubMed=10.1038/nature01183;
                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005515; F:protein binding;
InterPro; IPR002210; BTB POZ.
InterPro; IPR002083; MATH.
InterPro; IPR008974; Traf_like.
                                                                                                                                                 NCBI_TaxID=3702;
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Pfam; PF00651;
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SEQUENCE FROM N.A.
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8; Conserv
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61.5%;
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                                  EMBL/GenBank/DDBJ databases
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Pred. No.
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C.M., Benito M.-I.,
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                                                                  Nierman
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Matches 7
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EMBL; AF361831; AAX32943.1; --
EMBL; AB125257; BAD17858.1; --
EMBL; AB125257; BAD17858.1; --
EMBL; B84853; E84853.
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01-OCT-2000
01-OCT-2000
01-OCT-2002
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                                                                                                                                                                                       STRAIN-Friedlin;
STRAIN-Friedlin;
STRAIN-Friedlin;
STRAIN-Friedlin;
Myler P.J., Sisk E., Cawthra J., Handley F., Vogt C., Romyler P.J., Sisk E., Cawthra J., Handley F., Vogt C., Romyler P.J., Sisk E., Squyen D., Munden H., Stuart K.;
McDonagh P., Ivens A., Nguyen D., Munden H., Stuart K.;
McDonagh P., Ivens A., Nguyen D., Munden H., Stuart K.;
Submitted (MAY-2000) to the EMEL/GenBank/DDBJ databases
Submitted (MAY-2000) to the EMEL, AC022473; AAF69566 1; -
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                                                                                                                                                                                                                                                                                                                                                                            Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=L354.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L354.2
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                 Similarity
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                                               IEGPTLRQWLAARA
  VEAPLLTOWMTAAA
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450 AA; 50566 MW; 44DBE7B4AB689B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                   57.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                             Kinetoplastida;
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22,
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
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                                                                                             Score 42; DB
Pred. No. 1.2e
2; Mismatches
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Pred. No.
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                                                                                                                                          Length 586;
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               InterPro; IPR010659; RVT_connect.
InterPro; IPR010661; RVT_thumb.
Pfam; pF00552; Integrase; 1.
Pfam; pF00072; Integrase Zn; 1.
Pfam; pF00075; RnaseH; 1.
Pfam; pF00075; RVp; 1.
Pfam; pF00077; RVp; 1.
Pfam; pF00077; RVp; 1.
Pfam; pF00078; RVT; 1.
Pfam; pF00078; RVT; 1.
Pfam; pF00615; RVT_connect; 1.
Pfam; pF06817; RVT_thumb; 1.
PROSITE; pS00141; ASP_PROTEASE; 1.
PROSITE; pS00179; RNASE H; 1.
PROSITE; pS50878; RT_POL; 1.
PROSITE; pS50878; RT_POL; 1.
PROSITE; pS50878; RT_POL; 1.
PROSITE; pS50878; RT_POL; 1.
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zn_N.
InterPro; IPR003908; Peptidase_A2.
InterPro; IPR001995; Peptidase_A2.
InterPro; IPR001969; Pept_Aspartic.
InterPro; IPR001969; Pept_Asp_AS.
InterPro; IPR001566; RNaseH.
InterPro; IPR001584; RVIse.
InterPro; IPR001669; RVI_connect.
InterPro; IPR010661; RVI_thumb.
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SIVS4
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01-OCT-1989 (Rel. 12, Last sequence update)
05-OCT-2004 (Rel. 45, Last annotation update)
Pol polyprotein [Contains: Protease (Retropepsin)
Reverse transcriptase/fibonuclease H (EC 2.7.7.49)
Integrase (IN)].
Pfam; PFO
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
AIDS; Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a cbetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 339:389-392(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simian immunodeficiency virus
Viruses; Retroid viruses; Retr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X14307; -;
HSSP; P04584; 1M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                + + +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89262053; PubMed=2786147; DOI=10.1038/339389a0;
Hirsch V.M., Olmstead R.A., Murphey-Corb M., Purcell R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=POL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV; X14307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: During replicative cycle of retroviruses, transcribed viral DNA is integrated into the host of the viral integrase enzyme. RNase H activity is assuthe reverse transcriptase.

CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the retroviruses Pol I SIMILARITY: Contains 1 integrase-type zinc fi SIMILARITY: Contains 1 peptidase A2 domain. SIMILARITY: Contains 1 reverse transcriptase SIMILARITY: Contains 1 RNase H domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIVS4
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CATALYTIC ACTIVITY: N deoxynucleoside triphosphate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determined.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {DNA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (Some an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A02.002;
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  DNA integration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  irus (F236/smH4 isolate) (sooty mangabey)
Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SIVsm)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          closely
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     DNA recombination;
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(EC 3.1.26.4)
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Best Local S
Matches 7
                                                                                                                                                                                                              R HSSP; P04584; IMUZ.

R MEROPS; A02.002; -.

R MEROPS; A02.002; -.

R GO; GO:0004190; F:asspartic-type endopeptidase activity; IEA.

GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0008907; F:integrase activity; IEA.

R GO; GO:0008233; F:relbonuclease H activity; IEA.

R GO; GO:0008233; F:ribonuclease H activity; IEA.

R GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0016740; F:ranaferase activity; IEA.

R GO; GO:0006270; F:zinc ion binding; IEA.

R GO; GO:0006370; F:DNA integration; IEA.

R GO; GO:000630; F:DNA integration; IEA.

R GO; GO:000630; F:RNA-dependent DNA replication; IEA.

R GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I- SIMILARITY: Belongs to peptidase EMBL; U72748; AAC56559.1; -. PIR; T11560; T11560.
HSSP; P04584.
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SEQUENCE
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DOMAIN
DOMAIN
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STRAIN-SIVENE543;
MEDLINE-97151152; PubMed=8995688;
MAGGET-Johnson D., Campbell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endonuclease;
Nuclease; Poly
          InterPro;
InterPro;
InterPro;
                                                                                                                                                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirsch V., Adger-Johnson D., Campbell B., Goldstein S., Brown C., Elkins W.R., Monteficri D.C.; Rethough the Molecularly cloned, pathogenic, neutralization-resistant simian immunodeficiency virus, SIVsmE543-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P89154;
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hirsch V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SIVsmE543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency virus, SIVs
J. Virol. 71:1608-1620(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                        InterPro;
                                                                                            InterPro;
                                                                                                                  InterPro;
                                                                                                                                   InterPro;
                                                                                                                                                                                                   InterPro;
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                                                                      IPR009007;
IPR001969;
IPR002156;
IPR001584;
                                                                                                                                                         IPR001037;
IPR003308;
IPR001995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poly
                                IPR000477;
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401
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RVTse.
; RVT_connect.
; RVT_thumb
                                                                                                                               Integrase_C.
Integrase_Zn_N.
Peptidase_A2.
Pept_Aspartic.
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Last annotation update)
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MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases.
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RNase H.
Integrase-type.
By similarity.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,</u>
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Best Local S
Matches 7
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HSSP; P04584; 1MUZ.
GO; GO:0004190; F:as
GO; GO:00008273; F:ps
GO; GO:0008273; F:ps
GO; GO:0003723; F:rs
GO; GO:0003723; F:rs
GO; GO:0003724; F:rs
GO; GO:0016740; F:rs
GO; GO:0016740; F:rs
GO; GO:0006510; P:ps
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Pfam; PF00022; J
Pfam; PF00075; J
Pfam; PF00077; J
Pfam; PF00078; J
Pfam; PF00078; J
Pfam; PF00078; J
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01-JUN-2003
01-JUN-2003
                                                                                                                                                 InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Unique pattern of convergent envelope evolution immunodeficiency virus-infected rapid progressor with CD4-independent usage of CCRS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22628501; PubMed=12743298;
DOI=10.1128/JVI.77.11.6405-6418.2003;
Dehghani H., Puffer B.A., Doms R.W., Hirsch V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00141; ĀSP_PROTEASB; 1.
PROSITE; PS00175; ASP_PROT_REASB; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
Aspartyl protease; Hydrolase; Polyprotein; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=po1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0004190; F:aspartic-type endopeptidase ac GO; GO:0003677; F:NNA binding; IEA.
GO; GO:0008907; F:integrase activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008233; F:ribonuclease H activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA-directed DNA polymerase act GO:0003740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001877, F:DNA integration; IEA.
GO; GO:0016310; P:DNA recombination; IEA.
GO; GO:0006310; P:DNA recombination; IEA.
GO; GO:0006310; P:DNA recombination; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Virol
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    -!- SIMILARITY: Belongs to peptidase

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                                                                            InterPro;
                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 77:6405-6418(2003).
                                    | IPR009007;
| IPR001969;
| IPR002156;
| IPR001584;
| IPR000477;
| IPR010659;
| IPR010661;
                                                                                                                                                                                                                                                                                                           ; IPR001037;
; IPR003308;
; IPR001995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGPTLRQW 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1019 AA;
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(TrEMBLrel.
(TrEMBLrel.
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; RVT_1; 1.
; RVT_connect; 1.
; RVT_thumb; 1.
                                                                                                                                                                                                                                                          ); P:RNA-dependent DNA re
1)01037; Integrase_C.
103308; Integrase_Zn_N.
101995; Peptidase_A2.
1019007; Pept_Aspartic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RnaseH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P:proteolysis and peptidolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA067309.1;
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87.5%;
                                                                                                                                                                                     rept_Asp_AS.
RNaseH.
                                                                                                                                                                 Rve.
                                                                                                                     RVTse.
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Sug_transporter.
                                        RVT_connect.
RVT_thumb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24,
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Last annotation update)
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Last seq
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            replication;
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PROSITE; PS00141; ASP_PROT RETROV; 1.
PROSITE; PS00217; ASP_PROT RETROV; 1.
PROSITE; PS00217; SUGAR_TEARSPORT_2; UNK
ASPARTY1 protease; Hydrolase; Protease;
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01-JUN-2003
01-MAR-2004
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-I SINILARITY: Belongs to peptidase family A2. EMBL; AV221514; AAO67307.1; -...
HSSP, P04584; 1MU2.
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0008907; F:integrase activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008233; F:ribonuclease H activity; IEA.
GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:000370; F:transferase activity; IEA.
GO; GO:0006740; F:transferase activity; IEA.
GO; GO:0006740; F:transferase activity; IEA.
GO; GO:0006740; F:DNA integration; IEA.
GO; GO:0006501; F:DNA recombination; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0006508; F:RNA-dependent DNA replication; IEA.
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MEDLINE=22628501; PubMed=12743298;
DOI=10.1128/JVI.77.11.6405-6418.2003;
                     InterPro;
InterPro;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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PF00665; rve;
PF00077; RVP;
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PF06815; RVT_connect;
PF06817; RVT_thumb; 1
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7; Conserv
            J IPR001037; Integrase_C.

J IPR003308; Integrase_Zn N.

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J IPR001969; Pept_Aspartic.

J IPR001969; Pept_Aspartic.

J IPR00156; RNaseH.

J IPR001584; Rve.

J IPR001584; Rve.

J IPR000659; RVT_connect.

J IPR010661; RVT_thumb.

J IPR01661; RVT_thumb.

J IPR01661; RVT_thumb.
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Nature 417:459-463(2002).

Nature 417:459-463(2002).

RO, GO:0008433, F.transaminase activity; IEA.
GO, GO:0016740; F.transferase activity; IEA.
GO, GO:0009058; P.biosynthesis; IEA.
RO, GO:0009058; P.biosynthesis; IEA.
Query Match
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Matches
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Pfam; PF000665; rve; 1.
Pfam; PF00077; RVP; 1.
Pfam; PF00078; RVT 1; 1.
Pfam; PF06815; RVT_connect; 1
Pfam; PF06817; RVT_thumb; 1.
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Q8P9L5;
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01-OCT-2003 (TrEMBLrel. 25, Last anno
Valine-pyruvate aminotransferase.
Name=avtA; OrderedLocusNames=XCC1838;
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PROSITE; PS00175; ASP PROT RETROV; 1.
PROSITE; PS00217; SUGAR TRANSPORT 2; UNKNOWN
ASPARTYl protease; Hydrolase; Protease; RNA-d
                                                                                                                                 InterPro; IPR004839; Aminotrans_I/II.
Pfam; PF00155; Aminotran_1_2; 1.
Aminotransferase; Complete proteome;
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STRAIN=ACCC 33913 / NCDPB 528;

MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                           SEQUENCE
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7; Conserv
  Similarity
9; Conserv
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     Conservative
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                                                                                                           AA,
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87.5%;
                            56.8%;
56.2%;
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                                                                                                              e proteome; Pyruvate; '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB Pred. No. 2.1e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
     2
                            Score 41.5;
Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation
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                               1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNOWN 1.
RNA-directed
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Teixeira E.C., Tezza R.I.D., M., white F.F.,
                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
     <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1019
                                                                                                                 Transferase CRC64;
                                                        Length 410;
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           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA polymerase;
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GPT-----LRQWLAAR

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GPTEGYLPLREWVAAR

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Q98AJ1
ID Q98AJ
AC Q98AJ
AC Q98AJ
AC Q98AJ
AC TION-OC
DT 01-OC
DT 01-OC
DT 01-OC
DT O1-OC
DE Trans
GN Order
CO Rhize
OC Bacte
OC Bacte
OC Bacte
OC Bacte
IN NCB1
RN [1]
RN [1]
RR SEQUE
RC STRAI
RX MEDLIJ
RA Kanek
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Q8PLE2
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RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 417:459-463(2002).

EMBL; AED11819; AAM36720.1; -.

EQO; GO:00008483; F:transaminase activity; IEA.

GO; GO:0009056; P:biosynthesis; IEA.

InterPro; IPR004839; Aminotrans I/II.

Pfam; PF00155; Aminotran_1_2; 1.

Complete proteome.

SEQUENCE 427 AA; 45926 MW; BBDC205BDA06E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSPLE2;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
valine-pyruvate aminotransferase.
Valine-pyruvate aminotransferase.
Name=avtA; OrderedLocusNames=XAC188;
                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8PLE2
                                                                         SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=381;
                                                                                                                                                            Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                         OrderedLocusNames=msr5979;
                                                                                                                                                                                                                                 Transposase.
                                                                                                                                                                                                                                                                                                                        Q98AJ1;
                                                                                                                                                                                                                                                                                                                                                Q98AJ1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas axonopodis (pv. citri).
                                                                                                                                         Phyllobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPT-----LRQWLAAR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                         Mesorhizobium
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                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.5; DB 2; Length 427; Pred. No. 1.1e+02; 2; Mismatches 0; Indels
    S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BBDC205BDA06E56E CRC64;
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    Kato T.,
         Sasamoto
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                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                 Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoo M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium"
                                                                                                       Complete proteome. SEQUENCE 75 AA;
                                                                                                                                          Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                EMBL:
                                                                                                                              AP003008; BAB52338.1;
ω
                                                  7; Conserv
                         N
OGKACREWLAAR 14
                         EGPTLRQWLAAR 13
                                                   Conservative
                                                                                                       8363 MW;
                                                               56.2%;
58.3%;
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                                                   <u>ب</u>
                                                               Score 41; DB
Pred. No. 22;
                                                                                                       B76547C20DA52E4D CRC64;
                                                    Mismatches
                                                                             DB 2;
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T
                                                                           Length 75;
                                                    Indels
                                                    0,
                                                    Gaps
                                                    0,
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Search completed: September 1, 2005, 16:21:19
Job time: 55.0719 secs